

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

AM

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization  
International Bureau(43) International Publication Date  
19 July 2001 (19.07.2001)

PCT

(10) International Publication Number  
**WO 01/51633 A3**(51) International Patent Classification<sup>7</sup>: C12N 15/12,  
15/11, 1/21, 5/10, C07K 14/47, 16/18, 19/00, A61K 38/17,  
48/00, G01N 33/68, C12Q 1/68, C12N 5/08

(21) International Application Number: PCT/US01/01574

(22) International Filing Date: 16 January 2001 (16.01.2001)

(25) Filing Language: English

(26) Publication Language: English

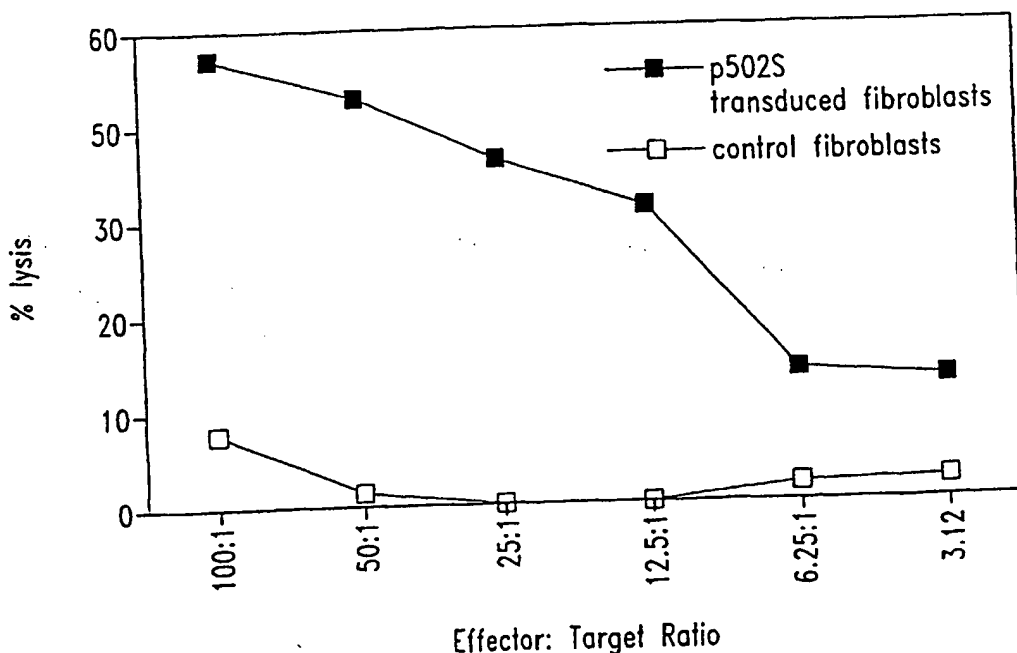
(30) Priority Data:  
09/483,672 14 January 2000 (14.01.2000) US(71) Applicant (for all designated States except US): CORIXA  
CORPORATION [US/US]: 1124 Columbia Street, Suite  
200, Seattle, WA 98104 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): XU, Jiangchun  
[US/US]: 15805 S.E. 43rd Place, Bellevue, WA 98006  
(US). DILLON, Davin, C. [US/US]: 18112 N.W. Mon-  
treux Drive, Issaquah, WA 98027 (US). MITCHAM,Jennifer, L. [US/US]: 16677 N.E. 88th Street, Redmond,  
WA 98052 (US). HARLOCKER, Susan, L. [US/US]:  
7522 13th Avenue W., Seattle, WA 98117 (US). JIANG,  
Yuqiu [CN/US]: 5001 South 232nd Street, Kent, WA  
98032 (US). REED, Steven, G. [US/US]: 2843 122nd  
Place N.E., Bellevue, WA 98005 (US). KALOS, Michael,  
D. [US/US]: 8116 Dayton Ave. N., Seattle, WA 98103  
(US). FANGER, Gary, Richard [US/US]: 15906 29th  
Drive S.E., Mill Creek, WA 98012 (US). DAY, Craig,  
H. [US/US]: 11501 Stone Ave. N., C122, Seattle, WA  
98133 (US). RETTER, Marc, W. [US/US]: 33402 N.E.  
43rd Place, Carnation, WA 98104 (US). STOLK, John,  
A. [US/US]: 7436 Northeast 144th Place, Bothell, WA  
98011 (US). SKEIKY, Yasir, A.W. [LB/US]: 15106 S.E.  
47th Place, Bellevue, WA 98006 (US). WANG, Aijun  
[CN/US]: 3106 213th Place S.E., Issaquah, WA 98029  
(US). MEAGHER, Madeleine, Joy [US/US]: 507 N.E.  
71st, #1, Seattle, WA 98115 (US).(74) Agents: POTTER, Jane, E.R.: Seed Intellectual Property  
Law Group PLLC, Suite 6300, 701 Fifth Avenue, Seattle,  
WA 98104-7092 et al. (US).

[Continued on next page]

(54) Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER



(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, particularly prostate cancer, are disclosed. Illustrative compositions comprise one or more prostate-specific polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly prostate cancer.

WO 01/51633 A3



(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

IT, LU, MC, NL, PT, SE, TR). OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

**Published:**

— with international search report

(88) Date of publication of the international search report:

20 June 2002

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE,

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

# INTERNATIONAL SEARCH REPORT

Inter:      nal Application No

PCT/US 01/01574

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7    C12N15/12    C12N15/11    C12N1/21    C12N5/10    C07K14/47  
           C07K16/18    C07K19/00    A61K38/17    A61K48/00    G01N33/68  
           C12Q1/68    C12N5/08

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7    C12N    A61K    C07K    G01N    C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, EMBL, BIOSIS, WPI Data, SEQUENCE SEARCH

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
------------	--	-----------------------

X Y	WO 98 37093 A (CORIXA CORP) 27 August 1998 (1998-08-27) the whole document ---	1-5,7,9, 12-14 6,10,11, 15-18
X Y	WO 98 37418 A (CORIXA CORP) 27 August 1998 (1998-08-27) the whole document ---	1-6,9, 15-17 6,15-17
A	WO 97 33909 A (CORIXA CORP) 18 September 1997 (1997-09-18) --- -/--	

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

### \* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance  
 "E" earlier document but published on or after the international filing date  
 "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)  
 "O" document referring to an oral disclosure, use, exhibition or other means  
 "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention  
 "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone  
 "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.  
 "&" document member of the same patent family

Date of the actual completion of the international search

4 September 2001

Date of mailing of the international search report

10.01.02

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2  
 NL - 2280 HV Rijswijk  
 Tel. (+31-70) 340-2040, Tx. 31 651 epo nl.  
 Fax: (+31-70) 340-3016

Authorized officer

VAN DER SCHAAL C.A.



## INTERNATIONAL SEARCH REPORT

Intern: al Application No

PCT/US 01/01574

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	<p>SJOGREN H O: "Therapeutic immunization against cancer antigens using genetically engineered cells"</p> <p>IMMUNOTECHNOLOGY, ELSEVIER SCIENCE PUBLISHERS BV, NL,</p> <p>vol. 3, no. 3,</p> <p>1 October 1997 (1997-10-01), pages 161-172, XP004097000</p> <p>ISSN: 1380-2933</p> <p>the whole document</p> <p>---</p>	10,11,18
P,X	<p>WO 00 04149 A (CORIXA CORP)</p> <p>27 January 2000 (2000-01-27)</p> <p>the whole document</p> <p>---</p>	1-7,9-18
E	<p>WO 01 25272 A (CORIXA CORP ; REED STEVEN G (US); XU JIANGCHUN (US); CHEEVER MARTIN)</p> <p>12 April 2001 (2001-04-12)</p> <p>SEQ ID NO 1</p> <p>claims</p> <p>---</p>	1-7,9-18
E	<p>WO 01 34802 A (HARLOCKER SUSAN L ; CORIXA CORP (US); DAY CRAIG H (US); JIANG YUQIU)</p> <p>17 May 2001 (2001-05-17)</p> <p>SEQ ID NO 1</p> <p>claims</p> <p>-----</p>	1-7,9-18

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US 01/01574

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:  
  
Although claims 10 13 14 and 18 are (partially) directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:  
  
Claims 1-7, 9-18 partially.
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: Invention 1: Claims 1-7 9-18 partially

A polypeptide comprising at least an immunogenic portion of a prostate tumor protein encoded by SEQ ID 1 (according to the Description of the Sequence Identifiers), fragments and variants thereof, fusion proteins comprising it, polynucleotides or oligonucleotides derived therefrom, antibodies binding to the polypeptide, their use in the treatment of cancer, in methods for diagnosing cancer, or for expanding and/or stimulating T-cells.

2. Claims: Inventions 2-527: Claims 1-18 partially and as far as applicable

As for subject 1 but concerning respectively SEQ IDs  
2-111,115-171,173-175,177,179-305,307-315,326,328,  
330,332-335,340-375,381,382,384-476,524,526,530,531,533,535  
536,552,569-572,587,591,593-606,618-626,630,631,634,636,639-6  
55,674,680,681,711,713,716,720-722,735,737-739,751,753,764,76  
5,773-776 and 786-788

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9837093	A	27-08-1998	US 6261562 B1	17-07-2001
			AU 731840 B2	05-04-2001
			AU 6181898 A	09-09-1998
			BR 9808881 A	11-09-2001
			CN 1252837 T	10-05-2000
			EP 1005546 A2	07-06-2000
			HU 0002095 A2	28-10-2000
			NO 994069 A	22-10-1999
			PL 335348 A1	25-04-2000
			TR 9902053 T2	21-04-2000
			US 6262245 B1	17-07-2001
			WO 9837093 A2	27-08-1998
			US 6329505 B1	11-12-2001
			ZA 9801585 A	04-09-1998
-----				
WO 9837418	A	27-08-1998	AU 6536898 A	09-09-1998
			BR 9807734 A	31-10-2000
			EP 0972201 A2	19-01-2000
			JP 2001513886 T	04-09-2001
			WO 9837418 A2	27-08-1998
			ZA 9801536 A	08-01-1999
-----				
WO 9733909	A	18-09-1997	AU 728186 B2	04-01-2001
			AU 2329597 A	01-10-1997
			BR 9708082 A	27-07-1999
			CA 2249742 A1	18-09-1997
			EP 0914335 A2	12-05-1999
			NO 984229 A	13-11-1998
			WO 9733909 A2	18-09-1997
			US 6034218 A	07-03-2000
-----				
WO 0004149	A	27-01-2000	AU 5314899 A	07-02-2000
			CN 1315998 T	03-10-2001
			EP 1097208 A2	09-05-2001
			NO 20010196 A	12-03-2001
			WO 0004149 A2	27-01-2000
			US 6329505 B1	11-12-2001
-----				
WO 0125272	A	12-04-2001	AU 7994200 A	10-05-2001
			WO 0125272 A2	12-04-2001
-----				
WO 0134802	A	17-05-2001	US 6329505 B1	11-12-2001
			AU 1656501 A	06-06-2001
			AU 6158700 A	30-01-2001
			WO 0104143 A2	18-01-2001
			WO 0134802 A2	17-05-2001
-----				

(19) World Intellectual Property Organization  
International Bureau(43) International Publication Date  
19 July 2001 (19.07.2001)

PCT

(10) International Publication Number  
**WO 01/51633 A2**(51) International Patent Classification<sup>7</sup>: C12N 15/12,  
C07K 14/47, C12N 5/10, 5/08, 1/21, C07K 16/18, G01N  
33/68, C07K 19/00, C12N 15/11, A61K 38/17, C12Q 1/68

(21) International Application Number: PCT/US01/01574

(22) International Filing Date: 16 January 2001 (16.01.2001)

(25) Filing Language: English

(26) Publication Language: English

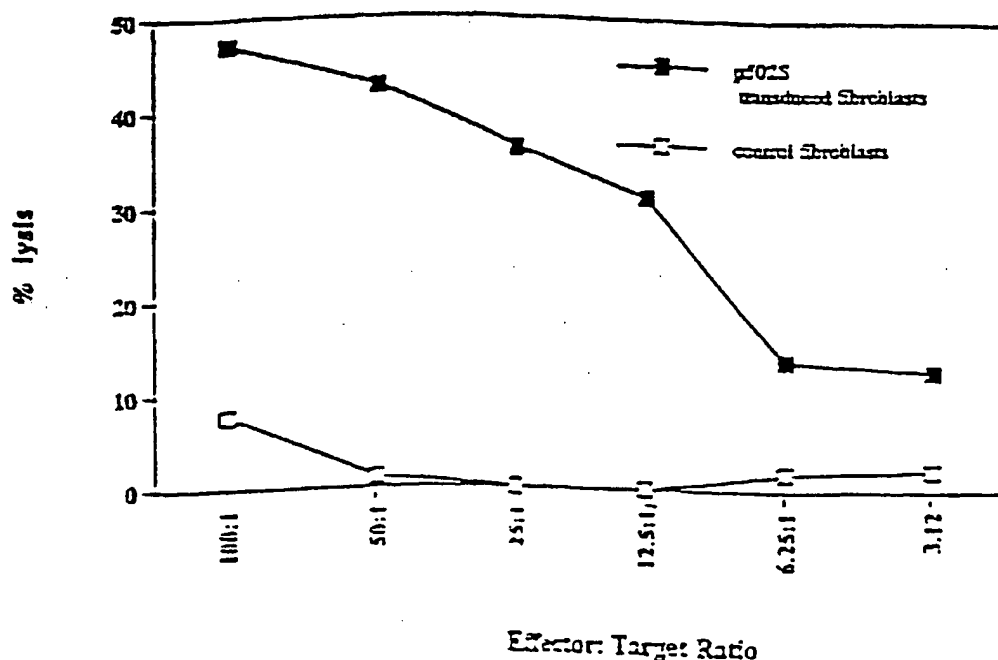
(30) Priority Data:  
09/483,672 14 January 2000 (14.01.2000) US(71) Applicant (for all designated States except US): CORIXA  
CORPORATION [US/US]; 1124 Columbia Street, Suite  
200, Seattle, WA 98104 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): XU, Jiangchun  
[US/US]; 15805 S.E. 43rd Place, Bellevue, WA 98006  
(US). DILLON, Davin, C. [US/US]; 18112 N.W. Mon-  
treux Drive, Issaquah, WA 98027 (US). MITCHAM,Jennifer, L. [US/US]; 16677 N.E. 88th Street, Redmond,  
WA 98052 (US). HARLOCKER, Susan, L. [US/US];  
7522 13th Avenue W., Seattle, WA 98117 (US). JIANG,  
Yuqiu [CN/US]; 5001 South 232nd Street, Kent, WA  
98032 (US). REED, Steven, G. [US/US]; 2843 122nd  
Place N.E., Bellevue, WA 98005 (US). KALOS, Michael,  
D. [US/US]; 8116 Dayton Ave. N., Seattle, WA 98103  
(US). FANGER, Gary, Richard [US/US]; 15906 29th  
Drive S.E., Mill Creek, WA 98012 (US). DAY, Craig,  
H. [US/US]; 11501 Stone Ave. N., C122, Seattle, WA  
98133 (US). RETTER, Marc, W. [US/US]; 33402 N.E.  
43rd Place, Carnation, WA 98104 (US). STOLK, John,  
A. [US/US]; 7436 Northeast 144th Place, Bothell, WA  
98011 (US). SKEIKY, Yasir, A.W. [LB/US]; 15106 S.E.  
47th Place, Bellevue, WA 98006 (US). WANG, Aijun  
[CN/US]; 3106 213th Place S.E., Issaquah, WA 98029  
(US). MEAGHER, Madeleine, Joy [US/US]; 507 N.E.  
71st, #1, Seattle, WA 98115 (US).(74) Agents: POTTER, Jane, E.R.; Seed Intellectual Property  
Law Group PLLC, Suite 6300, 701 Fifth Avenue, Seattle,  
WA 98104-7092 et al. (US).

[Continued on next page]

(54) Title: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER



(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, particularly prostate cancer, are disclosed. Illustrative compositions comprise one or more prostate-specific polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly prostate cancer.

WO 01/51633 A2



(81) **Designated States (national):** AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

**Published:**

— *without international search report and to be republished upon receipt of that report*

(84) **Designated States (regional):** ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European

*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

## COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER

### 5 TECHNICAL FIELD OF THE INVENTION

The present invention relates generally to therapy and diagnosis of cancer, such as prostate cancer. The invention is more specifically related to polypeptides, comprising at least a portion of a prostate-specific protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides  
10 are useful in pharmaceutical compositions, *e.g.*, vaccines, and other compositions for the diagnosis and treatment of prostate cancer.

### BACKGROUND OF THE INVENTION

Cancer is a significant health problem throughout the world. Although  
Cancer is a significant health problem throughout the world. Although advances have  
15 been made in detection and therapy of cancer, no vaccine or other universally successful method for prevention or treatment is currently available. Current therapies, which are generally based on a combination of chemotherapy or surgery and radiation, continue to prove inadequate in many patients.

Prostate cancer is the most common form of cancer among males, with  
20 an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

25 In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA)

and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

In spite of considerable research into therapies for these and other cancers, prostate cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating such cancers. The present invention fulfills these needs and further provides other related advantages.

## 10 SUMMARY OF THE INVENTION

In one aspect, the present invention provides polynucleotide compositions comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788;

(b) complements of the sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788;

(c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788;

(d) sequences that hybridize to a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375,



381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788, under moderately stringent conditions;

5 (e) sequences having at least 75% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788;

10 (f) sequences having at least 90% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788; and

15 (g) degenerate variants of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788.

20 In one preferred embodiment, the polynucleotide compositions of the invention are expressed in at least about 20%, more preferably in at least about 30%, and most preferably in at least about 50% of prostate tissue samples tested, at a level that is at least about 2-fold, preferably at least about 5-fold, and most preferably at least about 10-fold higher than that for other normal tissues.

25 The present invention, in another aspect, provides polypeptide compositions comprising an amino acid sequence that is encoded by a polynucleotide sequence described above.

The present invention further provides polypeptide compositions comprising an amino acid sequence selected from the group consisting of sequences  
30 recited in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383,

477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 627-629, 632, 633, 635, 637, 638, 656-671, 675, 683, 684, 710, 712, 714, 715, 717-719, 723-734, 736, 740-750, 752, 754, 755, 766-772, 777-785 and 789-791.

In certain preferred embodiments, the polypeptides and/or  
5 polynucleotides of the present invention are immunogenic, *i.e.*, they are capable of eliciting an immune response, particularly a humoral and/or cellular immune response, as further described herein.

The present invention further provides fragments, variants and/or derivatives of the disclosed polypeptide and/or polynucleotide sequences, wherein the  
10 fragments, variants and/or derivatives preferably have a level of immunogenic activity of at least about 50%, preferably at least about 70% and more preferably at least about 90% of the level of immunogenic activity of a polypeptide sequence set forth in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 627-  
15 629, 632, 633, 635, 637, 638, 656-671, 675, 683, 684, 710, 712, 714, 715, 717-719, 723-734, 736, 740-750, 752, 754, 755, 766-772, 777-785 or 789-791, or a polypeptide sequence encoded by a polynucleotide sequence set forth in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626,  
20 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788.

The present invention further provides polynucleotides that encode a polypeptide described above, expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

25 Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, pharmaceutical compositions, *e.g.*, vaccine compositions, are provided for prophylactic or therapeutic  
30 applications. Such compositions generally comprise an immunogenic polypeptide or

polynucleotide of the invention and an immunostimulant, such as an adjuvant, together with a physiologically acceptable carrier.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to  
5 a polypeptide of the present invention, or a fragment thereof; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Illustrative  
10 antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, pharmaceutical compositions are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

15 The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins, typically in the form of pharmaceutical compositions, *e.g.*, vaccine compositions, comprising a physiologically acceptable carrier and/or an immunostimulant. The fusions proteins may comprise multiple immunogenic  
20 polypeptides or portions/variants thereof, as described herein, and may further comprise one or more polypeptide segments for facilitating and/or enhancing the expression, purification and/or immunogenicity of the polypeptide(s).

Within further aspects, the present invention provides methods for stimulating an immune response in a patient, preferably a T cell response in a human  
25 patient, comprising administering a pharmaceutical composition described herein. The patient may be afflicted with prostate cancer, in which case the methods provide treatment for the disease, or a patient considered to be at risk for such a disease may be treated prophylactically.

Within further aspects, the present invention provides methods for  
30 inhibiting the development of a cancer in a patient, comprising administering to a

patient a pharmaceutical composition as recited above. The patient may be afflicted with prostate cancer, in which case the methods provide treatment for the disease, or a patient considered to be at risk for such a disease may be treated prophylactically.

The present invention further provides, within other aspects, methods for  
5 removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a polypeptide of the present invention, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the polypeptide from the sample.

Within related aspects, methods are provided for inhibiting the  
10 development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a polypeptide of the present invention, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a  
15 polynucleotide encoding such a polypeptide; and (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for  
20 inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with one or more of: (i) a polypeptide  
25 comprising at least an immunogenic portion of polypeptide disclosed herein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer, preferably a prostate cancer, in a patient comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b), and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide of the present invention; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide of the present invention, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to an inventive polynucleotide, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide of the present invention; (b) detecting in the sample an amount of a polynucleotide that  
5 hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b), and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as  
10 monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All  
15 references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 illustrates the ability of T cells to kill fibroblasts expressing the representative prostate-specific polypeptide P502S, as compared to control fibroblasts.  
20 The percentage lysis is shown as a series of effector:target ratios, as indicated.

Figures 2A and 2B illustrate the ability of T cells to recognize cells expressing the representative prostate-specific polypeptide P502S. In each case, the number of  $\gamma$ -interferon spots is shown for different numbers of responders. In Figure 2A, data is presented for fibroblasts pulsed with the P2S-12 peptide, as compared to  
25 fibroblasts pulsed with a control E75 peptide. In Figure 2B, data is presented for fibroblasts expressing P502S, as compared to fibroblasts expressing HER-2/*neu*.

Figure 3 represents a peptide competition binding assay showing that the P1S#10 peptide, derived from P501S, binds HLA-A2. Peptide P1S#10 inhibits HLA-A2 restricted presentation of fluM58 peptide to CTL clone D150M58 in TNF release

bioassay. D150M58 CTL is specific for the HLA-A2 binding influenza matrix peptide fluM58.

Figure 4 illustrates the ability of T cell lines generated from P1S#10 immunized mice to specifically lyse P1S#10-pulsed Jurkat A2Kb targets and P501S-  
5 transduced Jurkat A2Kb targets, as compared to EGFP-transduced Jurkat A2Kb. The percent lysis is shown as a series of effector to target ratios, as indicated.

Figure 5 illustrates the ability of a T cell clone to recognize and specifically lyse Jurkat A2Kb cells expressing the representative prostate-specific polypeptide P501S, thereby demonstrating that the P1S#10 peptide may be a naturally  
10 processed epitope of the P501S polypeptide.

Figures 6A and 6B are graphs illustrating the specificity of a CD8<sup>+</sup> cell line (3A-1) for a representative prostate-specific antigen (P501S). Figure 6A shows the results of a <sup>51</sup>Cr release assay. The percent specific lysis is shown as a series of effector:target ratios, as indicated. Figure 6B shows the production of interferon-  
15 gamma by 3A-1 cells stimulated with autologous B-LCL transduced with P501S, at varying effector:target ratios as indicated.

Figure 7 is a Western blot showing the expression of P501S in baculovirus.

Figure 8 illustrates the results of epitope mapping studies on P501S.

Figure 9 is a schematic representation of the P501S protein showing the location of transmembrane domains and predicted intracellular and extracellular domains.  
20

Figure 10 is a genomic map showing the location of the prostate genes P775P, P704P, B305D, P712P and P774P within the Cat Eye Syndrome region of  
25 chromosome 22q11.2

Figure 11 shows the results of an ELISA assay to determine the specificity of rabbit polyclonal antisera raised against P501S.

SEQ ID NO: 1 is the determined cDNA sequence for F1-13

SEQ ID NO: 2 is the determined 3' cDNA sequence for F1-12

30 SEQ ID NO: 3 is the determined 5' cDNA sequence for F1-12

SEQ ID NO: 4 is the determined 3' cDNA sequence for F1-16  
SEQ ID NO: 5 is the determined 3' cDNA sequence for H1-1  
SEQ ID NO: 6 is the determined 3' cDNA sequence for H1-9  
SEQ ID NO: 7 is the determined 3' cDNA sequence for H1-4  
5 SEQ ID NO: 8 is the determined 3' cDNA sequence for J1-17  
SEQ ID NO: 9 is the determined 5' cDNA sequence for J1-17  
SEQ ID NO: 10 is the determined 3' cDNA sequence for L1-12  
SEQ ID NO: 11 is the determined 5' cDNA sequence for L1-12  
SEQ ID NO: 12 is the determined 3' cDNA sequence for N1-1862  
10 SEQ ID NO: 13 is the determined 5' cDNA sequence for N1-1862  
SEQ ID NO: 14 is the determined 3' cDNA sequence for J1-13  
SEQ ID NO: 15 is the determined 5' cDNA sequence for J1-13  
SEQ ID NO: 16 is the determined 3' cDNA sequence for J1-19  
SEQ ID NO: 17 is the determined 5' cDNA sequence for J1-19  
15 SEQ ID NO: 18 is the determined 3' cDNA sequence for J1-25  
SEQ ID NO: 19 is the determined 5' cDNA sequence for J1-25  
SEQ ID NO: 20 is the determined 5' cDNA sequence for J1-24  
SEQ ID NO: 21 is the determined 3' cDNA sequence for J1-24  
SEQ ID NO: 22 is the determined 5' cDNA sequence for K1-58  
20 SEQ ID NO: 23 is the determined 3' cDNA sequence for K1-58  
SEQ ID NO: 24 is the determined 5' cDNA sequence for K1-63  
SEQ ID NO: 25 is the determined 3' cDNA sequence for K1-63  
SEQ ID NO: 26 is the determined 5' cDNA sequence for L1-4  
SEQ ID NO: 27 is the determined 3' cDNA sequence for L1-4  
25 SEQ ID NO: 28 is the determined 5' cDNA sequence for L1-14  
SEQ ID NO: 29 is the determined 3' cDNA sequence for L1-14  
SEQ ID NO: 30 is the determined 3' cDNA sequence for J1-12  
SEQ ID NO: 31 is the determined 3' cDNA sequence for J1-16  
SEQ ID NO: 32 is the determined 3' cDNA sequence for J1-21  
30 SEQ ID NO: 33 is the determined 3' cDNA sequence for K1-48



SEQ ID NO: 34 is the determined 3' cDNA sequence for K1-55  
SEQ ID NO: 35 is the determined 3' cDNA sequence for L1-2  
SEQ ID NO: 36 is the determined 3' cDNA sequence for L1-6  
SEQ ID NO: 37 is the determined 3' cDNA sequence for N1-1858  
5 SEQ ID NO: 38 is the determined 3' cDNA sequence for N1-1860  
SEQ ID NO: 39 is the determined 3' cDNA sequence for N1-1861  
SEQ ID NO: 40 is the determined 3' cDNA sequence for N1-1864  
SEQ ID NO: 41 is the determined cDNA sequence for P5  
SEQ ID NO: 42 is the determined cDNA sequence for P8  
10 SEQ ID NO: 43 is the determined cDNA sequence for P9  
SEQ ID NO: 44 is the determined cDNA sequence for P18  
SEQ ID NO: 45 is the determined cDNA sequence for P20  
SEQ ID NO: 46 is the determined cDNA sequence for P29  
SEQ ID NO: 47 is the determined cDNA sequence for P30  
15 SEQ ID NO: 48 is the determined cDNA sequence for P34  
SEQ ID NO: 49 is the determined cDNA sequence for P36  
SEQ ID NO: 50 is the determined cDNA sequence for P38  
SEQ ID NO: 51 is the determined cDNA sequence for P39  
SEQ ID NO: 52 is the determined cDNA sequence for P42  
20 SEQ ID NO: 53 is the determined cDNA sequence for P47  
SEQ ID NO: 54 is the determined cDNA sequence for P49  
SEQ ID NO: 55 is the determined cDNA sequence for P50  
SEQ ID NO: 56 is the determined cDNA sequence for P53  
SEQ ID NO: 57 is the determined cDNA sequence for P55  
25 SEQ ID NO: 58 is the determined cDNA sequence for P60  
SEQ ID NO: 59 is the determined cDNA sequence for P64  
SEQ ID NO: 60 is the determined cDNA sequence for P65  
SEQ ID NO: 61 is the determined cDNA sequence for P73  
SEQ ID NO: 62 is the determined cDNA sequence for P75  
30 SEQ ID NO: 63 is the determined cDNA sequence for P76

SEQ ID NO: 64 is the determined cDNA sequence for P79

SEQ ID NO: 65 is the determined cDNA sequence for P84

SEQ ID NO: 66 is the determined cDNA sequence for P68

SEQ ID NO: 67 is the determined cDNA sequence for P80 (also referred

5 to as P704P)

SEQ ID NO: 68 is the determined cDNA sequence for P82

SEQ ID NO: 69 is the determined cDNA sequence for U1-3064

SEQ ID NO: 70 is the determined cDNA sequence for U1-3065

SEQ ID NO: 71 is the determined cDNA sequence for V1-3692

10 SEQ ID NO: 72 is the determined cDNA sequence for 1A-3905

SEQ ID NO: 73 is the determined cDNA sequence for V1-3686

SEQ ID NO: 74 is the determined cDNA sequence for R1-2330

SEQ ID NO: 75 is the determined cDNA sequence for 1B-3976

SEQ ID NO: 76 is the determined cDNA sequence for V1-3679

15 SEQ ID NO: 77 is the determined cDNA sequence for 1G-4736

SEQ ID NO: 78 is the determined cDNA sequence for 1G-4738

SEQ ID NO: 79 is the determined cDNA sequence for 1G-4741

SEQ ID NO: 80 is the determined cDNA sequence for 1G-4744

SEQ ID NO: 81 is the determined cDNA sequence for 1G-4734

20 SEQ ID NO: 82 is the determined cDNA sequence for 1H-4774

SEQ ID NO: 83 is the determined cDNA sequence for 1H-4781

SEQ ID NO: 84 is the determined cDNA sequence for 1H-4785

SEQ ID NO: 85 is the determined cDNA sequence for 1H-4787

SEQ ID NO: 86 is the determined cDNA sequence for 1H-4796

25 SEQ ID NO: 87 is the determined cDNA sequence for 1I-4807

SEQ ID NO: 88 is the determined cDNA sequence for 1I-4810

SEQ ID NO: 89 is the determined cDNA sequence for 1I-4811

SEQ ID NO: 90 is the determined cDNA sequence for 1J-4876

SEQ ID NO: 91 is the determined cDNA sequence for 1K-4884

30 SEQ ID NO: 92 is the determined cDNA sequence for 1K-4896

- SEQ ID NO: 93 is the determined cDNA sequence for 1G-4761  
SEQ ID NO: 94 is the determined cDNA sequence for 1G-4762  
SEQ ID NO: 95 is the determined cDNA sequence for 1H-4766  
SEQ ID NO: 96 is the determined cDNA sequence for 1H-4770  
5 SEQ ID NO: 97 is the determined cDNA sequence for 1H-4771  
SEQ ID NO: 98 is the determined cDNA sequence for 1H-4772  
SEQ ID NO: 99 is the determined cDNA sequence for 1D-4297  
SEQ ID NO: 100 is the determined cDNA sequence for 1D-4309  
SEQ ID NO: 101 is the determined cDNA sequence for 1D.1-4278  
10 SEQ ID NO: 102 is the determined cDNA sequence for 1D-4288  
SEQ ID NO: 103 is the determined cDNA sequence for 1D-4283  
SEQ ID NO: 104 is the determined cDNA sequence for 1D-4304  
SEQ ID NO: 105 is the determined cDNA sequence for 1D-4296  
SEQ ID NO: 106 is the determined cDNA sequence for 1D-4280  
15 SEQ ID NO: 107 is the determined full length cDNA sequence for F1-12  
(also referred to as P504S)  
SEQ ID NO: 108 is the predicted amino acid sequence for F1-12  
SEQ ID NO: 109 is the determined full length cDNA sequence for J1-17  
SEQ ID NO: 110 is the determined full length cDNA sequence for L1-12  
20 (also referred to as P501S)  
SEQ ID NO: 111 is the determined full length cDNA sequence for N1-1862 (also referred to as P503S)  
SEQ ID NO: 112 is the predicted amino acid sequence for J1-17  
SEQ ID NO: 113 is the predicted amino acid sequence for L1-12 (also  
25 referred to as P501S)  
SEQ ID NO: 114 is the predicted amino acid sequence for N1-1862 (also referred to as P503S)  
SEQ ID NO: 115 is the determined cDNA sequence for P89  
SEQ ID NO: 116 is the determined cDNA sequence for P90  
30 SEQ ID NO: 117 is the determined cDNA sequence for P92

SEQ ID NO: 118 is the determined cDNA sequence for P95  
SEQ ID NO: 119 is the determined cDNA sequence for P98  
SEQ ID NO: 120 is the determined cDNA sequence for P102  
SEQ ID NO: 121 is the determined cDNA sequence for P110  
5 SEQ ID NO: 122 is the determined cDNA sequence for P111  
SEQ ID NO: 123 is the determined cDNA sequence for P114  
SEQ ID NO: 124 is the determined cDNA sequence for P115  
SEQ ID NO: 125 is the determined cDNA sequence for P116  
SEQ ID NO: 126 is the determined cDNA sequence for P124  
10 SEQ ID NO: 127 is the determined cDNA sequence for P126  
SEQ ID NO: 128 is the determined cDNA sequence for P130  
SEQ ID NO: 129 is the determined cDNA sequence for P133  
SEQ ID NO: 130 is the determined cDNA sequence for P138  
SEQ ID NO: 131 is the determined cDNA sequence for P143  
15 SEQ ID NO: 132 is the determined cDNA sequence for P151  
SEQ ID NO: 133 is the determined cDNA sequence for P156  
SEQ ID NO: 134 is the determined cDNA sequence for P157  
SEQ ID NO: 135 is the determined cDNA sequence for P166  
SEQ ID NO: 136 is the determined cDNA sequence for P176  
20 SEQ ID NO: 137 is the determined cDNA sequence for P178  
SEQ ID NO: 138 is the determined cDNA sequence for P179  
SEQ ID NO: 139 is the determined cDNA sequence for P185  
SEQ ID NO: 140 is the determined cDNA sequence for P192  
SEQ ID NO: 141 is the determined cDNA sequence for P201  
25 SEQ ID NO: 142 is the determined cDNA sequence for P204  
SEQ ID NO: 143 is the determined cDNA sequence for P208  
SEQ ID NO: 144 is the determined cDNA sequence for P211  
SEQ ID NO: 145 is the determined cDNA sequence for P213  
SEQ ID NO: 146 is the determined cDNA sequence for P219  
30 SEQ ID NO: 147 is the determined cDNA sequence for P237

SEQ ID NO: 148 is the determined cDNA sequence for P239  
SEQ ID NO: 149 is the determined cDNA sequence for P248  
SEQ ID NO: 150 is the determined cDNA sequence for P251  
SEQ ID NO: 151 is the determined cDNA sequence for P255  
5 SEQ ID NO: 152 is the determined cDNA sequence for P256  
SEQ ID NO: 153 is the determined cDNA sequence for P259  
SEQ ID NO: 154 is the determined cDNA sequence for P260  
SEQ ID NO: 155 is the determined cDNA sequence for P263  
SEQ ID NO: 156 is the determined cDNA sequence for P264  
10 SEQ ID NO: 157 is the determined cDNA sequence for P266  
SEQ ID NO: 158 is the determined cDNA sequence for P270  
SEQ ID NO: 159 is the determined cDNA sequence for P272  
SEQ ID NO: 160 is the determined cDNA sequence for P278  
SEQ ID NO: 161 is the determined cDNA sequence for P105  
15 SEQ ID NO: 162 is the determined cDNA sequence for P107  
SEQ ID NO: 163 is the determined cDNA sequence for P137  
SEQ ID NO: 164 is the determined cDNA sequence for P194  
SEQ ID NO: 165 is the determined cDNA sequence for P195  
SEQ ID NO: 166 is the determined cDNA sequence for P196  
20 SEQ ID NO: 167 is the determined cDNA sequence for P220  
SEQ ID NO: 168 is the determined cDNA sequence for P234  
SEQ ID NO: 169 is the determined cDNA sequence for P235  
SEQ ID NO: 170 is the determined cDNA sequence for P243  
SEQ ID NO: 171 is the determined cDNA sequence for P703P-DE1  
25 SEQ ID NO: 172 is the predicted amino acid sequence for P703P-DE1  
SEQ ID NO: 173 is the determined cDNA sequence for P703P-DE2  
SEQ ID NO: 174 is the determined cDNA sequence for P703P-DE6  
SEQ ID NO: 175 is the determined cDNA sequence for P703P-DE13  
SEQ ID NO: 176 is the predicted amino acid sequence for P703P-DE13  
30 SEQ ID NO: 177 is the determined cDNA sequence for P703P-DE14

SEQ ID NO: 178 is the predicted amino acid sequence for P703P-DE14

SEQ ID NO: 179 is the determined extended cDNA sequence for 1G-

4736

SEQ ID NO: 180 is the determined extended cDNA sequence for 1G-

5 4738

SEQ ID NO: 181 is the determined extended cDNA sequence for 1G-

4741

SEQ ID NO: 182 is the determined extended cDNA sequence for 1G-

4744

10 SEQ ID NO: 183 is the determined extended cDNA sequence for 1H-

4774

SEQ ID NO: 184 is the determined extended cDNA sequence for 1H-

4781

SEQ ID NO: 185 is the determined extended cDNA sequence for 1H-

15 4785

SEQ ID NO: 186 is the determined extended cDNA sequence for 1H-

4787

SEQ ID NO: 187 is the determined extended cDNA sequence for 1H-

4796

20 SEQ ID NO: 188 is the determined extended cDNA sequence for 1I-

4807

SEQ ID NO: 189 is the determined 3' cDNA sequence for 1I-4810

SEQ ID NO: 190 is the determined 3' cDNA sequence for 1I-4811

SEQ ID NO: 191 is the determined extended cDNA sequence for 1J-

25 4876

SEQ ID NO: 192 is the determined extended cDNA sequence for 1K-

4884

SEQ ID NO: 193 is the determined extended cDNA sequence for 1K-

4896

SEQ ID NO: 194 is the determined extended cDNA sequence for 1G-  
4761

SEQ ID NO: 195 is the determined extended cDNA sequence for 1G-  
4762

5 SEQ ID NO: 196 is the determined extended cDNA sequence for 1H-  
4766

SEQ ID NO: 197 is the determined 3' cDNA sequence for 1H-4770  
SEQ ID NO: 198 is the determined 3' cDNA sequence for 1H-4771  
SEQ ID NO: 199 is the determined extended cDNA sequence for 1H-  
10 4772

SEQ ID NO: 200 is the determined extended cDNA sequence for 1D-  
4309

SEQ ID NO: 201 is the determined extended cDNA sequence for 1D.1-  
4278

15 SEQ ID NO: 202 is the determined extended cDNA sequence for 1D-  
4288

SEQ ID NO: 203 is the determined extended cDNA sequence for 1D-  
4283

SEQ ID NO: 204 is the determined extended cDNA sequence for 1D-  
20 4304

SEQ ID NO: 205 is the determined extended cDNA sequence for 1D-  
4296

SEQ ID NO: 206 is the determined extended cDNA sequence for 1D-  
4280

25 SEQ ID NO: 207 is the determined cDNA sequence for 10-d8fwd  
SEQ ID NO: 208 is the determined cDNA sequence for 10-H10con  
SEQ ID NO: 209 is the determined cDNA sequence for 11-C8rev  
SEQ ID NO: 210 is the determined cDNA sequence for 7.g6fwd  
SEQ ID NO: 211 is the determined cDNA sequence for 7.g6rev  
30 SEQ ID NO: 212 is the determined cDNA sequence for 8-b5fwd

SEQ ID NO: 213 is the determined cDNA sequence for 8-b5rev  
SEQ ID NO: 214 is the determined cDNA sequence for 8-b6fwd  
SEQ ID NO: 215 is the determined cDNA sequence for 8-b6 rev  
SEQ ID NO: 216 is the determined cDNA sequence for 8-d4fwd  
5 SEQ ID NO: 217 is the determined cDNA sequence for 8-d9rev  
SEQ ID NO: 218 is the determined cDNA sequence for 8-g3fwd  
SEQ ID NO: 219 is the determined cDNA sequence for 8-g3rev  
SEQ ID NO: 220 is the determined cDNA sequence for 8-h11rev  
SEQ ID NO: 221 is the determined cDNA sequence for g-f12fwd  
10 SEQ ID NO: 222 is the determined cDNA sequence for g-f3rev  
SEQ ID NO: 223 is the determined cDNA sequence for P509S  
SEQ ID NO: 224 is the determined cDNA sequence for P510S  
SEQ ID NO: 225 is the determined cDNA sequence for P703DE5  
SEQ ID NO: 226 is the determined cDNA sequence for 9-A11  
15 SEQ ID NO: 227 is the determined cDNA sequence for 8-C6  
SEQ ID NO: 228 is the determined cDNA sequence for 8-H7  
SEQ ID NO: 229 is the determined cDNA sequence for JPTPN13  
SEQ ID NO: 230 is the determined cDNA sequence for JPTPN14  
SEQ ID NO: 231 is the determined cDNA sequence for JPTPN23  
20 SEQ ID NO: 232 is the determined cDNA sequence for JPTPN24  
SEQ ID NO: 233 is the determined cDNA sequence for JPTPN25  
SEQ ID NO: 234 is the determined cDNA sequence for JPTPN30  
SEQ ID NO: 235 is the determined cDNA sequence for JPTPN34  
SEQ ID NO: 236 is the determined cDNA sequence for PTPN35  
25 SEQ ID NO: 237 is the determined cDNA sequence for JPTPN36  
SEQ ID NO: 238 is the determined cDNA sequence for JPTPN38  
SEQ ID NO: 239 is the determined cDNA sequence for JPTPN39  
SEQ ID NO: 240 is the determined cDNA sequence for JPTPN40  
SEQ ID NO: 241 is the determined cDNA sequence for JPTPN41  
30 SEQ ID NO: 242 is the determined cDNA sequence for JPTPN42



SEQ ID NO: 243 is the determined cDNA sequence for JPTPN45  
SEQ ID NO: 244 is the determined cDNA sequence for JPTPN46  
SEQ ID NO: 245 is the determined cDNA sequence for JPTPN51  
SEQ ID NO: 246 is the determined cDNA sequence for JPTPN56  
5 SEQ ID NO: 247 is the determined cDNA sequence for PTPN64  
SEQ ID NO: 248 is the determined cDNA sequence for JPTPN65  
SEQ ID NO: 249 is the determined cDNA sequence for JPTPN67  
SEQ ID NO: 250 is the determined cDNA sequence for JPTPN76  
SEQ ID NO: 251 is the determined cDNA sequence for JPTPN84  
10 SEQ ID NO: 252 is the determined cDNA sequence for JPTPN85  
SEQ ID NO: 253 is the determined cDNA sequence for JPTPN86  
SEQ ID NO: 254 is the determined cDNA sequence for JPTPN87  
SEQ ID NO: 255 is the determined cDNA sequence for JPTPN88  
SEQ ID NO: 256 is the determined cDNA sequence for JP1F1  
15 SEQ ID NO: 257 is the determined cDNA sequence for JP1F2  
SEQ ID NO: 258 is the determined cDNA sequence for JP1C2  
SEQ ID NO: 259 is the determined cDNA sequence for JP1B1  
SEQ ID NO: 260 is the determined cDNA sequence for JP1B2  
SEQ ID NO: 261 is the determined cDNA sequence for JP1D3  
20 SEQ ID NO: 262 is the determined cDNA sequence for JP1A4  
SEQ ID NO: 263 is the determined cDNA sequence for JP1F5  
SEQ ID NO: 264 is the determined cDNA sequence for JP1E6  
SEQ ID NO: 265 is the determined cDNA sequence for JP1D6  
SEQ ID NO: 266 is the determined cDNA sequence for JP1B5  
25 SEQ ID NO: 267 is the determined cDNA sequence for JP1A6  
SEQ ID NO: 268 is the determined cDNA sequence for JP1E8  
SEQ ID NO: 269 is the determined cDNA sequence for JP1D7  
SEQ ID NO: 270 is the determined cDNA sequence for JP1D9  
SEQ ID NO: 271 is the determined cDNA sequence for JP1C10  
30 SEQ ID NO: 272 is the determined cDNA sequence for JP1A9

SEQ ID NO: 273 is the determined cDNA sequence for JP1F12  
SEQ ID NO: 274 is the determined cDNA sequence for JP1E12  
SEQ ID NO: 275 is the determined cDNA sequence for JP1D11  
SEQ ID NO: 276 is the determined cDNA sequence for JP1C11  
5 SEQ ID NO: 277 is the determined cDNA sequence for JP1C12  
SEQ ID NO: 278 is the determined cDNA sequence for JP1B12  
SEQ ID NO: 279 is the determined cDNA sequence for JP1A12  
SEQ ID NO: 280 is the determined cDNA sequence for JP8G2  
SEQ ID NO: 281 is the determined cDNA sequence for JP8H1  
10 SEQ ID NO: 282 is the determined cDNA sequence for JP8H2  
SEQ ID NO: 283 is the determined cDNA sequence for JP8A3  
SEQ ID NO: 284 is the determined cDNA sequence for JP8A4  
SEQ ID NO: 285 is the determined cDNA sequence for JP8C3  
SEQ ID NO: 286 is the determined cDNA sequence for JP8G4  
15 SEQ ID NO: 287 is the determined cDNA sequence for JP8B6  
SEQ ID NO: 288 is the determined cDNA sequence for JP8D6  
SEQ ID NO: 289 is the determined cDNA sequence for JP8F5  
SEQ ID NO: 290 is the determined cDNA sequence for JP8A8  
SEQ ID NO: 291 is the determined cDNA sequence for JP8C7  
20 SEQ ID NO: 292 is the determined cDNA sequence for JP8D7  
SEQ ID NO: 293 is the determined cDNA sequence for P8D8  
SEQ ID NO: 294 is the determined cDNA sequence for JP8E7  
SEQ ID NO: 295 is the determined cDNA sequence for JP8F8  
SEQ ID NO: 296 is the determined cDNA sequence for JP8G8  
25 SEQ ID NO: 297 is the determined cDNA sequence for JP8B10  
SEQ ID NO: 298 is the determined cDNA sequence for JP8C10  
SEQ ID NO: 299 is the determined cDNA sequence for JP8E9  
SEQ ID NO: 300 is the determined cDNA sequence for JP8E10  
SEQ ID NO: 301 is the determined cDNA sequence for JP8F9  
30 SEQ ID NO: 302 is the determined cDNA sequence for JP8H9

- SEQ ID NO: 303 is the determined cDNA sequence for JP8C12  
SEQ ID NO: 304 is the determined cDNA sequence for JP8E11  
SEQ ID NO: 305 is the determined cDNA sequence for JP8E12  
SEQ ID NO: 306 is the amino acid sequence for the peptide PS2#12  
5 SEQ ID NO: 307 is the determined cDNA sequence for P711P  
SEQ ID NO: 308 is the determined cDNA sequence for P712P  
SEQ ID NO: 309 is the determined cDNA sequence for CLONE23  
SEQ ID NO: 310 is the determined cDNA sequence for P774P  
SEQ ID NO: 311 is the determined cDNA sequence for P775P  
10 SEQ ID NO: 312 is the determined cDNA sequence for P715P  
SEQ ID NO: 313 is the determined cDNA sequence for P710P  
SEQ ID NO: 314 is the determined cDNA sequence for P767P  
SEQ ID NO: 315 is the determined cDNA sequence for P768P  
SEQ ID NO: 316-325 are the determined cDNA sequences of previously  
15 isolated genes  
SEQ ID NO: 326 is the determined cDNA sequence for P703PDE5  
SEQ ID NO: 327 is the predicted amino acid sequence for P703PDE5  
SEQ ID NO: 328 is the determined cDNA sequence for P703P6.26  
SEQ ID NO: 329 is the predicted amino acid sequence for P703P6.26  
20 SEQ ID NO: 330 is the determined cDNA sequence for P703PX-23  
SEQ ID NO: 331 is the predicted amino acid sequence for P703PX-23  
SEQ ID NO: 332 is the determined full length cDNA sequence for  
P509S  
SEQ ID NO: 333 is the determined extended cDNA sequence for P707P  
25 (also referred to as 11-C9)  
SEQ ID NO: 334 is the determined cDNA sequence for P714P  
SEQ ID NO: 335 is the determined cDNA sequence for P705P (also  
referred to as 9-F3)  
SEQ ID NO: 336 is the predicted amino acid sequence for P705P  
30 SEQ ID NO: 337 is the amino acid sequence of the peptide P1S#10

- SEQ ID NO: 338 is the amino acid sequence of the peptide p5
- SEQ ID NO: 339 is the predicted amino acid sequence of P509S
- SEQ ID NO: 340 is the determined cDNA sequence for P778P
- SEQ ID NO: 341 is the determined cDNA sequence for P786P
- 5 SEQ ID NO: 342 is the determined cDNA sequence for P789P
- SEQ ID NO: 343 is the determined cDNA sequence for a clone showing  
homology to Homo sapiens MM46 mRNA
- SEQ ID NO: 344 is the determined cDNA sequence for a clone showing  
homology to Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA
- 10 SEQ ID NO: 345 is the determined cDNA sequence for a clone showing  
homology to Homo sapiens mRNA for E-cadherin
- SEQ ID NO: 346 is the determined cDNA sequence for a clone showing  
homology to Human nuclear-encoded mitochondrial serine hydroxymethyltransferase  
(SHMT)
- 15 SEQ ID NO: 347 is the determined cDNA sequence for a clone showing  
homology to Homo sapiens natural resistance-associated macrophage protein2  
(NRAMP2)
- SEQ ID NO: 348 is the determined cDNA sequence for a clone showing  
homology to Homo sapiens phosphoglucomutase-related protein (PGMRP)
- 20 SEQ ID NO: 349 is the determined cDNA sequence for a clone showing  
homology to Human mRNA for proteosome subunit p40
- SEQ ID NO: 350 is the determined cDNA sequence for P777P
- SEQ ID NO: 351 is the determined cDNA sequence for P779P
- SEQ ID NO: 352 is the determined cDNA sequence for P790P
- 25 SEQ ID NO: 353 is the determined cDNA sequence for P784P
- SEQ ID NO: 354 is the determined cDNA sequence for P776P
- SEQ ID NO: 355 is the determined cDNA sequence for P780P
- SEQ ID NO: 356 is the determined cDNA sequence for P544S
- SEQ ID NO: 357 is the determined cDNA sequence for P745S
- 30 SEQ ID NO: 358 is the determined cDNA sequence for P782P

- SEQ ID NO: 359 is the determined cDNA sequence for P783P
- SEQ ID NO: 360 is the determined cDNA sequence for unknown 17984
- SEQ ID NO: 361 is the determined cDNA sequence for P787P
- SEQ ID NO: 362 is the determined cDNA sequence for P788P
- 5 SEQ ID NO: 363 is the determined cDNA sequence for unknown 17994
- SEQ ID NO: 364 is the determined cDNA sequence for P781P
- SEQ ID NO: 365 is the determined cDNA sequence for P785P
- SEQ ID NO: 366-375 are the determined cDNA sequences for splice variants of B305D.
- 10 SEQ ID NO: 376 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 366.
- SEQ ID NO: 377 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 372.
- SEQ ID NO: 378 is the predicted amino acid sequence encoded by the
- 15 sequence of SEQ ID NO: 373.
- SEQ ID NO: 379 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 374.
- SEQ ID NO: 380 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 375.
- 20 SEQ ID NO: 381 is the determined cDNA sequence for B716P.
- SEQ ID NO: 382 is the determined full-length cDNA sequence for P711P.
- SEQ ID NO: 383 is the predicted amino acid sequence for P711P.
- SEQ ID NO: 384 is the cDNA sequence for P1000C.
- 25 SEQ ID NO: 385 is the cDNA sequence for CGI-82.
- SEQ ID NO: 386 is the cDNA sequence for 23320.
- SEQ ID NO: 387 is the cDNA sequence for CGI-69.
- SEQ ID NO: 388 is the cDNA sequence for L-iditol-2-dehydrogenase.
- SEQ ID NO: 389 is the cDNA sequence for 23379.
- 30 SEQ ID NO: 390 is the cDNA sequence for 23381.

- SEQ ID NO:391 is the cDNA sequence for KIAA0122.
- SEQ ID NO:392 is the cDNA sequence for 23399.
- SEQ ID NO:393 is the cDNA sequence for a previously identified gene.
- SEQ ID NO:394 is the cDNA sequence for HCLBP.
- 5 SEQ ID NO:395 is the cDNA sequence for transglutaminase.
- SEQ ID NO:396 is the cDNA sequence for a previously identified gene.
- SEQ ID NO:397 is the cDNA sequence for PAP.
- SEQ ID NO:398 is the cDNA sequence for Ets transcription factor
- PDEF.
- 10 SEQ ID NO:399 is the cDNA sequence for hTGR.
- SEQ ID NO:400 is the cDNA sequence for KIAA0295.
- SEQ ID NO:401 is the cDNA sequence for 22545.
- SEQ ID NO:402 is the cDNA sequence for 22547.
- SEQ ID NO:403 is the cDNA sequence for 22548.
- 15 SEQ ID NO:404 is the cDNA sequence for 22550.
- SEQ ID NO:405 is the cDNA sequence for 22551.
- SEQ ID NO:406 is the cDNA sequence for 22552.
- SEQ ID NO:407 is the cDNA sequence for 22553 (also known as
- P1020C).
- 20 SEQ ID NO:408 is the cDNA sequence for 22558.
- SEQ ID NO:409 is the cDNA sequence for 22562.
- SEQ ID NO:410 is the cDNA sequence for 22565.
- SEQ ID NO:411 is the cDNA sequence for 22567.
- SEQ ID NO:412 is the cDNA sequence for 22568.
- 25 SEQ ID NO:413 is the cDNA sequence for 22570.
- SEQ ID NO:414 is the cDNA sequence for 22571.
- SEQ ID NO:415 is the cDNA sequence for 22572.
- SEQ ID NO:416 is the cDNA sequence for 22573.
- SEQ ID NO:417 is the cDNA sequence for 22573.
- 30 SEQ ID NO:418 is the cDNA sequence for 22575.

SEQ ID NO:419 is the cDNA sequence for 22580.  
SEQ ID NO:420 is the cDNA sequence for 22581.  
SEQ ID NO:421 is the cDNA sequence for 22582.  
SEQ ID NO:422 is the cDNA sequence for 22583.  
5 SEQ ID NO:423 is the cDNA sequence for 22584.  
SEQ ID NO:424 is the cDNA sequence for 22585.  
SEQ ID NO:425 is the cDNA sequence for 22586.  
SEQ ID NO:426 is the cDNA sequence for 22587.  
SEQ ID NO:427 is the cDNA sequence for 22588.  
10 SEQ ID NO:428 is the cDNA sequence for 22589.  
SEQ ID NO:429 is the cDNA sequence for 22590.  
SEQ ID NO:430 is the cDNA sequence for 22591.  
SEQ ID NO:431 is the cDNA sequence for 22592.  
SEQ ID NO:432 is the cDNA sequence for 22593.  
15 SEQ ID NO:433 is the cDNA sequence for 22594.  
SEQ ID NO:434 is the cDNA sequence for 22595.  
SEQ ID NO:435 is the cDNA sequence for 22596.  
SEQ ID NO:436 is the cDNA sequence for 22847.  
SEQ ID NO:437 is the cDNA sequence for 22848.  
20 SEQ ID NO:438 is the cDNA sequence for 22849.  
SEQ ID NO:439 is the cDNA sequence for 22851.  
SEQ ID NO:440 is the cDNA sequence for 22852.  
SEQ ID NO:441 is the cDNA sequence for 22853.  
SEQ ID NO:442 is the cDNA sequence for 22854.  
25 SEQ ID NO:443 is the cDNA sequence for 22855.  
SEQ ID NO:444 is the cDNA sequence for 22856.  
SEQ ID NO:445 is the cDNA sequence for 22857.  
SEQ ID NO:446 is the cDNA sequence for 23601.  
SEQ ID NO:447 is the cDNA sequence for 23602.  
30 SEQ ID NO:448 is the cDNA sequence for 23605.

- SEQ ID NO:449 is the cDNA sequence for 23606.  
SEQ ID NO:450 is the cDNA sequence for 23612.  
SEQ ID NO:451 is the cDNA sequence for 23614.  
SEQ ID NO:452 is the cDNA sequence for 23618.  
5 SEQ ID NO:453 is the cDNA sequence for 23622.  
SEQ ID NO:454 is the cDNA sequence for folate hydrolase.  
SEQ ID NO:455 is the cDNA sequence for LIM protein.  
SEQ ID NO:456 is the cDNA sequence for a known gene.  
SEQ ID NO:457 is the cDNA sequence for a known gene.  
10 SEQ ID NO:458 is the cDNA sequence for a previously identified gene.  
SEQ ID NO:459 is the cDNA sequence for 23045.  
SEQ ID NO:460 is the cDNA sequence for 23032.  
SEQ ID NO:461 is the cDNA sequence for clone 23054.  
SEQ ID NO:462-467 are cDNA sequences for known genes.  
15 SEQ ID NO:468-471 are cDNA sequences for P710P.  
SEQ ID NO:472 is a cDNA sequence for P1001C.  
SEQ ID NO: 473 is the determined cDNA sequence for a first splice  
variant of P775P (referred to as 27505).  
SEQ ID NO: 474 is the determined cDNA sequence for a second splice  
20 variant of P775P (referred to as 19947).  
SEQ ID NO: 475 is the determined cDNA sequence for a third splice  
variant of P775P (referred to as 19941).  
SEQ ID NO: 476 is the determined cDNA sequence for a fourth splice  
variant of P775P (referred to as 19937).  
25 SEQ ID NO: 477 is a first predicted amino acid sequence encoded by the  
sequence of SEQ ID NO: 474.  
SEQ ID NO: 478 is a second predicted amino acid sequence encoded by  
the sequence of SEQ ID NO: 474.  
SEQ ID NO: 479 is the predicted amino acid sequence encoded by the  
30 sequence of SEQ ID NO: 475.



SEQ ID NO: 480 is a first predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 481 is a second predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

5           SEQ ID NO: 482 is a third predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

SEQ ID NO: 483 is a fourth predicted amino acid sequence encoded by the sequence of SEQ ID NO: 473.

10           SEQ ID NO: 484 is the first 30 amino acids of the *M. tuberculosis* antigen Ra12.

SEQ ID NO: 485 is the PCR primer AW025.

SEQ ID NO: 486 is the PCR primer AW003.

SEQ ID NO: 487 is the PCR primer AW027.

SEQ ID NO: 488 is the PCR primer AW026.

15           SEQ ID NO: 489-501 are peptides employed in epitope mapping studies.

SEQ ID NO: 502 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody 20D4.

SEQ ID NO: 503 is the determined cDNA sequence of the complementarity determining region for the anti-P503S monoclonal antibody JA1.

20           SEQ ID NO: 504 & 505 are peptides employed in epitope mapping studies.

SEQ ID NO: 506 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 8H2.

25           SEQ ID NO: 507 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 7H8.

SEQ ID NO: 508 is the determined cDNA sequence of the complementarity determining region for the anti-P703P monoclonal antibody 2D4.

SEQ ID NO: 509-522 are peptides employed in epitope mapping studies.

30           SEQ ID NO: 523 is a mature form of P703P used to raise antibodies against P703P.

SEQ ID NO: 524 is the putative full-length cDNA sequence of P703P.

SEQ ID NO: 525 is the predicted amino acid sequence encoded by SEQ ID NO: 524.

SEQ ID NO: 526 is the full-length cDNA sequence for P790P.

5 SEQ ID NO: 527 is the predicted amino acid sequence for P790P.

SEQ ID NO: 528 & 529 are PCR primers.

SEQ ID NO: 530 is the cDNA sequence of a splice variant of SEQ ID NO: 366.

10 SEQ ID NO: 531 is the cDNA sequence of the open reading frame of SEQ ID NO: 530.

SEQ ID NO: 532 is the predicted amino acid encoded by the sequence of SEQ ID NO: 531.

SEQ ID NO: 533 is the DNA sequence of a putative ORF of P775P.

15 SEQ ID NO: 534 is the predicted amino acid sequence encoded by SEQ ID NO: 533.

SEQ ID NO: 535 is a first full-length cDNA sequence for P510S.

SEQ ID NO: 536 is a second full-length cDNA sequence for P510S.

SEQ ID NO: 537 is the predicted amino acid sequence encoded by SEQ ID NO: 535.

20 SEQ ID NO: 538 is the predicted amino acid sequence encoded by SEQ ID NO: 536.

SEQ ID NO: 539 is the peptide P501S-370.

SEQ ID NO: 540 is the peptide P501S-376.

SEQ ID NO: 541-551 are epitopes of P501S.

25 SEQ ID NO: 552 is an extended cDNA sequence for P712P.

SEQ ID NO: 553-568 are the amino acid sequences encoded by predicted open reading frames within SEQ ID NO: 552.

SEQ ID NO: 569 is an extended cDNA sequence for P776P.

30 SEQ ID NO: 570 is the determined cDNA sequence for a splice variant of P776P referred to as contig 6.

SEQ ID NO: 571 is the determined cDNA sequence for a splice variant of P776P referred to as contig 7.

SEQ ID NO: 572 is the determined cDNA sequence for a splice variant of P776P referred to as contig 14.

5           SEQ ID NO: 573 is the amino acid sequence encoded by a first predicted ORF of SEQ ID NO: 570.

SEQ ID NO: 574 is the amino acid sequence encoded by a second predicted ORF of SEQ ID NO: 570.

10           SEQ ID NO: 575 is the amino acid sequence encoded by a predicted ORF of SEQ ID NO: 571.

SEQ ID NO: 576-586 are amino acid sequences encoded by predicted ORFs of SEQ ID NO: 569.

SEQ ID NO: 587 is a DNA consensus sequence of the sequences of P767P and P777P.

15           SEQ ID NO: 588-590 are amino acid sequences encoded by predicted ORFs of SEQ ID NO: 587.

SEQ ID NO: 591 is an extended cDNA sequence for P1020C.

SEQ ID NO: 592 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: P1020C.

20           SEQ ID NO: 593 is a splice variant of P775P referred to as 50748.

SEQ ID NO: 594 is a splice variant of P775P referred to as 50717.

SEQ ID NO: 595 is a splice variant of P775P referred to as 45985.

SEQ ID NO: 596 is a splice variant of P775P referred to as 38769.

SEQ ID NO: 597 is a splice variant of P775P referred to as 37922.

25           SEQ ID NO: 598 is a splice variant of P510S referred to as 49274.

SEQ ID NO: 599 is a splice variant of P510S referred to as 39487.

SEQ ID NO: 600 is a splice variant of P504S referred to as 5167.16.

SEQ ID NO: 601 is a splice variant of P504S referred to as 5167.1.

SEQ ID NO: 602 is a splice variant of P504S referred to as 5163.46.

30           SEQ ID NO: 603 is a splice variant of P504S referred to as 5163.42.

SEQ ID NO: 604 is a splice variant of P504S referred to as 5163.34.

SEQ ID NO: 605 is a splice variant of P504S referred to as 5163.17.

SEQ ID NO: 606 is a splice variant of P501S referred to as 10640.

SEQ ID NO: 607-615 are the sequences of PCR primers.

5           SEQ ID NO: 616 is the determined cDNA sequence of a fusion of P703P  
and PSA.

SEQ ID NO: 617 is the amino acid sequence of the fusion of P703P and  
PSA.

SEQ ID NO: 618 is the cDNA sequence of the gene DD3.

10           SEQ ID NO: 619 is an extended cDNA sequence for P714P.

SEQ ID NO: 620-622 are the cDNA sequences for splice variants of  
P704P.

SEQ ID NO: 623 is the cDNA sequence of a splice variant of P553S  
referred to as P553S-14.

15           SEQ ID NO: 624 is the cDNA sequence of a splice variant of P553S  
referred to as P553S-12.

SEQ ID NO: 625 is the cDNA sequence of a splice variant of P553S  
referred to as P553S-10.

20           SEQ ID NO: 626 is the cDNA sequence of a splice variant of P553S  
referred to as P553S-6.

SEQ ID NO: 627 is the amino acid sequence encoded by SEQ ID NO:  
626.

SEQ ID NO: 628 is a first amino acid sequence encoded by SEQ ID NO:  
623.

25           SEQ ID NO: 629 is a second amino acid sequence encoded by SEQ ID  
NO: 623.

SEQ ID NO: 630 is a first full-length cDNA sequence for prostate-  
specific transglutaminase gene (also referred to herein as P558S).

30           SEQ ID NO: 631 is a second full-length cDNA sequence for prostate-  
specific transglutaminase gene.

SEQ ID NO: 632 is the amino acid sequence encoded by the sequence of  
SEQ ID NO: 630.

SEQ ID NO: 633 is the amino acid sequence encoded by the sequence of  
SEQ ID NO: 631.

5               SEQ ID NO: 634 is the full-length cDNA sequence for P788P.

SEQ ID NO: 635 is the amino acid sequence encoded by SEQ ID NO:  
634.

SEQ ID NO: 636 is the determined cDNA sequence for a polymorphic  
variant of P788P.

10             SEQ ID NO: 637 is the amino acid sequence encoded by SEQ ID NO:  
636.

SEQ ID NO: 638 is the amino acid sequence of peptide 4 from P703P.

SEQ ID NO: 639 is the cDNA sequence that encodes peptide 4 from  
P703P.

15             SEQ ID NO: 640-655 are cDNA sequences encoding epitopes of P703P.

SEQ ID NO: 656-671 are the amino acid sequences of epitopes of  
P703P.

SEQ ID NO: 672 and 673 are PCR primers.

20             SEQ ID NO: 674 is the cDNA sequence encoding an N-terminal portion  
of P788P expressed in *E. coli*.

SEQ ID NO: 675 is the amino acid sequence of the N-terminal portion of  
P788P expressed in *E. coli*.

SEQ ID NO: 676 is the amino acid sequence of the *M. tuberculosis*  
antigen Ra12.

25             SEQ ID NO: 677 and 678 are PCR primers.

SEQ ID NO: 679 is the cDNA sequence for the Ra12-P510S-C  
construct.

SEQ ID NO: 680 is the cDNA sequence for the P510S-C construct.

SEQ ID NO: 681 is the cDNA sequence for the P510S-E3 construct.

SEQ ID NO: 682 is the amino acid sequence for the Ra12-P510S-C construct.

SEQ ID NO: 683 is the amino acid sequence for the P510S-C construct.

SEQ ID NO: 684 is the amino acid sequence for the P510S-E3 construct.

5               SEQ ID NO: 685-690 are PCR primers.

SEQ ID NO: 691 is the cDNA sequence of the construct Ra12-P775P-ORF3.

SEQ ID NO: 692 is the amino acid sequence of the construct Ra12-P775P-ORF3.

10             SEQ ID NO: 693 and 694 are PCR primers.

SEQ ID NO: 695 is the determined amino acid sequence for a P703P His tag fusion protein.

SEQ ID NO: 696 is the determined cDNA sequence for a P703P His tag fusion protein.

15             SEQ ID NO: 697 and 698 are PCR primers.

SEQ ID NO: 699 is the determined amino acid sequence for a P705P His tag fusion protein.

SEQ ID NO: 700 is the determined cDNA sequence for a P705P His tag fusion protein.

20             SEQ ID NO: 701 and 702 are PCR primers.

SEQ ID NO: 703 is the determined amino acid sequence for a P711P His tag fusion protein.

SEQ ID NO: 704 is the determined cDNA sequence for a P711P His tag fusion protein.

25             SEQ ID NO: 705 is the amino acid sequence of the *M. tuberculosis* antigen Ra12.

SEQ ID NO: 706 and 707 are PCR primers.

SEQ ID NO: 708 is the determined cDNA sequence for the construct Ra12-P501S-E2.

SEQ ID NO: 709 is the determined amino acid sequence for the construct Ra12-P501S-E2.

SEQ ID NO: 710 is the amino acid sequence for an epitope of P501S.

SEQ ID NO: 711 is the DNA sequence encoding SEQ ID NO: 710.

5 SEQ ID NO: 712 is the amino acid sequence for an epitope of P501S.

SEQ ID NO: 713 is the DNA sequence encoding SEQ ID NO: 712.

SEQ ID NO: 714 is a peptide employed in epitope mapping studies.

SEQ ID NO: 715 is the amino acid sequence for an epitope of P501S.

SEQ ID NO: 716 is the DNA sequence encoding SEQ ID NO: 715.

10 SEQ ID NO: 717-719 are the amino acid sequences for CD4 epitopes of P501S.

SEQ ID NO: 720-722 are the DNA sequences encoding the sequences of SEQ ID NO: 717-719.

15 SEQ ID NO: 723-734 are the amino acid sequences for putative CTL epitopes of P703P.

SEQ ID NO: 735 is the full-length cDNA sequence for P789P.

SEQ ID NO: 736 is the amino acid sequence encoded by SEQ ID NO: 735.

20 SEQ ID NO: 737 is the determined full-length cDNA sequence for the splice variant of P776P referred to as contig 6.

SEQ ID NO: 738-739 are determined full-length cDNA sequences for the splice variant of P776P referred to as contig 7.

SEQ ID NO: 740-744 are amino acid sequences encoded by SEQ ID NO: 737.

25 SEQ ID NO: 745-750 are amino acid sequences encoded by the splice variant of P776P referred to as contig 7.

SEQ ID NO: 751 is the full-length cDNA sequence for human transmembrane protease serine 2.

30 SEQ ID NO: 752 is the amino acid sequence encoded by SEQ ID NO: 751.

SEQ ID NO: 753 is the cDNA sequence encoding the first 209 amino acids of human transmembrane protease serine 2.

SEQ ID NO: 754 is the first 209 amino acids of human transmembrane protease serine 2.

5               SEQ ID NO: 755 is the amino acid sequence of peptide 296-322 of P501S.

SEQ ID NO: 756-759 are PCR primers.

SEQ ID NO: 760 is the determined cDNA sequence of the Vb chain of a T cell receptor for the P501S-specific T cell clone 4E5.

10             SEQ ID NO: 761 is the determined cDNA sequence of the Va chain of a T cell receptor for the P501S-specific T cell clone 4E5.

SEQ ID NO: 762 is the amino acid sequence encoded by SEQ ID NO 760.

15             SEQ ID NO: 763 is the amino acid sequence encoded by SEQ ID NO 761.

SEQ ID NO: 764 is the full-length open reading frame for P768P including stop codon.

SEQ ID NO: 765 is the full-length open reading frame for P768P without stop codon.

20             SEQ ID NO: 766 is the amino acid sequence encoded by SEQ ID NO: 765.

SEQ ID NO: 767-772 are the amino acid sequences for predicted domains of P768P.

SEQ ID NO: 773 is the full-length cDNA sequence of P835P.

25             SEQ ID NO: 774 is the cDNA sequence of the previously identified clone FLJ13581.

SEQ ID NO: 775 is the cDNA sequence of the open reading frame for P835P with stop codon.

30             SEQ ID NO: 776 is the cDNA sequence of the open reading frame for P835P without stop codon.



SEQ ID NO: 777 is the full-length amino acid sequence for P835P.

SEQ ID NO: 778-785 are the amino acid sequences of extracellular and intracellular domains of P835P.

SEQ ID NO: 786 is the full-length cDNA sequence for P1000C.

5           SEQ ID NO: 787 is the cDNA sequence of the open reading frame for P1000C, including stop codon.

SEQ ID NO: 788 is the cDNA sequence of the open reading frame for P1000C, without stop codon.

SEQ ID NO: 789 is the full-length amino acid sequence for P1000C.

10           SEQ ID NO: 790 is amino acids 1-100 of SEQ ID NO: 789.

SEQ ID NO: 791 is amino acids 100-492 of SEQ ID NO: 789.

SEQ ID NO: 792 is the amino acid sequence of an  $\alpha$  prepro-P501S recombinant protein.

## 15   DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed generally to compositions and their use in the therapy and diagnosis of cancer, particularly prostate cancer. As described further below, illustrative compositions of the present invention include, but are not restricted to, polypeptides, particularly immunogenic polypeptides, polynucleotides encoding such  
20   polypeptides, antibodies and other binding agents, antigen presenting cells (APCs) and immune system cells (e.g., T cells).

The practice of the present invention will employ, unless indicated specifically to the contrary, conventional methods of virology, immunology, microbiology, molecular biology and recombinant DNA techniques within the skill of  
25   the art, many of which are described below for the purpose of illustration. Such techniques are explained fully in the literature. See, e.g., Sambrook, et al. Molecular Cloning: A Laboratory Manual (2nd Edition, 1989); Maniatis et al. Molecular Cloning: A Laboratory Manual (1982); DNA Cloning: A Practical Approach, vol. I & II (D. Glover, ed.); Oligonucleotide Synthesis (N. Gait, ed., 1984); Nucleic Acid

Hybridization (B. Hames & S. Higgins, eds., 1985); Transcription and Translation (B. Hames & S. Higgins, eds., 1984); Animal Cell Culture (R. Freshney, ed., 1986); Perbal, A Practical Guide to Molecular Cloning (1984).

All publications, patents and patent applications cited herein, whether  
5 supra or infra, are hereby incorporated by reference in their entirety.

As used in this specification and the appended claims, the singular forms "a," "an" and "the" include plural references unless the content clearly dictates otherwise.

### Polypeptide Compositions

10 As used herein, the term "polypeptide" is used in its conventional meaning, *i.e.*, as a sequence of amino acids. The polypeptides are not limited to a specific length of the product; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide, and such terms may be used interchangeably herein unless specifically indicated otherwise. This term also does not refer to or exclude post-  
15 expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like, as well as other modifications known in the art, both naturally occurring and non-naturally occurring. A polypeptide may be an entire protein, or a subsequence thereof. Particular polypeptides of interest in the context of this invention are amino acid subsequences comprising epitopes, *i.e.*, antigenic  
20 determinants substantially responsible for the immunogenic properties of a polypeptide and being capable of evoking an immune response.

Particularly illustrative polypeptides of the present invention comprise those encoded by a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382  
25 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788, or a sequence that hybridizes under moderately stringent conditions, or, alternatively, under highly stringent conditions, to a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175,

177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788. In specific embodiments, the polypeptides of the invention  
5 comprise amino acid sequences as set forth in any one of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 627-629, 632, 633, 635, 637, 638, 656-671, 675, 683, 684, 710, 712, 714, 715, 717-719, 723-734, 736, 740-750, 752, 754, 755, 766-772, 777-785 and 789-791.

10           The polypeptides of the present invention are sometimes herein referred to as prostate-specific proteins or prostate-specific polypeptides, as an indication that their identification has been based at least in part upon their increased levels of expression in prostate tissue samples. Thus, a "prostate-specific polypeptide" or "prostate-specific protein," refers generally to a polypeptide sequence of the present  
15 invention, or a polynucleotide sequence encoding such a polypeptide, that is expressed in a substantial proportion of prostate tissue samples, for example preferably greater than about 20%, more preferably greater than about 30%, and most preferably greater than about 50% or more of prostate tissue samples tested, at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in other  
20 normal tissues, as determined using a representative assay provided herein. A prostate-specific polypeptide sequence of the invention, based upon its increased level of expression in tumor cells, has particular utility both as a diagnostic marker as well as a therapeutic target, as further described below.

          In certain preferred embodiments, the polypeptides of the invention are  
25 immunogenic, *i.e.*, they react detectably within an immunoassay (such as an ELISA or T-cell stimulation assay) with antisera and/or T-cells from a patient with prostate cancer. Screening for immunogenic activity can be performed using techniques well known to the skilled artisan. For example, such screens can be performed using methods such as those described in Harlow and Lane, *Antibodies: A Laboratory*  
30 *Manual*, Cold Spring Harbor Laboratory, 1988. In one illustrative example, a

polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example,  $^{125}\text{I}$ -labeled Protein A.

- 5                   As would be recognized by the skilled artisan, immunogenic portions of the polypeptides disclosed herein are also encompassed by the present invention. An "immunogenic portion," as used herein, is a fragment of an immunogenic polypeptide of the invention that itself is immunologically reactive (*i.e.*, specifically binds) with the B-cells and/or T-cell surface antigen receptors that recognize the polypeptide.
- 10 Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they
- 15 specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well-known techniques.

- In one preferred embodiment, an immunogenic portion of a polypeptide of the present invention is a portion that reacts with antisera and/or T-cells at a level that
- 20 is not substantially less than the reactivity of the full-length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Preferably, the level of immunogenic activity of the immunogenic portion is at least about 50%, preferably at least about 70% and most preferably greater than about 90% of the immunogenicity for the full-length polypeptide. In some instances, preferred immunogenic portions will be identified that
- 25 have a level of immunogenic activity greater than that of the corresponding full-length polypeptide, *e.g.*, having greater than about 100% or 150% or more immunogenic activity.

- In certain other embodiments, illustrative immunogenic portions may include peptides in which an N-terminal leader sequence and/or transmembrane domain
- 30 has been deleted. Other illustrative immunogenic portions will contain a small N-

and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

In another embodiment, a polypeptide composition of the invention may also comprise one or more polypeptides that are immunologically reactive with T cells and/or antibodies generated against a polypeptide of the invention, particularly a  
5 polypeptide having an amino acid sequence disclosed herein, or to an immunogenic fragment or variant thereof.

In another embodiment of the invention, polypeptides are provided that comprise one or more polypeptides that are capable of eliciting T cells and/or antibodies  
10 that are immunologically reactive with one or more polypeptides described herein, or one or more polypeptides encoded by contiguous nucleic acid sequences contained in the polynucleotide sequences disclosed herein, or immunogenic fragments or variants thereof, or to one or more nucleic acid sequences which hybridize to one or more of these sequences under conditions of moderate to high stringency.

15 The present invention, in another aspect, provides polypeptide fragments comprising at least about 5, 10, 15, 20, 25, 50, or 100 contiguous amino acids, or more, including all intermediate lengths, of a polypeptide composition set forth herein, such as those set forth in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568,  
20 573-586, 588-590, 592, 627-629, 632, 633, 635, 637, 638, 656-671, 675, 683, 684, 710, 712, 714, 715, 717-719, 723-734, 736, 740-750, 752, 754, 755, 766-772, 777-785 and 789-791, or those encoded by a polynucleotide sequence set forth in a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591,  
25 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788.

In another aspect, the present invention provides variants of the polypeptide compositions described herein. Polypeptide variants generally encompassed by the present invention will typically exhibit at least about 70%, 75%,  
30 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more identity

(determined as described below), along its length, to a polypeptide sequence set forth herein.

In one preferred embodiment, the polypeptide fragments and variants provided by the present invention are immunologically reactive with an antibody and/or  
5 T-cell that reacts with a full-length polypeptide specifically set forth herein.

In another preferred embodiment, the polypeptide fragments and variants provided by the present invention exhibit a level of immunogenic activity of at least about 50%, preferably at least about 70%, and most preferably at least about 90% or more of that exhibited by a full-length polypeptide sequence specifically set forth  
10 herein.

A polypeptide "variant," as the term is used herein, is a polypeptide that typically differs from a polypeptide specifically disclosed herein in one or more substitutions, deletions, additions and/or insertions. Such variants may be naturally occurring or may be synthetically generated, for example, by modifying one or more of  
15 the above polypeptide sequences of the invention and evaluating their immunogenic activity as described herein using any of a number of techniques well known in the art.

For example, certain illustrative variants of the polypeptides of the invention include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other illustrative variants  
20 include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

In many instances, a variant will contain conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide  
25 chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. As described above, modifications may be made in the structure of the polynucleotides and polypeptides of the present invention and still obtain a functional molecule that encodes a variant or derivative polypeptide with desirable characteristics, *e.g.*, with immunogenic characteristics. When it is  
30 desired to alter the amino acid sequence of a polypeptide to create an equivalent, or

even an improved, immunogenic variant or portion of a polypeptide of the invention, one skilled in the art will typically change one or more of the codons of the encoding DNA sequence according to Table 1.

For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated that various changes may be made in the peptide sequences of the disclosed compositions, or corresponding DNA sequences which encode said peptides without appreciable loss of their biological utility or activity.

TABLE 1

Amino Acids			Codons						
Alanine	Ala	A	GCA	GCC	GCG	GCU			
Cysteine	Cys	C	UGC	UGU					
Aspartic acid	Asp	D	GAC	GAU					
Glutamic acid	Glu	E	GAA	GAG					
Phenylalanine	Phe	F	UUC	UUU					
Glycine	Gly	G	GGA	GGC	GGG	GGU			
Histidine	His	H	CAC	CAU					
Isoleucine	Ile	I	AUA	AUC	AUU				
Lysine	Lys	K	AAA	AAG					
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU	
Methionine	Met	M	AUG						
Asparagine	Asn	N	AAC	AAU					
Proline	Pro	P	CCA	CCC	CCG	CCU			
Glutamine	Gln	Q	CAA	CAG					
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU	
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU	
Threonine	Thr	T	ACA	ACC	ACG	ACU			
Valine	Val	V	GUA	GUC	GUG	GUU			
Tryptophan	Trp	W	UGG						
Tyrosine	Tyr	Y	UAC	UAU					

In making such changes, the hydrophatic index of amino acids may be considered. The importance of the hydrophatic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporated herein by reference). It is accepted that the relative hydrophatic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like. Each amino acid has been assigned a hydrophatic index on the basis of its



hydrophobicity and charge characteristics (Kyte and Doolittle, 1982). These values are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (−0.4); threonine (−0.7); serine (−0.8); tryptophan (−0.9); tyrosine (−1.3); proline (−1.6); histidine (−3.2); glutamate (−3.5);  
5 glutamine (−3.5); aspartate (−3.5); asparagine (−3.5); lysine (−3.9); and arginine (−4.5).

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, *i.e.* still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are  
10 within  $\pm 2$  is preferred, those within  $\pm 1$  are particularly preferred, and those within  $\pm 0.5$  are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U. S. Patent 4,554,101 (specifically incorporated herein by reference in its entirety), states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of  
15 its adjacent amino acids, correlates with a biological property of the protein.

As detailed in U. S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0  $\pm$  1); glutamate (+3.0  $\pm$  1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (−0.4); proline (−0.5  $\pm$  1); alanine (−0.5); histidine (−0.5); cysteine  
20 (−1.0); methionine (−1.3); valine (−1.5); leucine (−1.8); isoleucine (−1.8); tyrosine (−2.3); phenylalanine (−2.5); tryptophan (−3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within  $\pm 2$   
25 is preferred, those within  $\pm 1$  are particularly preferred, and those within  $\pm 0.5$  are even more particularly preferred.

As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions that  
30 take various of the foregoing characteristics into consideration are well known to those

of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

In addition, any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of  
5 flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl-methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

10 Amino acid substitutions may further be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values  
15 include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a  
20 preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydrophobic nature of the polypeptide.

25 As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein, which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For  
30 example, a polypeptide may be conjugated to an immunoglobulin Fc region.

When comparing polypeptide sequences, two sequences are said to be “identical” if the sequence of amino acids in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A “comparison window” as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA* 80:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics

Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides and polypeptides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. For amino acid sequences, a scoring matrix can be used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment.

In one preferred approach, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Within other illustrative embodiments, a polypeptide may be a fusion polypeptide that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known

tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the polypeptide or to enable the polypeptide to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the polypeptide.

Fusion polypeptides may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion polypeptide is expressed as a recombinant polypeptide, allowing the production of increased levels, relative to a non-fused polypeptide, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion polypeptide that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion polypeptide using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al.,

*Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to  
5 separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and  
10 transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

The fusion polypeptide can comprise a polypeptide as described herein together with an unrelated immunogenic protein, such as an immunogenic protein capable of eliciting a recall response. Examples of such proteins include tetanus,  
15 tuberculosis and hepatitis proteins (*see*, for example, Stoute et al. *New Engl. J. Med.*, 336:86-91, 1997).

In one preferred embodiment, the immunological fusion partner is derived from a *Mycobacterium* sp., such as a *Mycobacterium tuberculosis*-derived Ra12 fragment. Ra12 compositions and methods for their use in enhancing the expression  
20 and/or immunogenicity of heterologous polynucleotide/polypeptide sequences is described in U.S. Patent Application 60/158,585, the disclosure of which is incorporated herein by reference in its entirety. Briefly, Ra12 refers to a polynucleotide region that is a subsequence of a *Mycobacterium tuberculosis* MTB32A nucleic acid. MTB32A is a serine protease of 32 KD molecular weight encoded by a gene in virulent  
25 and avirulent strains of *M. tuberculosis*. The nucleotide sequence and amino acid sequence of MTB32A have been described (for example, U.S. Patent Application 60/158,585; *see also*, Skeiky et al., *Infection and Immun.* (1999) 67:3998-4007, incorporated herein by reference). C-terminal fragments of the MTB32A coding sequence express at high levels and remain as a soluble polypeptides throughout the  
30 purification process. Moreover, Ra12 may enhance the immunogenicity of heterologous

immunogenic polypeptides with which it is fused. One preferred Ra12 fusion polypeptide comprises a 14 KD C-terminal fragment corresponding to amino acid residues 192 to 323 of MTB32A. Other preferred Ra12 polynucleotides generally comprise at least about 15 consecutive nucleotides, at least about 30 nucleotides, at least  
5 about 60 nucleotides, at least about 100 nucleotides, at least about 200 nucleotides, or at least about 300 nucleotides that encode a portion of a Ra12 polypeptide. Ra12 polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a Ra12 polypeptide or a portion thereof) or may comprise a variant of such a sequence. Ra12 polynucleotide variants may contain one or more substitutions,  
10 additions, deletions and/or insertions such that the biological activity of the encoded fusion polypeptide is not substantially diminished, relative to a fusion polypeptide comprising a native Ra12 polypeptide. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native Ra12 polypeptide or a  
15 portion thereof.

Within other preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino  
20 acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells.  
25 Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is  
30 derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine

amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been  
5 exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (see *Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion polypeptide. A repeat portion is found in the C-terminal region starting at  
10 residue 178. A particularly preferred repeat portion incorporates residues 188-305.

Yet another illustrative embodiment involves fusion polypeptides, and the polynucleotides encoding them, wherein the fusion partner comprises a targeting signal capable of directing a polypeptide to the endosomal/lysosomal compartment, as described in U.S. Patent No. 5,633,234. An immunogenic polypeptide of the invention,  
15 when fused with this targeting signal, will associate more efficiently with MHC class II molecules and thereby provide enhanced in vivo stimulation of CD4<sup>+</sup> T-cells specific for the polypeptide.

Polypeptides of the invention are prepared using any of a variety of well known synthetic and/or recombinant techniques, the latter of which are further  
20 described below. Polypeptides, portions and other variants generally less than about 150 amino acids can be generated by synthetic means, using techniques well known to those of ordinary skill in the art. In one illustrative example, such polypeptides are synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a  
25 growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

In general, polypeptide compositions (including fusion polypeptides) of  
30 the invention are isolated. An "isolated" polypeptide is one that is removed from its



original environment. For example, a naturally-occurring protein or polypeptide is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are also purified, *e.g.*, are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99%  
5 pure.

### Polynucleotide Compositions

The present invention, in other aspects, provides polynucleotide compositions. The terms "DNA" and "polynucleotide" are used essentially interchangeably herein to refer to a DNA molecule that has been isolated free of total  
10 genomic DNA of a particular species. "Isolated," as used herein, means that a polynucleotide is substantially away from other coding sequences, and that the DNA molecule does not contain large portions of unrelated coding DNA, such as large chromosomal fragments or other functional genes or polypeptide coding regions. Of course, this refers to the DNA molecule as originally isolated, and does not exclude  
15 genes or coding regions later added to the segment by the hand of man.

As will be understood by those skilled in the art, the polynucleotide compositions of this invention can include genomic sequences, extra-genomic and plasmid-encoded sequences and smaller engineered gene segments that express, or may be adapted to express, proteins, polypeptides, peptides and the like. Such segments may  
20 be naturally isolated, or modified synthetically by the hand of man.

As will be also recognized by the skilled artisan, polynucleotides of the invention may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules may include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-  
25 to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a polypeptide/protein of the invention or a portion thereof) or may comprise a sequence that encodes a variant or derivative, preferably an immunogenic variant or derivative, of such a sequence.

5           Therefore, according to another aspect of the present invention, polynucleotide compositions are provided that comprise some or all of a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 10 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788, complements of a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 15 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788, and degenerate variants of a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 20 773-776 and 786-788. In certain preferred embodiments, the polynucleotide sequences set forth herein encode immunogenic polypeptides, as described above.

          In other related embodiments, the present invention provides polynucleotide variants having substantial identity to the sequences disclosed herein in SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332- 25 335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788, for example those comprising at least 70% sequence identity, preferably at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a 30 polynucleotide sequence of this invention using the methods described herein, (*e.g.*,

BLAST analysis using standard parameters, as described below). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the  
5 like.

Typically, polynucleotide variants will contain one or more substitutions, additions, deletions and/or insertions, preferably such that the immunogenicity of the polypeptide encoded by the variant polynucleotide is not substantially diminished relative to a polypeptide encoded by a polynucleotide sequence specifically set forth  
10 herein). The term "variants" should also be understood to encompass homologous genes of xenogenic origin.

In additional embodiments, the present invention provides polynucleotide fragments comprising various lengths of contiguous stretches of sequence identical to, or complementary to, one or more of the sequences disclosed  
15 herein. For example, polynucleotides are provided by this invention that comprise at least about 10, 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000 or more contiguous nucleotides of one or more of the sequences disclosed herein as well as all intermediate lengths there between. It will be readily understood that "intermediate lengths", in this context, means any length between the quoted values, such as 16, 17,  
20 18, 19, *etc.*; 21, 22, 23, *etc.*; 30, 31, 32, *etc.*; 50, 51, 52, 53, *etc.*; 100, 101, 102, 103, *etc.*; 150, 151, 152, 153, *etc.*; including all integers through 200-500; 500-1,000, and the like.

In another embodiment of the invention, polynucleotide compositions are provided that are capable of hybridizing under moderate to high stringency conditions to  
25 a polynucleotide sequence provided herein, or a fragment thereof, or a complementary sequence thereof. Hybridization techniques are well known in the art of molecular biology. For purposes of illustration, suitable moderately stringent conditions for testing the hybridization of a polynucleotide of this invention with other polynucleotides include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0);  
30 hybridizing at 50°C-60°C, 5 X SSC, overnight; followed by washing twice at 65°C for

20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. One skilled in the art will understand that the stringency of hybridization can be readily manipulated, such as by altering the salt content of the hybridization solution and/or the temperature at which the hybridization is performed. For example, in another embodiment, suitable  
5 highly stringent hybridization conditions include those described above, with the exception that the temperature of hybridization is increased, *e.g.*, to 60-65°C or 65-70°C.

In certain preferred embodiments, the polynucleotides described above, *e.g.*, polynucleotide variants, fragments and hybridizing sequences, encode polypeptides  
10 that are immunologically cross-reactive with a polypeptide sequence specifically set forth herein. In other preferred embodiments, such polynucleotides encode polypeptides that have a level of immunogenic activity of at least about 50%, preferably at least about 70%, and more preferably at least about 90% of that for a polypeptide sequence specifically set forth herein.

15 The polynucleotides of the present invention, or fragments thereof, regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment  
20 of almost any length may be employed, with the total length preferably being limited by the ease of preparation and use in the intended recombinant DNA protocol. For example, illustrative polynucleotide segments with total lengths of about 10,000, about 5000, about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated  
25 to be useful in many implementations of this invention.

When comparing polynucleotide sequences, two sequences are said to be "identical" if the sequence of nucleotides in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison  
30 window to identify and compare local regions of sequence similarity. A "comparison

window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, preferably 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

- 5                   Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships.
- 10 In Dayhoff, M.O. (ed.) Atlas of Protein Sequence and Structure, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson,
- 15 E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA* 80:726-730.

- Alternatively, optimal alignment of sequences for comparison may be
- 20 conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics
- 25 Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

- One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402
- 30 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST

2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. In one illustrative example, cumulative scores can be calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=-4 and a comparison of both strands.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides

that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions  
5 and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Therefore, in another embodiment of the invention, a mutagenesis approach, such as site-specific mutagenesis, is employed for the preparation of  
10 immunogenic variants and/or derivatives of the polypeptides described herein. By this approach, specific modifications in a polypeptide sequence can be made through mutagenesis of the underlying polynucleotides that encode them. These techniques provides a straightforward approach to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more  
15 nucleotide sequence changes into the polynucleotide.

Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on  
20 both sides of the deletion junction being traversed. Mutations may be employed in a selected polynucleotide sequence to improve, alter, decrease, modify, or otherwise change the properties of the polynucleotide itself, and/or alter the properties, activity, composition, stability, or primary sequence of the encoded polypeptide.

In certain embodiments of the present invention, the inventors  
25 contemplate the mutagenesis of the disclosed polynucleotide sequences to alter one or more properties of the encoded polypeptide, such as the immunogenicity of a polypeptide vaccine. The techniques of site-specific mutagenesis are well-known in the art, and are widely used to create variants of both polypeptides and polynucleotides. For example, site-specific mutagenesis is often used to alter a specific portion of a DNA  
30 molecule. In such embodiments, a primer comprising typically about 14 to about 25

nucleotides or so in length is employed, with about 5 to about 10 residues on both sides of the junction of the sequence being altered.

As will be appreciated by those of skill in the art, site-specific mutagenesis techniques have often employed a phage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially-available and their use is generally well-known to those skilled in the art. Double-stranded plasmids are also routinely employed in site directed mutagenesis that eliminates the step of transferring the gene of interest from a plasmid to a phage.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double-stranded vector that includes within its sequence a DNA sequence that encodes the desired peptide. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected peptide-encoding DNA segments using site-directed mutagenesis provides a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of peptides and the DNA sequences encoding them may be obtained. For example, recombinant vectors encoding the desired peptide sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants. Specific details regarding these methods and protocols are found in the teachings of Maloy *et al.*, 1994; Segal, 1976; Prokop and Bajpai, 1991; Kuby, 1994; and Maniatis *et al.*, 1982, each incorporated herein by reference, for that purpose.



As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable  
5 signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known  
10 rules of complementary base pairing (see, for example, Watson, 1987). Typically, vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U. S. Patent No. 4,237,224, specifically incorporated herein by reference in its entirety.

15 In another approach for the production of polypeptide variants of the present invention, recursive sequence recombination, as described in U.S. Patent No. 5,837,458, may be employed. In this approach, iterative cycles of recombination and screening or selection are performed to "evolve" individual polynucleotide variants of the invention having, for example, enhanced immunogenic activity.

20 In other embodiments of the present invention, the polynucleotide sequences provided herein can be advantageously used as probes or primers for nucleic acid hybridization. As such, it is contemplated that nucleic acid segments that comprise a sequence region of at least about 15 contiguous nucleotides that has the same sequence as, or is complementary to, a 15 nucleotide long contiguous sequence  
25 disclosed herein will find particular utility. Longer contiguous identical or complementary sequences, *e.g.*, those of about 20, 30, 40, 50, 100, 200, 500, 1000 (including all intermediate lengths) and even up to full length sequences will also be of use in certain embodiments.

The ability of such nucleic acid probes to specifically hybridize to a  
30 sequence of interest will enable them to be of use in detecting the presence of

complementary sequences in a given sample. However, other uses are also envisioned, such as the use of the sequence information for the preparation of mutant species primers, or primers for use in preparing other genetic constructions.

Polynucleotide molecules having sequence regions consisting of  
5 contiguous nucleotide stretches of 10-14, 15-20, 30, 50, or even of 100-200 nucleotides or so (including intermediate lengths as well), identical or complementary to a polynucleotide sequence disclosed herein, are particularly contemplated as hybridization probes for use in, *e.g.*, Southern and Northern blotting. This would allow a gene product, or fragment thereof, to be analyzed, both in diverse cell types and also in  
10 various bacterial cells. The total size of fragment, as well as the size of the complementary stretch(es), will ultimately depend on the intended use or application of the particular nucleic acid segment. Smaller fragments will generally find use in hybridization embodiments, wherein the length of the contiguous complementary region may be varied, such as between about 15 and about 100 nucleotides, but larger  
15 contiguous complementarity stretches may be used, according to the length complementary sequences one wishes to detect.

The use of a hybridization probe of about 15-25 nucleotides in length allows the formation of a duplex molecule that is both stable and selective. Molecules having contiguous complementary sequences over stretches greater than 15 bases in  
20 length are generally preferred, though, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of specific hybrid molecules obtained. One will generally prefer to design nucleic acid molecules having gene-complementary stretches of 15 to 25 contiguous nucleotides, or even longer where desired.

25 Hybridization probes may be selected from any portion of any of the sequences disclosed herein. All that is required is to review the sequences set forth herein, or to any continuous portion of the sequences, from about 15-25 nucleotides in length up to and including the full length sequence, that one wishes to utilize as a probe or primer. The choice of probe and primer sequences may be governed by various

factors. For example, one may wish to employ primers from towards the termini of the total sequence.

Small polynucleotide segments or fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer. Also, fragments may be obtained by application of nucleic acid reproduction technology, such as the PCR™ technology of U. S. Patent 4,683,202 (incorporated herein by reference), by introducing selected sequences into recombinant vectors for recombinant production, and by other recombinant DNA techniques generally known to those of skill in the art of molecular biology.

The nucleotide sequences of the invention may be used for their ability to selectively form duplex molecules with complementary stretches of the entire gene or gene fragments of interest. Depending on the application envisioned, one will typically desire to employ varying conditions of hybridization to achieve varying degrees of selectivity of probe towards target sequence. For applications requiring high selectivity, one will typically desire to employ relatively stringent conditions to form the hybrids, *e.g.*, one will select relatively low salt and/or high temperature conditions, such as provided by a salt concentration of from about 0.02 M to about 0.15 M salt at temperatures of from about 50°C to about 70°C. Such selective conditions tolerate little, if any, mismatch between the probe and the template or target strand, and would be particularly suitable for isolating related sequences.

Of course, for some applications, for example, where one desires to prepare mutants employing a mutant primer strand hybridized to an underlying template, less stringent (reduced stringency) hybridization conditions will typically be needed in order to allow formation of the heteroduplex. In these circumstances, one may desire to employ salt conditions such as those of from about 0.15 M to about 0.9 M salt, at temperatures ranging from about 20°C to about 55°C. Cross-hybridizing species can thereby be readily identified as positively hybridizing signals with respect to control hybridizations. In any case, it is generally appreciated that conditions can be rendered more stringent by the addition of increasing amounts of formamide, which serves to

destabilize the hybrid duplex in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and thus will generally be a method of choice depending on the desired results.

According to another embodiment of the present invention, polynucleotide compositions comprising antisense oligonucleotides are provided. Antisense oligonucleotides have been demonstrated to be effective and targeted inhibitors of protein synthesis, and, consequently, provide a therapeutic approach by which a disease can be treated by inhibiting the synthesis of proteins that contribute to the disease. The efficacy of antisense oligonucleotides for inhibiting protein synthesis is well established. For example, the synthesis of polygalacturonase and the muscarine type 2 acetylcholine receptor are inhibited by antisense oligonucleotides directed to their respective mRNA sequences (U. S. Patent 5,739,119 and U. S. Patent 5,759,829). Further, examples of antisense inhibition have been demonstrated with the nuclear protein cyclin, the multiple drug resistance gene (MDG1), ICAM-1, E-selectin, STK-1, striatal GABA<sub>A</sub> receptor and human EGF (Jaskulski *et al.*, Science. 1988 Jun 10;240(4858):1544-6; Vasanthakumar and Ahmed, Cancer Commun. 1989;1(4):225-32; Peris *et al.*, Brain Res Mol Brain Res. 1998 Jun 15;57(2):310-20; U. S. Patent 5,801,154; U.S. Patent 5,789,573; U. S. Patent 5,718,709 and U.S. Patent 5,610,288). Antisense constructs have also been described that inhibit and can be used to treat a variety of abnormal cellular proliferations, *e.g.* cancer (U. S. Patent 5,747,470; U. S. Patent 5,591,317 and U. S. Patent 5,783,683).

Therefore, in certain embodiments, the present invention provides oligonucleotide sequences that comprise all, or a portion of, any sequence that is capable of specifically binding to polynucleotide sequence described herein, or a complement thereof. In one embodiment, the antisense oligonucleotides comprise DNA or derivatives thereof. In another embodiment, the oligonucleotides comprise RNA or derivatives thereof. In a third embodiment, the oligonucleotides are modified DNAs comprising a phosphorothioated modified backbone. In a fourth embodiment, the oligonucleotide sequences comprise peptide nucleic acids or derivatives thereof. In each case, preferred compositions comprise a sequence region that is complementary,

and more preferably substantially-complementary, and even more preferably, completely complementary to one or more portions of polynucleotides disclosed herein. Selection of antisense compositions specific for a given gene sequence is based upon analysis of the chosen target sequence and determination of secondary structure,  $T_m$ ,  
5 binding energy, and relative stability. Antisense compositions may be selected based upon their relative inability to form dimers, hairpins, or other secondary structures that would reduce or prohibit specific binding to the target mRNA in a host cell. Highly preferred target regions of the mRNA, are those which are at or near the AUG translation initiation codon, and those sequences which are substantially complementary  
10 to 5' regions of the mRNA. These secondary structure analyses and target site selection considerations can be performed, for example, using v.4 of the OLIGO primer analysis software and/or the BLASTN 2.0.5 algorithm software (Altschul *et al.*, Nucleic Acids Res. 1997 Sep 1;25(17):3389-402).

The use of an antisense delivery method employing a short peptide  
15 vector, termed MPG (27 residues), is also contemplated. The MPG peptide contains a hydrophobic domain derived from the fusion sequence of HIV gp41 and a hydrophilic domain from the nuclear localization sequence of SV40 T-antigen (Morris *et al.*, Nucleic Acids Res. 1997 Jul 15;25(14):2730-6). It has been demonstrated that several molecules of the MPG peptide coat the antisense oligonucleotides and can be delivered  
20 into cultured mammalian cells in less than 1 hour with relatively high efficiency (90%). Further, the interaction with MPG strongly increases both the stability of the oligonucleotide to nuclease and the ability to cross the plasma membrane.

According to another embodiment of the invention, the polynucleotide compositions described herein are used in the design and preparation of ribozyme  
25 molecules for inhibiting expression of the tumor polypeptides and proteins of the present invention in tumor cells. Ribozymes are RNA-protein complexes that cleave nucleic acids in a site-specific fashion. Ribozymes have specific catalytic domains that possess endonuclease activity (Kim and Cech, Proc Natl Acad Sci U S A. 1987 Dec;84(24):8788-92; Forster and Symons, Cell. 1987 Apr 24;49(2):211-20). For  
30 example, a large number of ribozymes accelerate phosphoester transfer reactions with a

high degree of specificity, often cleaving only one of several phosphoesters in an oligonucleotide substrate (Cech *et al.*, Cell. 1981 Dec;27(3 Pt 2):487-96; Michel and Westhof, J Mol Biol. 1990 Dec 5;216(3):585-610; Reinhold-Hurek and Shub, Nature. 1992 May 14;357(6374):173-6). This specificity has been attributed to the requirement  
5 that the substrate bind via specific base-pairing interactions to the internal guide sequence ("IGS") of the ribozyme prior to chemical reaction.

Six basic varieties of naturally-occurring enzymatic RNAs are known presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds *in trans* (and thus can cleave other RNA molecules) under physiological conditions. In general,  
10 enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to  
15 cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme is advantageous over many  
20 technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its translation) since the concentration of ribozyme necessary to affect a therapeutic treatment is lower than that of an antisense oligonucleotide. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of  
25 target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme. Similar mismatches in antisense molecules do not prevent their action  
30 (Woolf *et al.*, Proc Natl Acad Sci U S A. 1992 Aug 15;89(16):7305-9). Thus, the

specificity of action of a ribozyme is greater than that of an antisense oligonucleotide binding the same RNA site.

The enzymatic nucleic acid molecule may be formed in a hammerhead, hairpin, a hepatitis  $\delta$  virus, group I intron or RNaseP RNA (in association with an RNA guide sequence) or Neurospora VS RNA motif. Examples of hammerhead motifs are described by Rossi *et al.* Nucleic Acids Res. 1992 Sep 11;20(17):4559-65. Examples of hairpin motifs are described by Hampel *et al.* (Eur. Pat. Appl. Publ. No. EP 0360257), Hampel and Tritz, Biochemistry 1989 Jun 13;28(12):4929-33; Hampel *et al.*, Nucleic Acids Res. 1990 Jan 25;18(2):299-304 and U. S. Patent 5,631,359. An example of the hepatitis  $\delta$  virus motif is described by Perrotta and Been, Biochemistry. 1992 Dec 1;31(47):11843-52; an example of the RNaseP motif is described by Guerrier-Takada *et al.*, Cell. 1983 Dec;35(3 Pt 2):849-57; Neurospora VS RNA ribozyme motif is described by Collins (Saville and Collins, Cell. 1990 May 18;61(4):685-96; Saville and Collins, Proc Natl Acad Sci U S A. 1991 Oct 1;88(19):8826-30; Collins and Olive, Biochemistry. 1993 Mar 23;32(11):2795-9); and an example of the Group I intron is described in (U. S. Patent 4,987,071). All that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart an RNA cleaving activity to the molecule. Thus the ribozyme constructs need not be limited to specific motifs mentioned herein.

Ribozymes may be designed as described in Int. Pat. Appl. Publ. No. WO 93/23569 and Int. Pat. Appl. Publ. No. WO 94/02595, each specifically incorporated herein by reference) and synthesized to be tested *in vitro* and *in vivo*, as described. Such ribozymes can also be optimized for delivery. While specific examples are provided, those in the art will recognize that equivalent RNA targets in other species can be utilized when necessary.

Ribozyme activity can be optimized by altering the length of the ribozyme binding arms, or chemically synthesizing ribozymes with modifications that prevent their degradation by serum ribonucleases (see *e.g.*, Int. Pat. Appl. Publ. No. WO

92/07065; Int. Pat. Appl. Publ. No. WO 93/15187; Int. Pat. Appl. Publ. No. WO 91/03162; Eur. Pat. Appl. Publ. No. 92110298.4; U. S. Patent 5,334,711; and Int. Pat. Appl. Publ. No. WO 94/13688, which describe various chemical modifications that can be made to the sugar moieties of enzymatic RNA molecules), modifications which enhance their efficacy in cells, and removal of stem II bases to shorten RNA synthesis times and reduce chemical requirements.

Sullivan *et al.* (Int. Pat. Appl. Publ. No. WO 94/02595) describes the general methods for delivery of enzymatic RNA molecules. Ribozymes may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, ribozymes may be directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles. Alternatively, the RNA/vehicle combination may be locally delivered by direct inhalation, by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of ribozyme delivery and administration are provided in Int. Pat. Appl. Publ. No. WO 94/02595 and Int. Pat. Appl. Publ. No. WO 93/23569, each specifically incorporated herein by reference.

Another means of accumulating high concentrations of a ribozyme(s) within cells is to incorporate the ribozyme-encoding sequences into a DNA expression vector. Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, *etc.*) present nearby. Prokaryotic RNA polymerase promoters may also be used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells. Ribozymes



expressed from such promoters have been shown to function in mammalian cells. Such transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated vectors), or viral RNA vectors (such as  
5 retroviral, semliki forest virus, sindbis virus vectors).

In another embodiment of the invention, peptide nucleic acids (PNAs) compositions are provided. PNA is a DNA mimic in which the nucleobases are attached to a pseudopeptide backbone (Good and Nielsen, *Antisense Nucleic Acid Drug Dev.* 1997 7(4) 431-37). PNA is able to be utilized in a number methods that  
10 traditionally have used RNA or DNA. Often PNA sequences perform better in techniques than the corresponding RNA or DNA sequences and have utilities that are not inherent to RNA or DNA. A review of PNA including methods of making, characteristics of, and methods of using, is provided by Corey (*Trends Biotechnol* 1997 Jun;15(6):224-9). As such, in certain embodiments, one may prepare PNA sequences  
15 that are complementary to one or more portions of the ACE mRNA sequence, and such PNA compositions may be used to regulate, alter, decrease, or reduce the translation of ACE-specific mRNA, and thereby alter the level of ACE activity in a host cell to which such PNA compositions have been administered.

PNAs have 2-aminoethyl-glycine linkages replacing the normal  
20 phosphodiester backbone of DNA (Nielsen *et al.*, *Science* 1991 Dec 6;254(5037):1497-500; Hanvey *et al.*, *Science*. 1992 Nov 27;258(5087):1481-5; Hyrup and Nielsen, *Bioorg Med Chem*. 1996 Jan;4(1):5-23). This chemistry has three important consequences: firstly, in contrast to DNA or phosphorothioate oligonucleotides, PNAs are neutral molecules; secondly, PNAs are achiral, which avoids the need to develop a  
25 stereoselective synthesis; and thirdly, PNA synthesis uses standard Boc or Fmoc protocols for solid-phase peptide synthesis, although other methods, including a modified Merrifield method, have been used.

PNA monomers or ready-made oligomers are commercially available from PerSeptive Biosystems (Framingham, MA). PNA syntheses by either Boc or  
30 Fmoc protocols are straightforward using manual or automated protocols (Norton *et al.*,

Bioorg Med Chem. 1995 Apr;3(4):437-45). The manual protocol lends itself to the production of chemically modified PNAs or the simultaneous synthesis of families of closely related PNAs.

As with peptide synthesis, the success of a particular PNA synthesis will depend on the properties of the chosen sequence. For example, while in theory PNAs can incorporate any combination of nucleotide bases, the presence of adjacent purines can lead to deletions of one or more residues in the product. In expectation of this difficulty, it is suggested that, in producing PNAs with adjacent purines, one should repeat the coupling of residues likely to be added inefficiently. This should be followed by the purification of PNAs by reverse-phase high-pressure liquid chromatography, providing yields and purity of product similar to those observed during the synthesis of peptides.

Modifications of PNAs for a given application may be accomplished by coupling amino acids during solid-phase synthesis or by attaching compounds that contain a carboxylic acid group to the exposed N-terminal amine. Alternatively, PNAs can be modified after synthesis by coupling to an introduced lysine or cysteine. The ease with which PNAs can be modified facilitates optimization for better solubility or for specific functional requirements. Once synthesized, the identity of PNAs and their derivatives can be confirmed by mass spectrometry. Several studies have made and utilized modifications of PNAs (for example, Norton *et al.*, Bioorg Med Chem. 1995 Apr;3(4):437-45; Petersen *et al.*, J Pept Sci. 1995 May-Jun;1(3):175-83; Orum *et al.*, Biotechniques. 1995 Sep;19(3):472-80; Footer *et al.*, Biochemistry. 1996 Aug 20;35(33):10673-9; Griffith *et al.*, Nucleic Acids Res. 1995 Aug 11;23(15):3003-8; Pardridge *et al.*, Proc Natl Acad Sci U S A. 1995 Jun 6;92(12):5592-6; Boffa *et al.*, Proc Natl Acad Sci U S A. 1995 Mar 14;92(6):1901-5; Gambacorti-Passerini *et al.*, Blood. 1996 Aug 15;88(4):1411-7; Armitage *et al.*, Proc Natl Acad Sci U S A. 1997 Nov 11;94(23):12320-5; Seeger *et al.*, Biotechniques. 1997 Sep;23(3):512-7). U.S. Patent No. 5,700,922 discusses PNA-DNA-PNA chimeric molecules and their uses in diagnostics, modulating protein in organisms, and treatment of conditions susceptible to therapeutics.

Methods of characterizing the antisense binding properties of PNAs are discussed in Rose (Anal Chem. 1993 Dec 15;65(24):3545-9) and Jensen *et al.* (Biochemistry. 1997 Apr 22;36(16):5072-7). Rose uses capillary gel electrophoresis to determine binding of PNAs to their complementary oligonucleotide, measuring the  
5 relative binding kinetics and stoichiometry. Similar types of measurements were made by Jensen *et al.* using BIAcore™ technology.

Other applications of PNAs that have been described and will be apparent to the skilled artisan include use in DNA strand invasion, antisense inhibition, mutational analysis, enhancers of transcription, nucleic acid purification, isolation of  
10 transcriptionally active genes, blocking of transcription factor binding, genome cleavage, biosensors, *in situ* hybridization, and the like.

#### Polynucleotide Identification, Characterization and Expression

Polynucleotide compositions of the present invention may be identified, prepared and/or manipulated using any of a variety of well established techniques (see  
15 generally, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989, and other like references). For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least two fold greater in a tumor than in normal tissue, as determined using a  
20 representative assay provided herein). Such screens may be performed, for example, using the microarray technology of Affymetrix, Inc. (Santa Clara, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polynucleotides may be amplified from cDNA  
25 prepared from cells expressing the proteins described herein, such as tumor cells.

Many template dependent processes are available to amplify a target sequences of interest present in a sample. One of the best known amplification methods is the polymerase chain reaction (PCR™) which is described in detail in U.S. Patent Nos. 4,683,195, 4,683,202 and 4,800,159, each of which is incorporated herein by

reference in its entirety. Briefly, in PCR<sup>TM</sup>, two primer sequences are prepared which are complementary to regions on opposite complementary strands of the target sequence. An excess of deoxynucleoside triphosphates is added to a reaction mixture along with a DNA polymerase (e.g., *Taq* polymerase). If the target sequence is present  
5 in a sample, the primers will bind to the target and the polymerase will cause the primers to be extended along the target sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the target to form reaction products, excess primers will bind to the target and to the reaction product and the process is repeated. Preferably reverse  
10 transcription and PCR<sup>TM</sup> amplification procedure may be performed in order to quantify the amount of mRNA amplified. Polymerase chain reaction methodologies are well known in the art.

Any of a number of other template dependent processes, many of which are variations of the PCR<sup>TM</sup> amplification technique, are readily known and available in  
15 the art. Illustratively, some such methods include the ligase chain reaction (referred to as LCR), described, for example, in Eur. Pat. Appl. Publ. No. 320,308 and U.S. Patent No. 4,883,750; Qbeta Replicase, described in PCT Intl. Pat. Appl. Publ. No. PCT/US87/00880; Strand Displacement Amplification (SDA) and Repair Chain Reaction (RCR). Still other amplification methods are described in Great Britain Pat.  
20 Appl. No. 2 202 328, and in PCT Intl. Pat. Appl. Publ. No. PCT/US89/01025. Other nucleic acid amplification procedures include transcription-based amplification systems (TAS) (PCT Intl. Pat. Appl. Publ. No. WO 88/10315), including nucleic acid sequence based amplification (NASBA) and 3SR. Eur. Pat. Appl. Publ. No. 329,822 describes a nucleic acid amplification process involving cyclically synthesizing single-stranded  
25 RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA). PCT Intl. Pat. Appl. Publ. No. WO 89/06700 describes a nucleic acid sequence amplification scheme based on the hybridization of a promoter/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. Other amplification methods such as "RACE" (Frohman, 1990), and "one-sided PCR" (Ohara,  
30 1989) are also well-known to those of skill in the art.

An amplified portion of a polynucleotide of the present invention may be used to isolate a full length gene from a suitable library (e.g., a tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification.

5 Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (e.g., by nick-translation or end-labeling with  $^{32}\text{P}$ ) using well known techniques. A bacterial or

10 bacteriophage library is then generally screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may

15 be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences can

20 then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, amplification techniques, such as those described above, can be useful for obtaining a full length coding sequence from a partial cDNA sequence. One such amplification technique is inverse PCR (see Triglia et al., *Nucl. Acids Res.*

25 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a

30 known region. The amplified sequences are typically subjected to a second round of

amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (e.g., NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

In other embodiments of the invention, polynucleotide sequences or fragments thereof which encode polypeptides of the invention, or fusion proteins or functional equivalents thereof, may be used in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences that encode substantially the same or a functionally equivalent amino acid sequence may be produced and these sequences may be used to clone and express a given polypeptide.

As will be understood by those of skill in the art, it may be advantageous in some instances to produce polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

Moreover, the polynucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter polypeptide encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. For example, DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. In addition, site-directed mutagenesis may be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, or introduce mutations, and so forth.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of polypeptide activity, it may be useful to encode a chimeric protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the polypeptide-encoding sequence and the heterologous protein sequence, so that the polypeptide may be cleaved and purified away from the heterologous moiety.

Sequences encoding a desired polypeptide may be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers, M. H. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 215-223, Horn, T. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 225-232). Alternatively, the protein itself may be produced using chemical methods to synthesize the amino acid sequence of a polypeptide, or a portion thereof. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, J. Y. et al. (1995) *Science* 269:202-204) and automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin Elmer, Palo Alto, CA).

A newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (e.g., Creighton, T. (1983) *Proteins, Structures and Molecular Principles*, WH Freeman and Co., New York, N.Y.) or other comparable techniques available in the art. The composition of the synthetic peptides may be

confirmed by amino acid analysis or sequencing (e.g., the Edman degradation procedure). Additionally, the amino acid sequence of a polypeptide, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

5           In order to express a desired polypeptide, the nucleotide sequences encoding the polypeptide, or functional equivalents, may be inserted into appropriate expression vector, *i.e.*, a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well known to those skilled in the art may be used to construct expression vectors containing  
10 sequences encoding a polypeptide of interest and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such techniques are described, for example, in Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. et al. (1989) Current Protocols in Molecular Biology, John Wiley & Sons, New York.  
15 N.Y.

A variety of expression vector/host systems may be utilized to contain and express polynucleotide sequences. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid,  
20 or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (e.g., baculovirus); plant cell systems transformed with virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems.

25           The "control elements" or "regulatory sequences" present in an expression vector are those non-translated regions of the vector--enhancers, promoters, 5' and 3' untranslated regions--which interact with host cellular proteins to carry out transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription  
30 and translation elements, including constitutive and inducible promoters, may be used.



For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the PBLUESCRIPT phagemid (Stratagene, La Jolla, Calif.) or PSPORT1 plasmid (Gibco BRL, Gaithersburg, MD) and the like may be used. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses  
5 are generally preferred. If it is necessary to generate a cell line that contains multiple copies of the sequence encoding a polypeptide, vectors based on SV40 or EBV may be advantageously used with an appropriate selectable marker.

In bacterial systems, any of a number of expression vectors may be selected depending upon the use intended for the expressed polypeptide. For example,  
10 when large quantities are needed, for example for the induction of antibodies, vectors which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the sequence encoding the polypeptide of interest may be ligated into the vector in frame with  
15 sequences for the amino-terminal Met and the subsequent 7 residues of .beta.-galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S. M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509); and the like. pGEX Vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are  
20 soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

25 In the yeast, *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. For reviews, see Ausubel et al. (supra) and Grant et al. (1987) *Methods Enzymol.* 153:516-544.

In cases where plant expression vectors are used, the expression of  
30 sequences encoding polypeptides may be driven by any of a number of promoters. For

example, viral promoters such as the 35S and 19S promoters of CaMV may be used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 6:307-311. Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; and Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (see, for example, Hobbs, S. or Murry, L. E. in McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York, N.Y.; pp. 191-196).

An insect system may also be used to express a polypeptide of interest. For example, in one such system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia* larvae. The sequences encoding the polypeptide may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of the polypeptide-encoding sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses may then be used to infect, for example, *S. frugiperda* cells or *Trichoplusia* larvae in which the polypeptide of interest may be expressed (Engelhard, E. K. et al. (1994) *Proc. Natl. Acad. Sci.* 91 :3224-3227).

In mammalian host cells, a number of viral-based expression systems are generally available. For example, in cases where an adenovirus is used as an expression vector, sequences encoding a polypeptide of interest may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain a viable virus which is capable of expressing the polypeptide in infected host cells (Logan, J. and Shenk, T. (1984) *Proc. Natl. Acad. Sci.* 81:3655-3659). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

Specific initiation signals may also be used to achieve more efficient translation of sequences encoding a polypeptide of interest. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding the polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162).

In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells such as CHO, COS, HeLa, MDCK, HEK293, and WI38, which have specific cellular machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.

For long-term, high-yield production of recombinant proteins, stable expression is generally preferred. For example, cell lines which stably express a polynucleotide of interest may be transformed using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer resistance to selection, and its presence allows growth and recovery of cells which

successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine  
5 kinase (Wigler, M. et al. (1977) *Cell* 11:223-32) and adenine phosphoribosyltransferase (Lowy, I. et al. (1990) *Cell* 22:817-23) genes which can be employed in tk.sup.- or aprt.sup.- cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler, M. et al. (1980) *Proc. Natl. Acad. Sci.* 77:3567-70); npt, which  
10 confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin, F. et al (1981) *J. Mol. Biol.* 150:1-14); and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*). Additional selectable genes have been described, for example, trpB, which allows cells to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in  
15 place of histidine (Hartman, S. C. and R. C. Mulligan (1988) *Proc. Natl. Acad. Sci.* 85:8047-51). The use of visible markers has gained popularity with such markers as anthocyanins, beta-glucuronidase and its substrate GUS, and luciferase and its substrate luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system  
20 (Rhodes, C. A. et al. (1995) *Methods Mol. Biol.* 55:121-131).

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding a polypeptide is inserted within a marker gene sequence, recombinant cells containing sequences can be identified by the  
25 absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a polypeptide-encoding sequence under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

Alternatively, host cells that contain and express a desired  
30 polynucleotide sequence may be identified by a variety of procedures known to those of

skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations and protein bioassay or immunoassay techniques which include, for example, membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

5           A variety of protocols for detecting and measuring the expression of polynucleotide-encoded products, using either polyclonal or monoclonal antibodies specific for the product are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal  
10 antibodies reactive to two non-interfering epitopes on a given polypeptide may be preferred for some applications, but a competitive binding assay may also be employed. These and other assays are described, among other places, in Hampton, R. et al. (1990; Serological Methods, a Laboratory Manual, APS Press, St Paul, Minn.) and Maddox, D. E. et al. (1983; *J. Exp. Med.* 158:1211-1216).

15           A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences, or any portions  
20 thereof may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits. Suitable reporter molecules or labels, which may be used  
25 include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with a polynucleotide sequence of interest may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a recombinant cell may be secreted or contained  
30 intracellularly depending on the sequence and/or the vector used. As will be understood

by those of skill in the art, expression vectors containing polynucleotides of the invention may be designed to contain signal sequences which direct secretion of the encoded polypeptide through a prokaryotic or eukaryotic cell membrane. Other recombinant constructions may be used to join sequences encoding a polypeptide of interest to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego, Calif.) between the purification domain and the encoded polypeptide may be used to facilitate purification. One such expression vector provides for expression of a fusion protein containing a polypeptide of interest and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography) as described in Porath, J. et al. (1992, *Prot. Exp. Purif.* 3:263-281) while the enterokinase cleavage site provides a means for purifying the desired polypeptide from the fusion protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D. J. et al. (1993; *DNA Cell Biol.* 12:441-453).

In addition to recombinant production methods, polypeptides of the invention, and fragments thereof, may be produced by direct peptide synthesis using solid-phase techniques (Merrifield J. (1963) *J. Am. Chem. Soc.* 85:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Alternatively, various fragments may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

Antibody Compositions, Fragments Thereof and Other Binding Agents

According to another aspect, the present invention further provides binding agents, such as antibodies and antigen-binding fragments thereof, that exhibit immunological binding to a tumor polypeptide disclosed herein, or to a portion, variant or derivative thereof. An antibody, or antigen-binding fragment thereof, is said to "specifically bind," "immunologically bind," and/or is "immunologically reactive" to a polypeptide of the invention if it reacts at a detectable level (within, for example, an ELISA assay) with the polypeptide, and does not react detectably with unrelated polypeptides under similar conditions.

Immunological binding, as used in this context, generally refers to the non-covalent interactions of the type which occur between an immunoglobulin molecule and an antigen for which the immunoglobulin is specific. The strength, or affinity of immunological binding interactions can be expressed in terms of the dissociation constant ( $K_d$ ) of the interaction, wherein a smaller  $K_d$  represents a greater affinity. Immunological binding properties of selected polypeptides can be quantified using methods well known in the art. One such method entails measuring the rates of antigen-binding site/antigen complex formation and dissociation, wherein those rates depend on the concentrations of the complex partners, the affinity of the interaction, and on geometric parameters that equally influence the rate in both directions. Thus, both the "on rate constant" ( $K_{on}$ ) and the "off rate constant" ( $K_{off}$ ) can be determined by calculation of the concentrations and the actual rates of association and dissociation. The ratio of  $K_{off}/K_{on}$  enables cancellation of all parameters not related to affinity, and is thus equal to the dissociation constant  $K_d$ . See, generally, Davies et al. (1990) Annual Rev. Biochem. 59:439-473.

An "antigen-binding site," or "binding portion" of an antibody refers to the part of the immunoglobulin molecule that participates in antigen binding. The antigen binding site is formed by amino acid residues of the N-terminal variable ("V") regions of the heavy ("H") and light ("L") chains. Three highly divergent stretches within the V regions of the heavy and light chains are referred to as "hypervariable regions" which are interposed between more conserved flanking stretches known as

"framework regions," or "FRs". Thus the term "FR" refers to amino acid sequences which are naturally found between and adjacent to hypervariable regions in immunoglobulins. In an antibody molecule, the three hypervariable regions of a light chain and the three hypervariable regions of a heavy chain are disposed relative to each other in three dimensional space to form an antigen-binding surface. The antigen-binding surface is complementary to the three-dimensional surface of a bound antigen, and the three hypervariable regions of each of the heavy and light chains are referred to as "complementarity-determining regions," or "CDRs."

Binding agents may be further capable of differentiating between patients with and without a cancer, such as prostate cancer, using the representative assays provided herein. For example, antibodies or other binding agents that bind to a tumor protein will preferably generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, more preferably at least about 30% of patients. Alternatively, or in addition, the antibody will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (e.g., blood, sera, sputum, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. Preferably, a statistically significant number of samples with and without the disease will be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation



of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

A number of therapeutically useful molecules are known in the art which comprise antigen-binding sites that are capable of exhibiting immunological binding properties of an antibody molecule. The proteolytic enzyme papain preferentially cleaves IgG molecules to yield several fragments, two of which (the "F(ab)" fragments) each comprise a covalent heterodimer that includes an intact antigen-binding site. The enzyme pepsin is able to cleave IgG molecules to provide several fragments, including the "F(ab')<sub>2</sub>" fragment which comprises both antigen-binding sites. An "Fv" fragment can be produced by preferential proteolytic cleavage of an IgM, and on rare occasions IgG or IgA immunoglobulin molecule. Fv fragments are, however, more commonly derived using recombinant techniques known in the art. The Fv fragment includes a non-covalent V<sub>H</sub>::V<sub>L</sub> heterodimer including an antigen-binding site which retains much of the antigen recognition and binding capabilities of the native antibody molecule. Inbar et al. (1972) Proc. Nat. Acad. Sci. USA 69:2659-2662; Hochman et al. (1976) Biochem 15:2706-2710; and Ehrlich et al. (1980) Biochem 19:4091-4096.

A single chain Fv ("sFv") polypeptide is a covalently linked V<sub>H</sub>::V<sub>L</sub> heterodimer which is expressed from a gene fusion including V<sub>H</sub>- and V<sub>L</sub>-encoding genes linked by a peptide-encoding linker. Huston et al. (1988) Proc. Nat. Acad. Sci. USA 85(16):5879-5883. A number of methods have been described to discern chemical structures for converting the naturally aggregated--but chemically separated--light and heavy polypeptide chains from an antibody V region into an sFv molecule which will fold into a three dimensional structure substantially similar to the structure of an

antigen-binding site. See, *e.g.*, U.S. Pat. Nos. 5,091,513 and 5,132,405, to Huston et al.; and U.S. Pat. No. 4,946,778, to Ladner et al.

Each of the above-described molecules includes a heavy chain and a light chain CDR set, respectively interposed between a heavy chain and a light chain FR set which provide support to the CDRs and define the spatial relationship of the CDRs relative to each other. As used herein, the term "CDR set" refers to the three hypervariable regions of a heavy or light chain V region. Proceeding from the N-terminus of a heavy or light chain, these regions are denoted as "CDR1," "CDR2," and "CDR3" respectively. An antigen-binding site, therefore, includes six CDRs, comprising the CDR set from each of a heavy and a light chain V region. A polypeptide comprising a single CDR, (*e.g.*, a CDR1, CDR2 or CDR3) is referred to herein as a "molecular recognition unit." Crystallographic analysis of a number of antigen-antibody complexes has demonstrated that the amino acid residues of CDRs form extensive contact with bound antigen, wherein the most extensive antigen contact is with the heavy chain CDR3. Thus, the molecular recognition units are primarily responsible for the specificity of an antigen-binding site.

As used herein, the term "FR set" refers to the four flanking amino acid sequences which frame the CDRs of a CDR set of a heavy or light chain V region. Some FR residues may contact bound antigen; however, FRs are primarily responsible for folding the V region into the antigen-binding site, particularly the FR residues directly adjacent to the CDRs. Within FRs, certain amino residues and certain structural features are very highly conserved. In this regard, all V region sequences contain an internal disulfide loop of around 90 amino acid residues. When the V regions fold into a binding-site, the CDRs are displayed as projecting loop motifs which form an antigen-binding surface. It is generally recognized that there are conserved structural regions of FRs which influence the folded shape of the CDR loops into certain "canonical" structures--regardless of the precise CDR amino acid sequence. Further, certain FR residues are known to participate in non-covalent interdomain contacts which stabilize the interaction of the antibody heavy and light chains.

A number of "humanized" antibody molecules comprising an antigen-binding site derived from a non-human immunoglobulin have been described, including chimeric antibodies having rodent V regions and their associated CDRs fused to human constant domains (Winter et al. (1991) *Nature* 349:293-299; Lobuglio et al. (1989) *Proc. Nat. Acad. Sci. USA* 86:4220-4224; Shaw et al. (1987) *J Immunol.* 138:4534-4538; and Brown et al. (1987) *Cancer Res.* 47:3577-3583), rodent CDRs grafted into a human supporting FR prior to fusion with an appropriate human antibody constant domain (Riechmann et al. (1988) *Nature* 332:323-327; Verhoeyen et al. (1988) *Science* 239:1534-1536; and Jones et al. (1986) *Nature* 321:522-525), and rodent CDRs supported by recombinantly veneered rodent FRs (European Patent Publication No. 519,596, published Dec. 23, 1992). These "humanized" molecules are designed to minimize unwanted immunological response toward rodent antihuman antibody molecules which limits the duration and effectiveness of therapeutic applications of those moieties in human recipients.

As used herein, the terms "veneered FRs" and "recombinantly veneered FRs" refer to the selective replacement of FR residues from, *e.g.*, a rodent heavy or light chain V region, with human FR residues in order to provide a xenogeneic molecule comprising an antigen-binding site which retains substantially all of the native FR polypeptide folding structure. Veneering techniques are based on the understanding that the ligand binding characteristics of an antigen-binding site are determined primarily by the structure and relative disposition of the heavy and light chain CDR sets within the antigen-binding surface. Davies et al. (1990) *Ann. Rev. Biochem.* 59:439-473. Thus, antigen binding specificity can be preserved in a humanized antibody only wherein the CDR structures, their interaction with each other, and their interaction with the rest of the V region domains are carefully maintained. By using veneering techniques, exterior (*e.g.*, solvent-accessible) FR residues which are readily encountered by the immune system are selectively replaced with human residues to provide a hybrid molecule that comprises either a weakly immunogenic, or substantially non-immunogenic veneered surface.

The process of veneering makes use of the available sequence data for human antibody variable domains compiled by Kabat et al., in Sequences of Proteins of Immunological Interest, 4th ed., (U.S. Dept. of Health and Human Services, U.S. Government Printing Office, 1987), updates to the Kabat database, and other accessible U.S. and foreign databases (both nucleic acid and protein). Solvent accessibilities of V region amino acids can be deduced from the known three-dimensional structure for human and murine antibody fragments. There are two general steps in veneering a murine antigen-binding site. Initially, the FRs of the variable domains of an antibody molecule of interest are compared with corresponding FR sequences of human variable domains obtained from the above-identified sources. The most homologous human V regions are then compared residue by residue to corresponding murine amino acids. The residues in the murine FR which differ from the human counterpart are replaced by the residues present in the human moiety using recombinant techniques well known in the art. Residue switching is only carried out with moieties which are at least partially exposed (solvent accessible), and care is exercised in the replacement of amino acid residues which may have a significant effect on the tertiary structure of V region domains, such as proline, glycine and charged amino acids.

In this manner, the resultant "veneered" murine antigen-binding sites are thus designed to retain the murine CDR residues, the residues substantially adjacent to the CDRs, the residues identified as buried or mostly buried (solvent inaccessible), the residues believed to participate in non-covalent (*e.g.*, electrostatic and hydrophobic) contacts between heavy and light chain domains, and the residues from conserved structural regions of the FRs which are believed to influence the "canonical" tertiary structures of the CDR loops. These design criteria are then used to prepare recombinant nucleotide sequences which combine the CDRs of both the heavy and light chain of a murine antigen-binding site into human-appearing FRs that can be used to transfect mammalian cells for the expression of recombinant human antibodies which exhibit the antigen specificity of the murine antibody molecule.

In another embodiment of the invention, monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in

this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include  $^{90}\text{Y}$ ,  $^{123}\text{I}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{211}\text{At}$ , and  $^{212}\text{Bi}$ . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, Shigella toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the

intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by  
5 serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody.  
10 Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers that provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent  
15 bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for  
20 radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For  
25 example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

### T Cell Compositions

The present invention, in another aspect, provides T cells specific for a tumor polypeptide disclosed herein, or for a variant or derivative thereof. Such cells

may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the Isolex™ System, available from Nexell Therapeutics, Inc. (Irvine, CA; see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a polypeptide, polynucleotide encoding a polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide of interest. Preferably, a tumor polypeptide or polynucleotide of the invention is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a polypeptide of the present invention if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days will typically result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN-γ) is indicative of T cell activation (see Coligan et



al., Current Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4<sup>+</sup> and/or CD8<sup>+</sup>. Tumor polypeptide-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from a patient, a related donor or an unrelated donor, and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4<sup>+</sup> or CD8<sup>+</sup> T cells that proliferate in response to a tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of the tumor polypeptide can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

#### Pharmaceutical Compositions

In additional embodiments, the present invention concerns formulation of one or more of the polynucleotide, polypeptide, T-cell and/or antibody compositions disclosed herein in pharmaceutically-acceptable carriers for administration to a cell or an animal, either alone, or in combination with one or more other modalities of therapy.

It will be understood that, if desired, a composition as disclosed herein may be administered in combination with other agents as well, such as, *e.g.*, other proteins or polypeptides or various pharmaceutically-active agents. In fact, there is virtually no limit to other components that may also be included, given that the additional agents do not cause a significant adverse effect upon contact with the target cells or host tissues. The compositions may thus be delivered along with various other agents as required in the particular instance. Such compositions may be purified from host cells or other biological sources, or alternatively may be chemically synthesized as

described herein. Likewise, such compositions may further comprise substituted or derivatized RNA or DNA compositions.

Therefore, in another aspect of the present invention, pharmaceutical compositions are provided comprising one or more of the polynucleotide, polypeptide, antibody, and/or T-cell compositions described herein in combination with a physiologically acceptable carrier. In certain preferred embodiments, the pharmaceutical compositions of the invention comprise immunogenic polynucleotide and/or polypeptide compositions of the invention for use in prophylactic and therapeutic vaccine applications. Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Generally, such compositions will comprise one or more polynucleotide and/or polypeptide compositions of the present invention in combination with one or more immunostimulants.

It will be apparent that any of the pharmaceutical compositions described herein can contain pharmaceutically acceptable salts of the polynucleotides and polypeptides of the invention. Such salts can be prepared, for example, from pharmaceutically acceptable non-toxic bases, including organic bases (e.g., salts of primary, secondary and tertiary amines and basic amino acids) and inorganic bases (e.g., sodium, potassium, lithium, ammonium, calcium and magnesium salts).

In another embodiment, illustrative immunogenic compositions, e.g., vaccine compositions, of the present invention comprise DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the polynucleotide may be administered within any of a variety of delivery systems known to those of ordinary skill in the art. Indeed, numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate polynucleotide expression systems will, of course, contain the necessary regulatory DNA regulatory sequences for expression in a patient (such as a suitable promoter and terminating signal). Alternatively, bacterial delivery systems may involve

the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope.

Therefore, in certain embodiments, polynucleotides encoding immunogenic polypeptides described herein are introduced into suitable mammalian host cells for expression using any of a number of known viral-based systems. In one illustrative embodiment, retroviruses provide a convenient and effective platform for gene delivery systems. A selected nucleotide sequence encoding a polypeptide of the present invention can be inserted into a vector and packaged in retroviral particles using techniques known in the art. The recombinant virus can then be isolated and delivered to a subject. A number of illustrative retroviral systems have been described (*e.g.*, U.S. Pat. No. 5,219,740; Miller and Rosman (1989) *BioTechniques* 7:980-990; Miller, A. D. (1990) *Human Gene Therapy* 1:5-14; Scarpa et al. (1991) *Virology* 180:849-852; Burns et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:8033-8037; and Boris-Lawrie and Temin (1993) *Cur. Opin. Genet. Develop.* 3:102-109.

In addition, a number of illustrative adenovirus-based systems have also been described. Unlike retroviruses which integrate into the host genome, adenoviruses persist extrachromosomally thus minimizing the risks associated with insertional mutagenesis (Haj-Ahmad and Graham (1986) *J. Virol.* 57:267-274; Bett et al. (1993) *J. Virol.* 67:5911-5921; Mittereder et al. (1994) *Human Gene Therapy* 5:717-729; Seth et al. (1994) *J. Virol.* 68:933-940; Barr et al. (1994) *Gene Therapy* 1:51-58; Berkner, K. L. (1988) *BioTechniques* 6:616-629; and Rich et al. (1993) *Human Gene Therapy* 4:461-476).

Various adeno-associated virus (AAV) vector systems have also been developed for polynucleotide delivery. AAV vectors can be readily constructed using techniques well known in the art. See, *e.g.*, U.S. Pat. Nos. 5,173,414 and 5,139,941; International Publication Nos. WO 92/01070 and WO 93/03769; Lebkowski et al. (1988) *Molec. Cell. Biol.* 8:3988-3996; Vincent et al. (1990) *Vaccines 90* (Cold Spring Harbor Laboratory Press); Carter, B. J. (1992) *Current Opinion in Biotechnology* 3:533-539; Muzyczka, N. (1992) *Current Topics in Microbiol. and Immunol.* 158:97-129;

Kotin, R. M. (1994) Human Gene Therapy 5:793-801; Shelling and Smith (1994) Gene Therapy 1:165-169; and Zhou et al. (1994) J. Exp. Med. 179:1867-1875.

Additional viral vectors useful for delivering the polynucleotides encoding polypeptides of the present invention by gene transfer include those derived from the pox family of viruses, such as vaccinia virus and avian poxvirus. By way of example, vaccinia virus recombinants expressing the novel molecules can be constructed as follows. The DNA encoding a polypeptide is first inserted into an appropriate vector so that it is adjacent to a vaccinia promoter and flanking vaccinia DNA sequences, such as the sequence encoding thymidine kinase (TK). This vector is then used to transfect cells which are simultaneously infected with vaccinia. Homologous recombination serves to insert the vaccinia promoter plus the gene encoding the polypeptide of interest into the viral genome. The resulting TK.sup.(-) recombinant can be selected by culturing the cells in the presence of 5-bromodeoxyuridine and picking viral plaques resistant thereto.

15 A vaccinia-based infection/transfection system can be conveniently used to provide for inducible, transient expression or coexpression of one or more polypeptides described herein in host cells of an organism. In this particular system, cells are first infected in vitro with a vaccinia virus recombinant that encodes the bacteriophage T7 RNA polymerase. This polymerase displays exquisite specificity in that it only transcribes templates bearing T7 promoters. Following infection, cells are transcribed with the polynucleotide or polynucleotides of interest, driven by a T7 promoter. The polymerase expressed in the cytoplasm from the vaccinia virus recombinant transcribes the transfected DNA into RNA which is then translated into polypeptide by the host translational machinery. The method provides for high level, transient, cytoplasmic production of large quantities of RNA and its translation products. See, *e.g.*, Elroy-Stein and Moss, Proc. Natl. Acad. Sci. USA (1990) 87:6743-6747; Fuerst et al. Proc. Natl. Acad. Sci. USA (1986) 83:8122-8126.

Alternatively, avipoxviruses, such as the fowlpox and canarypox viruses, can also be used to deliver the coding sequences of interest. Recombinant avipox viruses, expressing immunogens from mammalian pathogens, are known to confer

protective immunity when administered to non-avian species. The use of an Avipox vector is particularly desirable in human and other mammalian species since members of the Avipox genus can only productively replicate in susceptible avian species and therefore are not infective in mammalian cells. Methods for producing recombinant  
5 Avipoxviruses are known in the art and employ genetic recombination, as described above with respect to the production of vaccinia viruses. See, e.g., WO 91/12882; WO 89/03429; and WO 92/03545.

Any of a number of alphavirus vectors can also be used for delivery of polynucleotide compositions of the present invention, such as those vectors described in  
10 U.S. Patent Nos. 5,843,723; 6,015,686; 6,008,035 and 6,015,694. Certain vectors based on Venezuelan Equine Encephalitis (VEE) can also be used, illustrative examples of which can be found in U.S. Patent Nos. 5,505,947 and 5,643,576.

Moreover, molecular conjugate vectors, such as the adenovirus chimeric vectors described in Michael et al. *J. Biol. Chem.* (1993) 268:6866-6869 and Wagner et  
15 al. *Proc. Natl. Acad. Sci. USA* (1992) 89:6099-6103, can also be used for gene delivery under the invention.

Additional illustrative information on these and other known viral-based delivery systems can be found, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner  
20 et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al.,  
25 *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993.

In certain embodiments, a polynucleotide may be integrated into the genome of a target cell. This integration may be in a specific location and orientation via homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the  
30 polynucleotide may be stably maintained in the cell as a separate, episomal segment of

DNA. Such polynucleotide segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host cell cycle. The manner in which the expression construct is delivered to a cell and where in the cell the polynucleotide remains is dependent on the type of expression  
5 construct employed.

In another embodiment of the invention, a polynucleotide is administered/delivered as "naked" DNA, for example as described in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable  
10 beads, which are efficiently transported into the cells.

In still another embodiment, a composition of the present invention can be delivered via a particle bombardment approach, many of which have been described. In one illustrative example, gas-driven particle acceleration can be achieved with devices such as those manufactured by Powderject Pharmaceuticals PLC (Oxford, UK)  
15 and Powderject Vaccines Inc. (Madison, WI), some examples of which are described in U.S. Patent Nos. 5,846,796; 6,010,478; 5,865,796; 5,584,807; and EP Patent No. 0500 799. This approach offers a needle-free delivery approach wherein a dry powder formulation of microscopic particles, such as polynucleotide or polypeptide particles, are accelerated to high speed within a helium gas jet generated by a hand held device,  
20 propelling the particles into a target tissue of interest.

In a related embodiment, other devices and methods that may be useful for gas-driven needle-less injection of compositions of the present invention include those provided by Bioject, Inc. (Portland, OR), some examples of which are described in U.S. Patent Nos. 4,790,824; 5,064,413; 5,312,335; 5,383,851; 5,399,163; 5,520,639  
25 and 5,993,412.

According to another embodiment, the pharmaceutical compositions described herein will comprise one or more immunostimulants in addition to the immunogenic polynucleotide, polypeptide, antibody, T-cell and/or APC compositions of this invention. An immunostimulant refers to essentially any substance that enhances  
30 or potentiates an immune response (antibody and/or cell-mediated) to an exogenous

antigen. One preferred type of immunostimulant comprises an adjuvant. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins.

5 Certain adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated

10 sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Within certain embodiments of the invention, the adjuvant composition

15 is preferably one that induces an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- $\gamma$ , TNF $\alpha$ , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as

20 provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman,

25 *Ann. Rev. Immunol.* 7:145-173, 1989.

Certain preferred adjuvants for eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A, together with an aluminum salt. MPL<sup>®</sup> adjuvants are available from Corixa Corporation (Seattle, WA; see, for example, US

30 Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing

oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555, WO 99/33488 and U.S. Patent Nos. 6,008,200 and 5,856,462. Immunostimulatory DNA sequences are also described, for example, by

5 Sato et al., *Science* 273:352, 1996. Another preferred adjuvant comprises a saponin, such as Quil A, or derivatives thereof, including QS21 and QS7 (Aquila Biopharmaceuticals Inc., Framingham, MA); Escin; Digitonin; or *Gypsophila* or *Chenopodium quinoa* saponins. Other preferred formulations include more than one saponin in the adjuvant combinations of the present invention, for example

10 combinations of at least two of the following group comprising QS21, QS7, Quil A,  $\beta$ -escin, or digitonin.

Alternatively the saponin formulations may be combined with vaccine vehicles composed of chitosan or other polycationic polymers, polylactide and polylactide-co-glycolide particles, poly-N-acetyl glucosamine-based polymer matrix,

15 particles composed of polysaccharides or chemically modified polysaccharides, liposomes and lipid-based particles, particles composed of glycerol monoesters, etc. The saponins may also be formulated in the presence of cholesterol to form particulate structures such as liposomes or ISCOMs. Furthermore, the saponins may be formulated together with a polyoxyethylene ether or ester, in either a non-particulate solution or

20 suspension, or in a particulate structure such as a paucilamellar liposome or ISCOM. The saponins may also be formulated with excipients such as Carbopol<sup>R</sup> to increase viscosity, or may be formulated in a dry powder form with a powder excipient such as lactose.

In one preferred embodiment, the adjuvant system includes the

25 combination of a monophosphoryl lipid A and a saponin derivative, such as the combination of QS21 and 3D-MPL<sup>®</sup> adjuvant, as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. Another particularly preferred adjuvant formulation employing QS21, 3D-

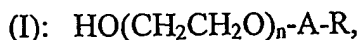


MPL<sup>®</sup> adjuvant and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

Another enhanced adjuvant system involves the combination of a CpG-containing oligonucleotide and a saponin derivative particularly the combination of  
5 CpG and QS21 is disclosed in WO 00/09159. Preferably the formulation additionally comprises an oil in water emulsion and tocopherol.

Additional illustrative adjuvants for use in the pharmaceutical compositions of the invention include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series  
10 of adjuvants (*e.g.*, SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Enhanzyn<sup>®</sup>; Corixa, Hamilton, MT), RC-529 (Corixa, Hamilton, MT) and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described in pending U.S. Patent Application Serial Nos. 08/853,826 and 09/074,720, the disclosures of which are incorporated herein by reference in their entireties, and polyoxyethylene  
15 ether adjuvants such as those described in WO 99/52549A1.

Other preferred adjuvants include adjuvant molecules of the general formula



wherein,  $n$  is 1-50,  $A$  is a bond or  $-\text{C}(\text{O})-$ ,  $R$  is  $\text{C}_{1-50}$  alkyl or Phenyl  $\text{C}_{1-50}$  alkyl.

20 One embodiment of the present invention consists of a vaccine formulation comprising a polyoxyethylene ether of general formula (I), wherein  $n$  is between 1 and 50, preferably 4-24, most preferably 9; the  $R$  component is  $\text{C}_{1-50}$ , preferably  $\text{C}_4\text{-C}_{20}$  alkyl and most preferably  $\text{C}_{12}$  alkyl, and  $A$  is a bond. The concentration of the polyoxyethylene ethers should be in the range 0.1-20%, preferably  
25 from 0.1-10%, and most preferably in the range 0.1-1%. Preferred polyoxyethylene ethers are selected from the following group: polyoxyethylene-9-lauryl ether, polyoxyethylene-9-stearyl ether, polyoxyethylene-8-stearyl ether, polyoxyethylene-4-lauryl ether, polyoxyethylene-35-lauryl ether, and polyoxyethylene-23-lauryl ether. Polyoxyethylene ethers such as polyoxyethylene lauryl ether are described in the Merck  
30 index (12<sup>th</sup> edition: entry 7717). These adjuvant molecules are described in WO

99/52549. The polyoxyethylene ether according to the general formula (I) above may, if desired, be combined with another adjuvant. For example, a preferred adjuvant combination is preferably with CpG as described in the pending UK patent application GB 9820956.2.

5                   According to another embodiment of this invention, an immunogenic composition described herein is delivered to a host via antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or  
10 maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

15                   Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In  
20 general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex*  
25 *vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med.* 4:594-600, 1998).

                  Dendritic cells and progenitors may be obtained from peripheral blood,  
30 bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph

nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF $\alpha$  to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from  
5 peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF $\alpha$ , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature"  
10 cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc $\gamma$  receptor and mannose receptor. The mature  
15 phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide of the  
20 invention (or portion or other variant thereof) such that the encoded polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a pharmaceutical composition comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be  
25 administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or  
30 progenitor cells with the tumor polypeptide, DNA (naked or within a plasmid vector) or

RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will typically vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, mucosal, intravenous, intracranial, intraperitoneal, subcutaneous and intramuscular administration.

Carriers for use within such pharmaceutical compositions are biocompatible, and may also be biodegradable. In certain embodiments, the formulation preferably provides a relatively constant level of active component release. In other embodiments, however, a more rapid rate of release immediately upon administration may be desired. The formulation of such compositions is well within the level of ordinary skill in the art using known techniques. Illustrative carriers useful in this regard include microparticles of poly(lactide-co-glycolide), polyacrylate, latex, starch, cellulose, dextran and the like. Other illustrative delayed-release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (*e.g.*, a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (*see e.g.*, U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

In another illustrative embodiment, biodegradable microspheres (*e.g.*, polylactate polyglycolate) are employed as carriers for the compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268; 5,075,109; 5,928,647; 5,811,128; 5,820,883; 5,853,763;

5,814,344, 5,407,609 and 5,942,252. Modified hepatitis B core protein carrier systems, such as described in WO/99 40934, and references cited therein, will also be useful for many applications. Another illustrative carrier/delivery system employs a carrier comprising particulate-protein complexes, such as those described in U.S. Patent No. 5 5,928,647, which are capable of inducing a class I-restricted cytotoxic T lymphocyte responses in a host.

The pharmaceutical compositions of the invention will often further comprise one or more buffers (*e.g.*, neutral buffered saline or phosphate buffered saline), carbohydrates (*e.g.*, glucose, mannose, sucrose or dextrans), mannitol, proteins, 10 polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (*e.g.*, aluminum hydroxide), solutes that render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate.

15 The pharmaceutical compositions described herein may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers are typically sealed in such a way to preserve the sterility and stability of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, a pharmaceutical composition 20 may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

The development of suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including *e.g.*, oral, parenteral, intravenous, intranasal, and intramuscular administration and 25 formulation, is well known in the art, some of which are briefly discussed below for general purposes of illustration.

In certain applications, the pharmaceutical compositions disclosed herein may be delivered *via* oral administration to an animal. As such, these compositions may be formulated with an inert diluent or with an assimilable edible carrier, or they

may be enclosed in hard- or soft-shell gelatin capsule, or they may be compressed into tablets, or they may be incorporated directly with the food of the diet.

The active compounds may even be incorporated with excipients and used in the form of ingestible tablets, buccal tables, troches, capsules, elixirs, suspensions, syrups, wafers, and the like (see, for example, Mathiowitz *et al.*, Nature 5 1997 Mar 27;386(6623):410-4; Hwang *et al.*, Crit Rev Ther Drug Carrier Syst 1998;15(3):243-84; U. S. Patent 5,641,515; U. S. Patent 5,580,579 and U. S. Patent 5,792,451). Tablets, troches, pills, capsules and the like may also contain any of a variety of additional components, for example, a binder, such as gum tragacanth, acacia, 10 cornstarch, or gelatin; excipients, such as dicalcium phosphate; a disintegrating agent, such as corn starch, potato starch, alginic acid and the like; a lubricant, such as magnesium stearate; and a sweetening agent, such as sucrose, lactose or saccharin may be added or a flavoring agent, such as peppermint, oil of wintergreen, or cherry flavoring. When the dosage unit form is a capsule, it may contain, in addition to 15 materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar, or both. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compounds 20 may be incorporated into sustained-release preparation and formulations.

Typically, these formulations will contain at least about 0.1% of the active compound or more, although the percentage of the active ingredient(s) may, of course, be varied and may conveniently be between about 1 or 2% and about 60% or 70% or more of the weight or volume of the total formulation. Naturally, the amount of 25 active compound(s) in each therapeutically useful composition may be prepared in such a way that a suitable dosage will be obtained in any given unit dose of the compound. Factors such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations will be contemplated by one skilled in the art of preparing such pharmaceutical formulations, and as such, a 30 variety of dosages and treatment regimens may be desirable.

For oral administration, the compositions of the present invention may alternatively be incorporated with one or more excipients in the form of a mouthwash, dentifrice, buccal tablet, oral spray, or sublingual orally-administered formulation. Alternatively, the active ingredient may be incorporated into an oral solution such as one containing sodium borate, glycerin and potassium bicarbonate, or dispersed in a dentifrice, or added in a therapeutically-effective amount to a composition that may include water, binders, abrasives, flavoring agents, foaming agents, and humectants. Alternatively the compositions may be fashioned into a tablet or solution form that may be placed under the tongue or otherwise dissolved in the mouth.

10 In certain circumstances it will be desirable to deliver the pharmaceutical compositions disclosed herein parenterally, intravenously, intramuscularly, or even intraperitoneally. Such approaches are well known to the skilled artisan, some of which are further described, for example, in U. S. Patent 5,543,158; U. S. Patent 5,641,515 and U. S. Patent 5,399,363. In certain embodiments, solutions of the active compounds as free base or pharmacologically acceptable salts may be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions may also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations generally will contain a preservative to prevent the growth of microorganisms.

20 Illustrative pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions (for example, see U. S. Patent 5,466,468). In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (e.g., glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and/or

25  
30

by the use of surfactants. The prevention of the action of microorganisms can be facilitated by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride.

- 5 Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

In one embodiment, for parenteral administration in an aqueous solution, the solution should be suitably buffered if necessary and the liquid diluent first rendered  
10 isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, a sterile aqueous medium that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml  
15 of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. Moreover, for human administration, preparations will of course preferably meet sterility, pyrogenicity, and the general safety and purity  
20 standards as required by FDA Office of Biologics standards.

In another embodiment of the invention, the compositions disclosed herein may be formulated in a neutral or salt form. Illustrative pharmaceutically-acceptable salts include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for  
25 example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be



administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective.

The carriers can further comprise any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption  
5 delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions. The phrase  
10 "pharmaceutically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human.

In certain embodiments, the pharmaceutical compositions may be delivered by intranasal sprays, inhalation, and/or other aerosol delivery vehicles. Methods for delivering genes, nucleic acids, and peptide compositions directly to the  
15 lungs *via* nasal aerosol sprays has been described, *e.g.*, in U. S. Patent 5,756,353 and U. S. Patent 5,804,212. Likewise, the delivery of drugs using intranasal microparticle resins (Takenaga *et al.*, J Controlled Release 1998 Mar 2;52(1-2):81-7) and lysophosphatidyl-glycerol compounds (U. S. Patent 5,725,871) are also well-known in the pharmaceutical arts. Likewise, illustrative transmucosal drug delivery in the form of  
20 a polytetrafluoroethylene support matrix is described in U. S. Patent 5,780,045.

In certain embodiments, liposomes, nanocapsules, microparticles, lipid particles, vesicles, and the like, are used for the introduction of the compositions of the present invention into suitable host cells/organisms. In particular, the compositions of the present invention may be formulated for delivery either encapsulated in a lipid  
25 particle, a liposome, a vesicle, a nanosphere, or a nanoparticle or the like. Alternatively, compositions of the present invention can be bound, either covalently or non-covalently, to the surface of such carrier vehicles.

The formation and use of liposome and liposome-like preparations as potential drug carriers is generally known to those of skill in the art (see for example,  
30 Lasic, Trends Biotechnol 1998 Jul;16(7):307-21; Takakura, Nippon Rinsho 1998

Mar;56(3):691-5; Chandran *et al.*, Indian J Exp Biol. 1997 Aug;35(8):801-9; Margalit, Crit Rev Ther Drug Carrier Syst. 1995;12(2-3):233-61; U.S. Patent 5,567,434; U.S. Patent 5,552,157; U.S. Patent 5,565,213; U.S. Patent 5,738,868 and U.S. Patent 5,795,587, each specifically incorporated herein by reference in its entirety).

5               Liposomes have been used successfully with a number of cell types that are normally difficult to transfect by other procedures, including T cell suspensions, primary hepatocyte cultures and PC 12 cells (Renneisen *et al.*, J Biol Chem. 1990 Sep 25;265(27):16337-42; Muller *et al.*, DNA Cell Biol. 1990 Apr;9(3):221-9). In addition, liposomes are free of the DNA length constraints that are typical of viral-based delivery  
10 systems. Liposomes have been used effectively to introduce genes, various drugs, radiotherapeutic agents, enzymes, viruses, transcription factors, allosteric effectors and the like, into a variety of cultured cell lines and animals. Furthermore, the use of liposomes does not appear to be associated with autoimmune responses or unacceptable toxicity after systemic delivery.

15               In certain embodiments, liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs)).

                  Alternatively, in other embodiments, the invention provides for pharmaceutically-acceptable nanocapsule formulations of the compositions of the  
20 present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (see, for example, Quintanar-Guerrero *et al.*, Drug Dev Ind Pharm. 1998 Dec;24(12):1113-28). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1  $\mu\text{m}$ ) may be designed using polymers able to be degraded *in vivo*. Such particles can be made as described, for  
25 example, by Couvreur *et al.*, Crit Rev Ther Drug Carrier Syst. 1988;5(1):1-20; zur Muhlen *et al.*, Eur J Pharm Biopharm. 1998 Mar;45(2):149-55; Zambaux *et al.* J Controlled Release. 1998 Jan 2;50(1-3):31-40; and U. S. Patent 5,145,684.

Cancer Therapeutic Methods

In further aspects of the present invention, the pharmaceutical compositions described herein may be used for the treatment of cancer, particularly for the immunotherapy of prostate cancer. Within such methods, the pharmaceutical compositions described herein are administered to a patient, typically a warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs. As discussed above, administration of the pharmaceutical compositions may be by any suitable method, including administration by intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intradermal, anal, vaginal, topical and oral routes.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides as provided herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8<sup>+</sup> cytotoxic T lymphocytes and CD4<sup>+</sup> T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The

polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast and/or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see, for example, Cheever et al., Immunological Reviews 157:177, 1997*).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions described herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g., intracutaneous,*

intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 25 µg to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

#### Cancer Detection and Diagnostic Compositions, Methods and Kits

In general, a cancer may be detected in a patient based on the presence of one or more prostate tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, sputum urine and/or tumor biopsies)

obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as prostate cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the  
5 biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a prostate tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in  
10 the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c)  
15 comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding  
20 agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized  
25 binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length prostate tumor proteins and polypeptide portions thereof to which the binding agent binds, as  
30 described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10  $\mu$ g, and preferably about 100 ng to about 1  $\mu$ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized

on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a  
5 different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically  
10 blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact  
15 time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve  
20 equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second  
25 antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of  
30 binding that occurs over a period of time. Unbound detection reagent is then removed



and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

10 To determine the presence or absence of a cancer, such as prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with  
15 samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985,  
20 p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a  
25 signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 $\mu$ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient is incubated with a tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with polypeptide (*e.g.*, 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of tumor polypeptide to serve as a control. For CD4<sup>+</sup> T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8<sup>+</sup> T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a tumor protein of the invention that is at least 10

nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the  
5 diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence as disclosed herein. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis et al., *Cold*  
10 *Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules.  
15 PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold  
20 or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the compositions described herein may be used as markers for the progression of cancer. In this embodiment, assays as described above  
25 for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the

cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound  
5 binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific  
10 for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

15 The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a tumor protein.  
20 Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

25 Alternatively, a kit may be designed to detect the level of mRNA encoding a tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be

present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

5

## EXAMPLES

### EXAMPLE 1

#### ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES

10

This Example describes the isolation of certain prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A<sup>+</sup> RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following  
15 the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A<sup>+</sup> RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen,  
20 Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA), the cDNA was ligated into the EcoRI/NotI site of  
25 pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the  
30 percentage of clones that carried insert, the average insert size and by sequence analysis.

The prostate tumor library contained  $1.64 \times 10^7$  independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained  $3.3 \times 10^6$  independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70  $\mu$ g) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100  $\mu$ l of H<sub>2</sub>O, heat-denatured and mixed with 100  $\mu$ l (100  $\mu$ g) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50  $\mu$ l) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23  $\mu$ l H<sub>2</sub>O to form the driver DNA.

To form the tracer DNA, 10  $\mu$ g prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5  $\mu$ l H<sub>2</sub>O. Tracer DNA was mixed with 15  $\mu$ l driver DNA and 20  $\mu$ l of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12  $\mu$ l H<sub>2</sub>O, mixed with 8  $\mu$ l driver DNA and 20  $\mu$ l of 2 x hybridization buffer, and subjected to a hybridization at 68

<sup>0</sup>C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK<sup>+</sup> (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted  
5 cDNA library (referred to as "prostate subtraction 1").

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems  
10 Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided  
15 in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA),  
20 human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence  
25 for F1-12 (also referred to as P504S). This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108. cDNA splice variants of P504S are provided in SEQ ID NO: 600-605.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described  
30 above with the normal pancreas cDNA library and with the three most abundant genes



in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1  $\mu$ g each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114. L1-12 is also referred to as P501S. A cDNA splice variant of P501S is provided in SEQ ID NO: 606.

5           In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (referred to as "prostate subtraction 2"). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively.

10       Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (referred to as "prostate subtraction spike 2") was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17,

15       pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences

20       with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones,

25       referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and

30       1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the

isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810  
5 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

Additional studies with prostate subtraction spike 2 resulted in the isolation of three more clones. Their sequences were determined as described above and compared to the most recent GenBank. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280  
10 (SEQ ID NO: 317, 319, and 320, respectively). Further analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were over-expressed in most prostate tumors and prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

An additional subtraction was performed by subtracting a normal  
15 prostate cDNA library with normal pancreas cDNA (referred to as "prostate subtraction 3"). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the  
20 isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of  
25 polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS:  
30 103 and 104, respectively). Further analysis of the isolated clones led to the

determination of extended cDNA sequences for 1D-4309, 1D-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction  
5 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested,  
10 reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other  
15 normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously  
20 identified ESTs.

Additional, studies led to the isolation of the full-length cDNA sequence for P509S. This sequence is provided in SEQ ID NO: 332, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 339. Two variant full-length cDNA sequences for P510S are provided in SEQ ID NO: 535 and 536, with the  
25 corresponding predicted amino acid sequences being provided in SEQ ID NO: 537 and 538, respectively. Additional splice variants of P510S are provided in SEQ ID NO: 598 and 599.

## EXAMPLE 2

## DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE-SPECIFIC POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the  
5 representative prostate-specific polypeptides F1-16, H1-1, J1-17 (also referred to as P502S), L1-12 (also referred to as P501S), F1-12 (also referred to as P504S) and N1-1862 (also referred to as P503S) were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor  
10 tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2  $\mu$ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR,  $\beta$ -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the  
15 first strand cDNAs were prepared and RT-PCR assays were performed using  $\beta$ -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the  $\beta$ -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the  $\beta$ -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was  
20 minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver,  
25 lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon  
30 and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin,

small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 (P502S) and L1-12 (P501S) appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 (P503S) was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17 (P502S), N1-1862 (P503S) and L1-12 (P501S) are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 (P504S) is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 (P501S) is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 (P502S) was detected in two prostate tumors and not in the other tissues tested. N1-1862 (P503S) was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 (P504S) was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The microarray technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 (P501S) was found to be

over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 (P504S) were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 (P503S) was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Further microarray analysis to specifically address the extent to which P501S (SEQ ID NO: 110) was expressed in breast tumor revealed moderate over-expression not only in breast tumor, but also in metastatic breast tumor (2/31), with negligible to low expression in normal tissues. This data suggests that P501S may be over-expressed in various breast tumors as well as in prostate tumors.

The expression levels of 32 ESTs (expressed sequence tags) described by Vasmatazis *et al.* (*Proc. Natl. Acad. Sci. USA* 95:300-304, 1998) in a variety of tumor and normal tissues were examined by microarray technology as described above. Two of these clones (referred to as P1000C and P1001C) were found to be over-expressed in prostate tumor and normal prostate, and expressed at low to undetectable levels in all other tissues tested (normal aorta, thymus, resting and activated PBMC, epithelial cells, spinal cord, adrenal gland, fetal tissues, skin, salivary gland, large intestine, bone marrow, liver, lung, dendritic cells, stomach, lymph nodes, brain, heart, small intestine, skeletal muscle, colon and kidney. The determined cDNA sequences for P1000C and P1001C are provided in SEQ ID NO: 384 and 472, respectively. The sequence of P1001C was found to show some homology to the previously isolated Human mRNA for JM27 protein. Subsequent comparison of the sequence of SEQ ID NO: 384 with sequences in the public databases, led to the identification of a full-length cDNA sequence of P1000C (SEQ ID NO: 786), which encodes a 492 amino acid sequence. Analysis of the amino acid sequence using the PSORT II program led to the

identification of a putative transmembrane domain from amino acids 84-100. The cDNA sequence of the open reading frame of P1000C, including the stop codon, is provided in SEQ ID NO: 787, with the open reading frame without the stop codon being provided in SEQ ID NO: 788. The full-length amino acid sequence of P1000C is  
5 provided in SEQ ID NO: 789. SEQ ID NO: 790 and 791 represent amino acids 1-100 and 100-492 of P1000C, respectively.

The expression of the polypeptide encoded by the full length cDNA sequence for F1-12 (also referred to as P504S; SEQ ID NO: 108) was investigated by immunohistochemical analysis. Rabbit-anti-P504S polyclonal antibodies were  
10 generated against the full length P504S protein by standard techniques. Subsequent isolation and characterization of the polyclonal antibodies were also performed by techniques well known in the art. Immunohistochemical analysis showed that the P504S polypeptide was expressed in 100% of prostate carcinoma samples tested (n=5).

The rabbit-anti-P504S polyclonal antibody did not appear to label benign  
15 prostate cells with the same cytoplasmic granular staining, but rather with light nuclear staining. Analysis of normal tissues revealed that the encoded polypeptide was found to be expressed in some, but not all normal human tissues. Positive cytoplasmic staining with rabbit-anti-P504S polyclonal antibody was found in normal human kidney, liver, brain, colon and lung-associated macrophages, whereas heart and bone marrow were  
20 negative.

This data indicates that the P504S polypeptide is present in prostate cancer tissues, and that there are qualitative and quantitative differences in the staining between benign prostatic hyperplasia tissues and prostate cancer tissues, suggesting that this polypeptide may be detected selectively in prostate tumors and therefore be useful  
25 in the diagnosis of prostate cancer.



## EXAMPLE 3

ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC  
POLYPEPTIDES BY PCR-BASED SUBTRACTION

5           A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The  
10   resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

          Fifty-nine positive clones were sequenced. Comparison of the DNA  
15   sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO: 41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID  
20   NO: 46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

          Further studies employing the sequence of SEQ ID NO: 67 as a probe in standard full-length cloning methods, resulted in the isolation of three cDNA sequences  
25   which appear to be splice variants of P80 (also known as P704P). These sequences are provided in SEQ ID NO: 620-622.

          Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant homologies to known sequences. The determined cDNA  
30   sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145,

147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. Larger cDNA clones  
5 containing the P20 sequence represent splice variants of a gene referred to as P703P. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The determined cDNA sequence for an extended spliced form of P703 is  
10 provided in SEQ ID NO: 225. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine  
15 and brain), and activated and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed  
20 comparable expression. P20, a portion of the P703P gene, was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor  
25 compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal  
30 prostate and prostate tumor, compared to six of twelve other normal tissues tested.

Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and  
5 normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-  
10 h11, 9-f12 and 9-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, 9-f12 and 9-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in  
15 the gene bank revealed no significant homologies to the sequence of 9-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and 9-f12 were found to show some homology to previously identified genes. Further characterization of 7-G6 and 8-G3 showed identity to the known genes PAP and PSA, respectively.

20 mRNA expression levels for these clones were determined using the micro-array technology described above. The clones 7-G6, 8-G3, 8-B5, 8-B6, 8-D4, 8-D9, 9-F3, 9-F12, 9-H3, 10-A2, 10-A4, 11-C9 and 11-F2 were found to be over-expressed in prostate tumor and normal prostate, with expression in other tissues tested being low or undetectable. Increased expression of 8-F11 was seen in prostate tumor  
25 and normal prostate, bladder, skeletal muscle and colon. Increased expression of 10-H10 was seen in prostate tumor and normal prostate, bladder, lung, colon, brain and large intestine. Increased expression of 9-B1 was seen in prostate tumor, breast tumor, and normal prostate, salivary gland, large intestine and skin, with increased expression of 11-C8 being seen in prostate tumor, and normal prostate and large intestine.

An additional cDNA fragment derived from the PCR-based normal prostate subtraction, described above, was found to be prostate specific by both microarray technology and RT-PCR. The determined cDNA sequence of this clone (referred to as 9-A11) is provided in SEQ ID NO: 226. Comparison of this sequence with those  
5 in the public databases revealed 99% identity to the known gene HOXB13.

Further studies led to the isolation of the clones 8-C6 and 8-H7. The determined cDNA sequences for these clones are provided in SEQ ID NO: 227 and 228, respectively. These sequences were found to show some homology to previously isolated ESTs.

10 PCR and hybridization-based methodologies were employed to obtain longer cDNA sequences for clone P20 (also referred to as P703P), yielding three additional cDNA fragments that progressively extend the 5' end of the gene. These fragments, referred to as P703PDE5, P703P6.26, and P703PX-23 (SEQ ID NO: 326, 328 and 330, with the predicted corresponding amino acid sequences being provided in  
15 SEQ ID NO: 327, 329 and 331, respectively) contain additional 5' sequence. P703PDE5 was recovered by screening of a cDNA library (#141-26) with a portion of P703P as a probe. P703P6.26 was recovered from a mixture of three prostate tumor cDNAs and P703PX\_23 was recovered from cDNA library (#438-48). Together, the additional sequences include all of the putative mature serine protease along with part of  
20 the putative signal sequence. The full-length cDNA sequence for P703P is provided in SEQ ID NO: 524, with the corresponding amino acid sequence being provided in SEQ ID NO: 525.

Using computer algorithms, the following regions of P703P were predicted to represent potential HLA A2-binding CTL epitopes: amino acids 164-172  
25 of SEQ ID NO: 525 (SEQ ID NO: 723); amino acids 160-168 of SEQ ID NO: 525 (SEQ ID NO: 724); amino acids 239-247 of SEQ ID NO: 525 (SEQ ID NO: 725); amino acids 118-126 of SEQ ID NO: 525 (SEQ ID NO: 726); amino acids 112-120 of SEQ ID NO: 525 (SEQ ID NO: 727); amino acids 155-164 of SEQ ID NO: 525 (SEQ ID NO: 728); amino acids 117-126 of SEQ ID NO: 525 (SEQ ID NO: 729); amino acids  
30 164-173 of SEQ ID NO: 525 (SEQ ID NO: 730); amino acids 154-163 of SEQ ID NO:

525 (SEQ ID NO: 731); amino acids 163-172 of SEQ ID NO: 525 (SEQ ID NO: 732); amino acids 58-66 of SEQ ID NO: 525 (SEQ ID NO: 733); and amino acids 59-67 of SEQ ID NO: 525 (SEQ ID NO: 734).

P703P was found to show some homology to previously identified  
5 proteases, such as thrombin. The thrombin receptor has been shown to be preferentially expressed in highly metastatic breast carcinoma cells and breast carcinoma biopsy samples. Introduction of thrombin receptor antisense cDNA has been shown to inhibit the invasion of metastatic breast carcinoma cells in culture. Antibodies against thrombin receptor inhibit thrombin receptor activation and thrombin-induced platelet  
10 activation. Furthermore, peptides that resemble the receptor's tethered ligand domain inhibit platelet aggregation by thrombin. P703P may play a role in prostate cancer through a protease-activated receptor on the cancer cell or on stromal cells. The potential trypsin-like protease activity of P703P may either activate a protease-activated receptor on the cancer cell membrane to promote tumorigenesis or activate a protease-  
15 activated receptor on the adjacent cells (such as stromal cells) to secrete growth factors and/or proteases (such as matrix metalloproteinases) that could promote tumor angiogenesis, invasion and metastasis. P703P may thus promote tumor progression and/or metastasis through the activation of protease-activated receptor. Polypeptides and antibodies that block the P703P-receptor interaction may therefore be usefully  
20 employed in the treatment of prostate cancer.

To determine whether P703P expression increases with increased severity of Gleason grade, an indicator of tumor stage, quantitative PCR analysis was performed on prostate tumor samples with a range of Gleason scores from 5 to > 8. The mean level of P703P expression increased with increasing Gleason score, indicating that  
25 P703P expression may correlate with increased disease severity.

Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known GenBank sequences. The determined cDNA sequences  
30 for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are

provided in SEQ ID NO: 307-311, 313 and 315, respectively. The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to  
5 normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression levels in all normal tissues. Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression  
10 in normal prostate.

Further studies led to the isolation of an extended cDNA sequence for P712P (SEQ ID NO: 552). The amino acid sequences encoded by 16 predicted open reading frames present within the sequence of SEQ ID NO: 552 are provided in SEQ ID NO: 553-568.

15 The full-length cDNA for P711P was obtained by employing the partial sequence of SEQ ID NO: 307 to screen a prostate cDNA library. Specifically, a directionally cloned prostate cDNA library was prepared using standard techniques. One million colonies of this library were plated onto LB/Amp plates. Nylon membrane filters were used to lift these colonies, and the cDNAs which were picked up by these  
20 filters were denatured and cross-linked to the filters by UV light. The P711P cDNA fragment of SEQ ID NO: 307 was radio-labeled and used to hybridize with these filters. Positive clones were selected, and cDNAs were prepared and sequenced using an automatic Perkin Elmer/Applied Biosystems sequencer. The determined full-length sequence of P711P is provided in SEQ ID NO: 382, with the corresponding predicted  
25 amino acid sequence being provided in SEQ ID NO: 383.

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent GenBank, P707P was found to be a splice  
30 variant of the known gene HoxB13. In contrast, no significant homologies to P714P

were found. Further studies employing the sequence of SEQ ID NO: 334 as a probe in standard full-length cloning methods, resulted in an extended cDNA sequence for P714P. This sequence is provided in SEQ ID NO: 619. This sequence was found to show some homology to the gene that encodes human ribosomal L23A protein.

5 Clones 8-B3, P89, P98, P130 and P201 (as disclosed in U.S. Patent Application No. 09/020,956, filed February 9, 1998) were found to be contained within one contiguous sequence, referred to as P705P (SEQ ID NO: 335, with the predicted amino acid sequence provided in SEQ ID NO: 336), which was determined to be a splice variant of the known gene NKX 3.1.

10 Further studies on P775P resulted in the isolation of four additional sequences (SEQ ID NO: 473-476) which are all splice variants of the P775P gene. The sequence of SEQ ID NO: 474 was found to contain two open reading frames (ORFs). The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 477 and 478. The cDNA sequence of SEQ ID NO: 475 was found to contain an  
15 ORF which encodes the amino acid sequence of SEQ ID NO: 479. The cDNA sequence of SEQ ID NO: 473 was found to contain four ORFs. The predicted amino acid sequences encoded by these ORFs are provided in SEQ ID NO: 480-483. Additional splice variants of P775P are provided in SEQ ID NO: 593-597.

Subsequent studies led to the identification of a genomic region on  
20 chromosome 22q11.2, known as the Cat Eye Syndrome region, that contains the five prostate genes P704P, P712P, P774P, P775P and B305D. The relative location of each of these five genes within the genomic region is shown in Fig. 10. This region may therefore be associated with malignant tumors; and other potential tumor genes may be contained within this region. These studies also led to the identification of a potential  
25 open reading frame (ORF) for P775P (provided in SEQ ID NO: 533), which encodes the amino acid sequence of SEQ ID NO: 534.

Comparison of the clone of SEQ ID NO: 325 (referred to as P558S) with sequences in the GenBank and GeneSeq DNA databases showed that P558S is identical to the prostate-specific transglutaminase gene, which is known to have two forms. The  
30 full-length sequences for the two forms are provided in SEQ ID NO: 630 and 631, with

the corresponding amino acid sequences being provided in SEQ ID NO: 632 and 633, respectively. The cDNA sequence of SEQ ID NO: 631 has a 15 pair base insert, resulting in a 5 amino acid insert in the corresponding amino acid sequence (SEQ ID NO: 633). This insert is not present in the sequence of SEQ ID NO: 630.

5                   Further studies on P768P (SEQ ID NO: 315) led to the identification of the putative full-length open reading frame (ORF). The cDNA sequence of the ORF with stop codon is provided in SEQ ID NO: 764. The cDNA sequence of the ORF without stop codon is provided in SEQ ID NO: 765, with the corresponding amino acid sequence being provided in SEQ ID NO: 766. This sequence was found to show 86%  
10 identity to a rat calcium transporter protein, indicating that P768P may represent a human calcium transporter protein. The locations of transmembrane domains within P768P were predicted using the PSORT II computer algorithm. Six transmembrane domains were predicted at amino acid positions 118-134, 172-188, 211-227, 230-246, 282-298 and 348-364. The amino acid sequences of SEQ ID NO: 767-772 represent  
15 amino acids 1-134, 135-188, 189-227, 228-246, 247-298 and 299-511 of P768P, respectively.

#### EXAMPLE 4

##### SYNTHESIS OF POLYPEPTIDES

20

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of  
25 conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid  
30 (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of



0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

5

## EXAMPLE 5

### FURTHER ISOLATION AND CHARACTERIZATION OF PROSTATE-SPECIFIC POLYPEPTIDES BY PCR-BASED SUBTRACTION

10           A cDNA library generated from prostate primary tumor mRNA as described above was subtracted with cDNA from normal prostate. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were separately digested with five restriction enzymes that recognize six-nucleotide  
15   restriction sites (MluI, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

20           The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate  
25   hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences  
30   which could be used as templates for PCR amplification with adaptor-specific primers.

The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich  
5 differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are overexpressed in prostate tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.

10 In addition to genes known to be overexpressed in prostate tumor, seventy-seven further clones were identified. Sequences of these partial cDNAs are provided in SEQ ID NO: 29 to 305. Most of these clones had no significant homology to database sequences. Exceptions were JPTPN23 (SEQ ID NO: 231; similarity to pig valosin-containing protein), JPTPN30 (SEQ ID NO: 234; similarity to rat mRNA for  
15 proteasome subunit), JPTPN45 (SEQ ID NO: 243; similarity to rat *norvegicus* cytosolic NADP-dependent isocitrate dehydrogenase), JPTPN46 (SEQ ID NO: 244; similarity to human subclone H8 4 d4 DNA sequence), JP1D6 (SEQ ID NO: 265; similarity to *G. gallus* dynein light chain-A), JP8D6 (SEQ ID NO: 288; similarity to human BAC clone RG016J04), JP8F5 (SEQ ID NO: 289; similarity to human subclone H8 3 b5 DNA  
20 sequence), and JP8E9 (SEQ ID NO: 299; similarity to human Alu sequence).

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most recent release of GenBank revealed no significant  
25 homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most  
30 prostate tumors and BPH tissues by a factor of three or greater, with elevated expression

seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

5 Further analysis, by microarray as described above, of the PT-PN PCR subtraction library and of a DNA subtraction library containing cDNA from prostate tumor subtracted with a pool of normal tissue cDNAs, led to the isolation of 27 additional clones (SEQ ID NO: 340-365 and 381) which were determined to be over-expressed in prostate tumor. The clones of SEQ ID NO: 341, 342, 345, 347, 348, 349,  
10 351, 355-359, 361, 362 and 364 were also found to be expressed in normal prostate. Expression of all 26 clones in a variety of normal tissues was found to be low or undetectable, with the exception of P544S (SEQ ID NO: 356) which was found to be expressed in small intestine. Of the 26 clones, 11 (SEQ ID NO: 340-349 and 362) were found to show some homology to previously identified sequences. No significant  
15 homologies were found to the clones of SEQ ID NO: 350, 351, 353-361, and 363-365.

Comparison of the sequence of SEQ ID NO: 362 with sequences in the GenBank and GeneSeq DNA databases showed that this clone (referred to as P788P) is identical to GeneSeq Accession No. X27262, which encodes a protein found in the GeneSeq protein Accession No. Y00931. The full length cDNA sequence of P788P is  
20 provided in SEQ ID NO: 634, with the corresponding predicted amino acid being provided in SEQ ID NO: 635. Subsequently, a full-length cDNA sequence for P788P that contains polymorphisms not found in the sequence of SEQ ID NO: 634, was cloned multiple times by PCR amplification from cDNA prepared from several RNA templates from three individuals. This determined cDNA sequence of this polymorphic variant of  
25 P788P is provided in SEQ ID NO: 636, with the corresponding amino acid sequence being provided in SEQ ID NO: 637. The sequence of SEQ ID NO: 637 differs from that of SEQ ID NO: 635 by six amino acid residues. The P788P protein has 7 potential transmembrane domains at the C-terminal portion and is predicted to be a plasma membrane protein with an extracellular N-terminal region.

Further studies on the clone of SEQ ID NO: 352 (referred to as P790P) led to the isolation of the full-length cDNA sequence of SEQ ID NO: 526. The corresponding predicted amino acid is provided in SEQ ID NO: 527. Data from two quantitative PCR experiments indicated that P790P is over-expressed in 11/15 tested prostate tumor samples and is expressed at low levels in spinal cord, with no expression being seen in all other normal samples tested. Data from further PCR experiments and microarray experiments showed over-expression in normal prostate and prostate tumor with little or no expression in other tissues tested. P790P was subsequently found to show significant homology to a previously identified G-protein coupled prostate tissue receptor.

Additional studies on the clone of SEQ ID NO: 354 (referred to as P776P) led to the isolation of an extended cDNA sequence, provided in SEQ ID NO: 569. The determined cDNA sequences of three additional splice variants of P776P are provided in SEQ ID NO: 570-572. The amino acid sequences encoded by two predicted open reading frames (ORFs) contained within SEQ ID NO: 570, one predicted ORF contained within SEQ ID NO: 571, and 11 predicted ORFs contained within SEQ ID NO: 569, are provided in SEQ ID NO: 573-586, respectively. Further studies led to the isolation of the full-length sequence for the clone of SEQ ID NO: 570 (provided in SEQ ID NO: 737). Full-length cloning efforts on the clone of SEQ ID NO: 571 led to the isolation of two sequences (provided in SEQ ID NO: 738 and 739), representing a single clone, that are identical with the exception of a polymorphic insertion/deletion at position 1293. Specifically, the clone of SEQ ID NO: 739 (referred to as clone F1) has a C at position 1293. The clone of SEQ ID NO: 738 (referred to as clone F2) has a single base pair deletion at position 1293. The predicted amino acid sequences encoded by 5 open reading frames located within SEQ ID NO: 737 are provided in SEQ ID NO: 740-744, with the predicted amino acid sequences encoded by the clone of SEQ ID NO: 738 and 739 being provided in SEQ ID NO: 745-750.

Comparison of the cDNA sequences for the clones P767P (SEQ ID NO: 314) and P777P (SEQ ID NO: 350) with sequences in the GenBank human EST database showed that the two clones matched many EST sequences in common,

suggesting that P767P and P777P may represent the same gene. A DNA consensus sequence derived from a DNA sequence alignment of P767P, P777P and multiple EST clones is provided in SEQ ID NO: 587. The amino acid sequences encoded by three putative ORFs located within SEQ ID NO: 587 are provided in SEQ ID NO: 588-590.

5           The clone of SEQ ID NO: 342 (referred to as P789P) was found to show homology to a previously identified gene. The full length cDNA sequence for P789P and the corresponding amino acid sequence are provided in SEQ ID NO: 735 and 736, respectively.

10

## EXAMPLE 6

## PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

6.1. This Example illustrates the preparation of a CTL cell line specific for cells expressing the P502S gene.

15           Mice expressing the transgene for human HLA A2Kb (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with P2S#12 peptide (VLGWVAEL; SEQ ID NO: 306), which is derived from the P502S gene (also referred to herein as J1-17, SEQ ID NO: 8), as described by Theobald et al., *Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995 with the following modifications. Mice were  
20 immunized with 100µg of P2S#12 and 120µg of an I-A<sup>b</sup> binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and using a nylon mesh single cell suspensions prepared. Cells were then resuspended at  $6 \times 10^6$  cells/ml in complete media (RPMI-1640; Gibco BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium  
25 pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL),  $2 \times 10^{-5}$  M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) P2S#12-pulsed (5mg/ml P2S#12 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). Six days later, cells ( $5 \times 10^5$ /ml) were  
30 restimulated with  $2.5 \times 10^6$ /ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells

(Sherman et al, *Science* 258:815-818, 1992) and  $3 \times 10^6$ /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20U/ml IL-2. Cells continued to be restimulated on a weekly basis as described, in preparation for cloning the line.

P2S#12 line was cloned by limiting dilution analysis with peptide pulsed  
5 EL4 A2Kb tumor cells ( $1 \times 10^4$  cells/ well) as stimulators and A2 transgenic spleen cells as feeders ( $5 \times 10^5$  cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, clones that were growing were isolated and maintained in culture. Several of these clones demonstrated significantly higher reactivity (lysis) against human fibroblasts (HLA A2Kb expressing) transduced with  
10 P502S than against control fibroblasts. An example is presented in Figure 1.

This data indicates that P2S #12 represents a naturally processed epitope of the P502S protein that is expressed in the context of the human HLA A2Kb molecule.

15 6.2. This Example illustrates the preparation of murine CTL lines and CTL clones specific for cells expressing the P501S gene.

This series of experiments were performed similarly to that described above. Mice were immunized with the P1S#10 peptide (SEQ ID NO: 337), which is  
20 derived from the P501S gene (also referred to herein as L1-12, SEQ ID NO: 110). The P1S#10 peptide was derived by analysis of the predicted polypeptide sequence for P501S for potential HLA-A2 binding sequences as defined by published HLA-A2 binding motifs (Parker, KC, et al, *J. Immunol.*, 152:163, 1994). P1S#10 peptide was synthesized as described in Example 4, and empirically tested for HLA-A2 binding  
25 using a T cell based competition assay. Predicted A2 binding peptides were tested for their ability to compete HLA-A2 specific peptide presentation to an HLA-A2 restricted CTL clone (D150M58), which is specific for the HLA-A2 binding influenza matrix peptide fluM58. D150M58 CTL secretes TNF in response to self-presentation of peptide fluM58. In the competition assay, test peptides at 100-200  $\mu$ g/ml were added to  
30 cultures of D150M58 CTL in order to bind HLA-A2 on the CTL. After thirty minutes,

CTL cultured with test peptides, or control peptides, were tested for their antigen dose response to the fluM58 peptide in a standard TNF bioassay. As shown in Figure 3, peptide P1S#10 competes HLA-A2 restricted presentation of fluM58, demonstrating that peptide P1S#10 binds HLA-A2.

5 Mice expressing the transgene for human HLA A2Kb were immunized as described by Theobald et al. (*Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995) with the following modifications. Mice were immunized with 62.5 $\mu$ g of P1S #10 and 120 $\mu$ g of an I-A<sup>b</sup> binding peptide derived from Hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and single  
10 cell suspensions prepared using a nylon mesh. Cells were then resuspended at  $6 \times 10^6$  cells/ml in complete media (as described above) and cultured in the presence of irradiated (3000 rads) P1S#10-pulsed (2 $\mu$ g/ml P1S#10 and 10mg/ml  $\beta$ 2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7 $\mu$ g/ml dextran sulfate and 25 $\mu$ g/ml LPS for 3 days). Six days later cells ( $5 \times 10^5$ /ml) were restimulated  
15 with  $2.5 \times 10^6$ /ml peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells, as described above, and  $3 \times 10^6$ /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20 U/ml IL-2. Cells were restimulated on a weekly basis in preparation for cloning. After three rounds of *in vitro* stimulations, one line was generated that recognized P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat targets as  
20 shown in Figure 4.

A P1S#10-specific CTL line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells ( $1 \times 10^4$  cells/ well) as stimulators and A2 transgenic spleen cells as feeders ( $5 \times 10^5$  cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, viable clones were  
25 isolated and maintained in culture. As shown in Figure 5, five of these clones demonstrated specific cytolytic reactivity against P501S-transduced Jurkat A2Kb targets. This data indicates that P1S#10 represents a naturally processed epitope of the P501S protein that is expressed in the context of the human HLA-A2.1 molecule.

## EXAMPLE 7

PRIMING OF CTL *IN VIVO* USING NAKED DNA IMMUNIZATION

## WITH A PROSTATE ANTIGEN

The prostate-specific antigen L1-12, as described above, is also referred  
5 to as P501S. HLA A2Kb Tg mice (provided by Dr L. Sherman, The Scripps Research  
Institute, La Jolla, CA) were immunized with 100 µg P501S in the vector VR1012  
either intramuscularly or intradermally. The mice were immunized three times, with a  
two week interval between immunizations. Two weeks after the last immunization,  
immune spleen cells were cultured with Jurkat A2Kb-P501S transduced stimulator  
10 cells. CTL lines were stimulated weekly. After two weeks of *in vitro* stimulation, CTL  
activity was assessed against P501S transduced targets. Two out of 8 mice developed  
strong anti-P501S CTL responses. These results demonstrate that P501S contains at  
least one naturally processed HLA-A2-restricted CTL epitope.

15

## EXAMPLE 8

## ABILITY OF HUMAN T CELLS TO RECOGNIZE PROSTATE-SPECIFIC POLYPEPTIDES

This Example illustrates the ability of T cells specific for a prostate  
tumor polypeptide to recognize human tumor.

20

Human CD8<sup>+</sup> T cells were primed *in vitro* to the P2S-12 peptide (SEQ  
ID NO: 306) derived from P502S (also referred to as J1-17) using dendritic cells  
according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology* 18:65-75,  
1998). The resulting CD8<sup>+</sup> T cell microcultures were tested for their ability to  
recognize the P2S-12 peptide presented by autologous fibroblasts or fibroblasts which  
25 were transduced to express the P502S gene in a  $\gamma$ -interferon ELISPOT assay (see  
Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). Briefly, titrating numbers of T cells  
were assayed in duplicate on 10<sup>4</sup> fibroblasts in the presence of 3 µg/ml human  $\beta$ 2-  
microglobulin and 1 µg/ml P2S-12 peptide or control E75 peptide. In addition, T cells  
were simultaneously assayed on autologous fibroblasts transduced with the P502S gene  
30 or as a control, fibroblasts transduced with HER-2/*neu*. Prior to the assay, the



fibroblasts were treated with 10 ng/ml  $\gamma$ -interferon for 48 hours to upregulate class I MHC expression. One of the microcultures (#5) demonstrated strong recognition of both peptide pulsed fibroblasts as well as transduced fibroblasts in a  $\gamma$ -interferon ELISPOT assay. Figure 2A demonstrates that there was a strong increase in the number of  $\gamma$ -interferon spots with increasing numbers of T cells on fibroblasts pulsed with the P2S-12 peptide (solid bars) but not with the control E75 peptide (open bars). This shows the ability of these T cells to specifically recognize the P2S-12 peptide. As shown in Figure 2B, this microculture also demonstrated an increase in the number of  $\gamma$ -interferon spots with increasing numbers of T cells on fibroblasts transduced to express the P502S gene but not the HER-2/*neu* gene. These results provide additional confirmatory evidence that the P2S-12 peptide is a naturally processed epitope of the P502S protein. Furthermore, this also demonstrates that there exists in the human T cell repertoire, high affinity T cells which are capable of recognizing this epitope. These T cells should also be capable of recognizing human tumors which express the P502S gene.

## EXAMPLE 9

### ELICITATION OF PROSTATE ANTIGEN-SPECIFIC CTL RESPONSES IN HUMAN BLOOD

20

This Example illustrates the ability of a prostate-specific antigen to elicit a CTL response in blood of normal humans.

Autologous dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal donors by growth for five days in RPMI medium containing 10% human serum, 50 ng/ml GMCSF and 30 ng/ml IL-4. Following culture, DC were infected overnight with recombinant P501S-expressing vaccinia virus at an M.O.I. of 5 and matured for 8 hours by the addition of 2 micrograms/ml CD40 ligand. Virus was inactivated by UV irradiation, CD8<sup>+</sup> cells were isolated by positive selection using magnetic beads, and priming cultures were initiated in 24-well plates. Following five stimulation cycles using autologous fibroblasts

retrovirally transduced to express P501S and CD80, CD8+ lines were identified that specifically produced interferon-gamma when stimulated with autologous P501S-transduced fibroblasts. The P501S-specific activity of cell line 3A-1 could be maintained following additional stimulation cycles on autologous B-LCL transduced with P501S. Line 3A-1 was shown to specifically recognize autologous B-LCL transduced to express P501S, but not EGFP-transduced autologous B-LCL, as measured by cytotoxicity assays ( $^{51}\text{Cr}$  release) and interferon-gamma production (Interferon-gamma Elispot; *see above and Lalvani et al., J. Exp. Med. 186:859-865, 1997*). The results of these assays are presented in Figures 6A and 6B.

10

## EXAMPLE 10

IDENTIFICATION OF A NATURALLY PROCESSED CTL EPIOTOPE CONTAINED WITHIN THE  
PROSTATE-SPECIFIC ANTIGEN P703P

The 9-mer peptide p5 (SEQ ID NO: 338) was derived from the P703P antigen (also referred to as P20). The p5 peptide is immunogenic in human HLA-A2 donors and is a naturally processed epitope. Antigen specific human CD8+ T cells can be primed following repeated *in vitro* stimulations with monocytes pulsed with p5 peptide. These CTL specifically recognize p5-pulsed and P703P-transduced target cells in both ELISPOT (as described above) and chromium release assays. Additionally, immunization of HLA-A2Kb transgenic mice with p5 leads to the generation of CTL lines which recognize a variety of HLA-A2Kb or HLA-A2 transduced target cells expressing P703P.

Initial studies demonstrating that p5 is a naturally processed epitope were done using HLA-A2Kb transgenic mice. HLA-A2Kb transgenic mice were immunized subcutaneously in the footpad with 100  $\mu\text{g}$  of p5 peptide together with 140  $\mu\text{g}$  of hepatitis B virus core peptide (a Th peptide) in Freund's incomplete adjuvant. Three weeks post immunization, spleen cells from immunized mice were stimulated *in vitro* with peptide-pulsed LPS blasts. CTL activity was assessed by chromium release assay five days after primary *in vitro* stimulation. Retrovirally transduced cells expressing the

30

control antigen P703P and HLA-A2Kb were used as targets. CTL lines that specifically recognized both p5-pulsed targets as well as P703P-expressing targets were identified.

Human *in vitro* priming experiments demonstrated that the p5 peptide is immunogenic in humans. Dendritic cells (DC) were differentiated from monocyte  
5 cultures derived from PBMC of normal human donors by culturing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, the DC were pulsed with 1 ug/ml p5 peptide and cultured with CD8+ T cell enriched PBMC. CTL lines were restimulated on a weekly basis with p5-pulsed monocytes. Five to six weeks after initiation of the CTL cultures,  
10 CTL recognition of p5-pulsed target cells was demonstrated. CTL were additionally shown to recognize human cells transduced to express P703P, demonstrating that p5 is a naturally processed epitope.

Studies identifying a further peptide epitope (referred to as peptide 4) derived from the prostate tumor-specific antigen P703P that is capable of being  
15 recognized by CD4 T cells on the surface of cells in the context of HLA class II molecules were carried out as follows. The amino acid sequence for peptide 4 is provided in SEQ ID NO: 638, with the corresponding cDNA sequence being provided in SEQ ID NO: 639.

Twenty 15-mer peptides overlapping by 10 amino acids and derived  
20 from the carboxy-terminal fragment of P703P were generated using standard procedures. Dendritic cells (DC) were derived from PBMC of a normal female donor using GM-CSF and IL-4 by standard protocols. CD4 T cells were generated from the same donor as the DC using MACS beads and negative selection. DC were pulsed overnight with pools of the 15-mer peptides, with each peptide at a final concentration  
25 of 0.25 microgram/ml. Pulsed DC were washed and plated at  $1 \times 10^4$  cells/well of 96-well V-bottom plates and purified CD4 T cells were added at  $1 \times 10^5$ /well. Cultures were supplemented with 60 ng/ml IL-6 and 10 ng/ml IL-12 and incubated at 37 °C. Cultures were restimulated as above on a weekly basis using DC generated and pulsed as above as antigen presenting cells, supplemented with 5 ng/ml IL-7 and 10 u/ml IL-2.  
30 Following 4 *in vitro* stimulation cycles, 96 lines (each line corresponding to one well) were tested for specific proliferation and cytokine production in response to the

stimulating pools with an irrelevant pool of peptides derived from mammaglobin being used as a control.

One line (referred to as 1-F9) was identified from pool #1 that demonstrated specific proliferation (measured by <sup>3</sup>H proliferation assays) and cytokine production (measured by interferon-gamma ELISA assays) in response to pool #1 of P703P peptides. This line was further tested for specific recognition of the peptide pool, specific recognition of individual peptides in the pool, and in HLA mismatch analyses to identify the relevant restricting allele. Line 1-F9 was found to specifically proliferate and produce interferon-gamma in response to peptide pool #1, and also to peptide 4 (SEQ ID NO: 638). Peptide 4 corresponds to amino acids 126-140 of SEQ ID NO: 327. Peptide titration experiments were conducted to assess the sensitivity of line 1-F9 for the specific peptide. The line was found to specifically respond to peptide 4 at concentrations as low as 0.25 ng/ml, indicating that the T cells are very sensitive and therefore likely to have high affinity for the epitope.

To determine the HLA restriction of the P703P response, a panel of antigen presenting cells (APC) was generated that was partially matched with the donor used to generate the T cells. The APC were pulsed with the peptide and used in proliferation and cytokine assays together with line 1-F9. APC matched with the donor at HLA-DRB0701 and HLA-DQB02 alleles were able to present the peptide to the T cells, indicating that the P703P-specific response is restricted to one of these alleles.

Antibody blocking assays were utilized to determine if the restricting allele was HLA-DR0701 or HLA-DQ02. The anti-HLA-DR blocking antibody L243 or an irrelevant isotype matched IgG2a were added to T cells and APC cultures pulsed with the peptide RMPTVLQCVNVS VVS (SEQ ID NO: 638) at 250 ng/ml. Standard interferon-gamma and proliferation assays were performed. Whereas the control antibody had no effect on the ability of the T cells to recognize peptide-pulsed APC, in both assays the anti-HLA-DR antibody completely blocked the ability of the T cells to specifically recognize peptide-pulsed APC.

To determine if the peptide epitope RMPTVLQCVNVS VVS (SEQ ID NO: 638) was naturally processed, the ability of line 1-F9 to recognize APC pulsed with recombinant P703P protein was examined. For these experiments a number of

recombinant P703P sources were utilized; *E. coli*-derived P703P, Pichia-derived P703P and baculovirus-derived P703P. Irrelevant protein controls used were *E. coli*-derived L3E (a lung-specific antigen) and baculovirus-derived mammaglobin. In interferon-gamma ELISA assays, line 1-F9 was able to efficiently recognize both *E. coli* forms of P703P as well as Pichia-derived recombinant P703P, while baculovirus-derived P703P was recognized less efficiently. Subsequent Western blot analysis revealed that the *E. coli* and Pichia P703P protein preparations were intact while the baculovirus P703P preparation was approximately 75% degraded. Thus, peptide RMPTVLQCVNVS VVS (SEQ ID NO: 638) from P703P is a naturally processed peptide epitope derived from P703P and presented to T cells in the context of HLA-DRB-0701

In further studies, twenty-four 15-mer peptides overlapping by 10 amino acids and derived from the N-terminal fragment of P703P (corresponding to amino acids 27-154 of SEQ ID NO: 525) were generated by standard procedures and their ability to be recognized by CD4 cells was determined essentially as described above. DC were pulsed overnight with pools of the peptides with each peptide at a final concentration of 10 microgram/ml. A large number of individual CD4 T cell lines (65/480) demonstrated significant proliferation and cytokine release (IFN-gamma) in response to the P703P peptide pools but not to a control peptide pool. The CD4 T cell lines which demonstrated specific activity were restimulated on the appropriate pool of P703P peptides and reassayed on the individual peptides of each pool as well as a peptide dose titration of the pool of peptides in a IFN-gamma release assay and in a proliferation assay.

Sixteen immunogenic peptides were recognized by the T cells from the entire set of peptide antigens tested. The amino acid sequences of these peptides are provided in SEQ ID NO: 656-671, with the corresponding cDNA sequences being provided in SEQ ID NO: 640-655, respectively. In some cases the peptide reactivity of the T cell line could be mapped to a single peptide, however some could be mapped to more than one peptide in each pool. Those CD4 T cell lines that displayed a representative pattern of recognition from each peptide pool with a reasonable affinity for peptide were chosen for further analysis (I-1A, -6A; II-4C, -5E; III-6E, IV-4B, -3F, -9B, -10F, V-5B, -4D, and -10F). These CD4 T cell lines were restimulated on the

appropriate individual peptide and reassayed on autologous DC pulsed with a truncated form of recombinant P703P protein made in *E. coli* (a.a. 96 - 254 of SEQ ID NO: 525), full-length P703P made in the baculovirus expression system, and a fusion between influenza virus NS1 and P703P made in *E. coli*. Of the T cell lines tested, line I-1A  
5 recognized specifically the truncated form of P703P (*E. coli*) but no other recombinant form of P703P. This line also recognized the peptide used to elicit the T cells. Line 2-4C recognized the truncated form of P703P (*E. coli*) and the full length form of P703P made in baculovirus, as well as peptide. The remaining T cell lines tested were either peptide-specific only (II-5E, II-6F, IV-4B, IV-3F, IV-9B, IV-10F, V-5B and V-4D) or  
10 were non-responsive to any antigen tested (V-10F). These results demonstrate that the peptide sequence RPLLANDLMLIKLDE (SEQ ID NO: 671; corresponding to a.a. 110-124 of SEQ ID NO: 525) recognized by the T cell line I-1A, and the peptide sequences SVSESDTIRSISIAS (SEQ ID NO: 668; corresponding to a.a. 125-139 of SEQ ID NO: 525) and ISIASQCPTAGNSCL (SEQ ID NO: 667; corresponding to a.a. 135-149 of  
15 SEQ ID NO: 525) recognized by the T cell line II-4C may be naturally processed epitopes of the P703P protein.

#### EXAMPLE 11

##### EXPRESSION OF A BREAST TUMOR-DERIVED ANTIGEN IN PROSTATE

Isolation of the antigen B305D from breast tumor by differential display is described in US Patent Application No. 08/700,014, filed August 20, 1996. Several different splice forms of this antigen were isolated. The determined cDNA sequences  
25 for these splice forms are provided in SEQ ID NO: 366-375, with the predicted amino acid sequences corresponding to the sequences of SEQ ID NO: 292, 298 and 301-303 being provided in SEQ ID NO: 299-306, respectively. In further studies, a splice variant of the cDNA sequence of SEQ ID NO: 366 was isolated which was found to contain an additional guanine residue at position 884 (SEQ ID NO: 530), leading to a  
30 frameshift in the open reading frame. The determined DNA sequence of this ORF is

provided in SEQ ID NO: 531. This frameshift generates a protein sequence (provided in SEQ ID NO: 532) of 293 amino acids that contains the C-terminal domain common to the other isoforms of B305D but that differs in the N-terminal region.

The expression levels of B305D in a variety of tumor and normal tissues were examined by real time PCR and by Northern analysis. The results indicated that B305D is highly expressed in breast tumor, prostate tumor, normal prostate and normal testes, with expression being low or undetectable in all other tissues examined (colon tumor, lung tumor, ovary tumor, and normal bone marrow, colon, kidney, liver, lung, ovary, skin, small intestine, stomach). Using real-time PCR on a panel of prostate tumors, expression of B305D in prostate tumors was shown to increase with increasing Gleason grade, demonstrating that expression of B305D increases as prostate cancer progresses.

#### EXAMPLE 12

##### 15 GENERATION OF HUMAN CTL *IN VITRO* USING WHOLE GENE PRIMING AND STIMULATION TECHNIQUES WITH THE PROSTATE-SPECIFIC ANTIGEN P501S

Using *in vitro* whole-gene priming with P501S-vaccinia infected DC (see, for example, Yee et al, *The Journal of Immunology*, 157(9):4079-86, 1996), human CTL lines were derived that specifically recognize autologous fibroblasts transduced with P501S (also known as L1-12), as determined by interferon- $\gamma$  ELISPOT analysis as described above. Using a panel of HLA-mismatched B-LCL lines transduced with P501S, these CTL lines were shown to be likely restricted to HLAB class I allele. Specifically, dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by growing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, DC were infected overnight with recombinant P501S vaccinia virus at a multiplicity of infection (M.O.I) of five, and matured overnight by the addition of 3  $\mu$ g/ml CD40 ligand. Virus was inactivated by UV irradiation. CD8+ T cells were isolated using a magnetic bead system, and priming cultures were initiated

using standard culture techniques. Cultures were restimulated every 7-10 days using autologous primary fibroblasts retrovirally transduced with P501S and CD80. Following four stimulation cycles, CD8<sup>+</sup> T cell lines were identified that specifically produced interferon- $\gamma$  when stimulated with P501S and CD80-transduced autologous  
5 fibroblasts. A panel of HLA-mismatched B-LCL lines transduced with P501S were generated to define the restriction allele of the response. By measuring interferon- $\gamma$  in an ELISPOT assay, the P501S specific response was shown to be likely restricted by HLA B alleles. These results demonstrate that a CD8<sup>+</sup> CTL response to P501S can be elicited.

10 To identify the epitope(s) recognized, cDNA encoding P501S was fragmented by various restriction digests, and sub-cloned into the retroviral expression vector pBIB-KS. Retroviral supernatants were generated by transfection of the helper packaging line Phoenix-Ampho. Supernatants were then used to transduce Jurkat/A2Kb cells for CTL screening. CTL were screened in IFN-gamma ELISPOT  
15 assays against these A2Kb targets transduced with the "library" of P501S fragments. Initial positive fragments P501S/H3 and P501S/F2 were sequenced and found to encode amino acids 106-553 and amino acids 136-547, respectively, of SEQ ID NO: 113. A truncation of H3 was made to encode amino acid residues 106-351 of SEQ ID NO: 113, which was unable to stimulate the CTL, thus localizing the epitope to amino acid  
20 residues 351-547. Additional fragments encoding amino acids 1-472 (Fragment A) and amino acids 1-351 (Fragment B) were also constructed. Fragment A but not Fragment B stimulated the CTL thus localizing the epitope to amino acid residues 351-472. Overlapping 20-mer and 18-mer peptides representing this region were tested by pulsing Jurkat/A2Kb cells versus CTL in an IFN-gamma assay. Only peptides P501S-369(20)  
25 and P501S-369(18) stimulated the CTL. Nine-mer and 10-mer peptides representing this region were synthesized and similarly tested. Peptide P501S-370 (SEQ ID NO: 539) was the minimal 9-mer giving a strong response. Peptide P501S-376 (SEQ ID NO: 540) also gave a weak response, suggesting that it might represent a cross-reactive epitope.



In subsequent studies, the ability of primary human B cells transduced with P501S to prime MHC class I-restricted, P501S-specific, autologous CD8 T cells was examined. Primary B cells were derived from PBMC of a homozygous HLA-A2 donor by culture in CD40 ligand and IL-4, transduced at high frequency with recombinant P501S in the vector pBIB, and selected with blastocidin-S. For *in vitro* priming, purified CD8<sup>+</sup> T cells were cultured with autologous CD40 ligand + IL-4 derived, P501S-transduced B cells in a 96-well microculture format. These CTL microcultures were re-stimulated with P501S-transduced B cells and then assayed for specificity. Following this initial screen, microcultures with significant signal above background were cloned on autologous EBV-transformed B cells (BLCL), also transduced with P501S. Using IFN-gamma ELISPOT for detection, several of these CD8 T cell clones were found to be specific for P501S, as demonstrated by reactivity to BLCL/P501S but not BLCL transduced with control antigen. It was further demonstrated that the anti-P501S CD8 T cell specificity is HLA-A2-restricted. First, antibody blocking experiments with anti-HLA-A,B,C monoclonal antibody (W6.32), anti-HLA-B,C monoclonal antibody (B1.23.2) and a control monoclonal antibody showed that only the anti-HLA-A,B,C antibody blocked recognition of P501S-expressing autologous BLCL. Secondly, the anti-P501S CTL also recognized an HLA-A2 matched, heterologous BLCL transduced with P501S, but not the corresponding EGFP transduced control BLCL.

A naturally processed, CD8, class I-restricted peptide epitope of P501S was identified as follows. Dendritic Cells (DC) were isolated by Percol gradient followed by differential adherence, and cultured for 5 days in the presence of RPMI medium containing 1% human serum, 50ng/ml GM-CSF and 30ng/ml IL-4. Following culture, DC were infected for 24 hours with P501S-expressing adenovirus at an MOI of 10 and matured for an additional 24 hours by the addition of 2ug/ml CD40 ligand. CD8 cells were enriched for by the subtraction of CD4<sup>+</sup>, CD14<sup>+</sup> and CD16<sup>+</sup> populations from PBMC with magnetic beads. Priming cultures containing 10,000 P501S-expressing DC and 100,000 CD8<sup>+</sup> T cells per well were set up in 96-well V-bottom plates with RPMI containing 10% human serum, 5ng/ml IL-12 and 10ng/ml IL-6. Cultures were stimulated every 7 days using autologous fibroblasts retrovirally

transduced to express P501S and CD80, and were treated with IFN-gamma for 48-72 hours to upregulate MHC Class I expression. 10u/ml IL-2 was added at the time of stimulation and on days 2 and 5 following stimulation. Following 4 stimulation cycles, one P501S-specific CD8+ T cell line (referred to as 2A2) was identified that produced IFN-gamma in response to IFN-gamma-treated P501S/CD80 expressing autologous fibroblasts, but not in response to IFN-gamma-treated P703P/CD80 expressing autologous fibroblasts in a  $\gamma$ -IFN Elispot assay. Line 2A2 was cloned in 96-well plates with 0.5 cell/well or 2 cells/well in the presence of 75,000 PBMC/well, 10,000 B-LCL/well, 30ng/ml OKT3 and 50u/ml IL-2. Twelve clones were isolated that showed strong P501S specificity in response to transduced fibroblasts.

Fluorescence activated cell sorting (FACS) analysis was performed on P501S-specific clones using CD3-, CD4- and CD8-specific antibodies conjugated to PercP, FITC and PE respectively. Consistent with the use of CD8 enriched T cells in the priming cultures, P5401S-specific clones were determined to be CD3+, CD8+ and CD4-.

To identify the relevant P501S epitope recognized by P501S specific CTL, pools of 18-20 mer or 30-mer peptides that spanned the majority of the amino acid sequence of P501S were loaded onto autologous B-LCL and tested in  $\gamma$ -IFN Elispot assays for the ability to stimulate two P501S-specific CTL clones, referred to as 4E5 and 4E7. One pool, composed of five 18-20 mer peptides that spanned amino acids 411-486 of P501S (SEQ ID NO: 113), was found to be recognized by both P501S-specific clones. To identify the specific 18-20 mer peptide recognized by the clones, each of the 18-20 mer peptides that comprised the positive pool were tested individually in  $\gamma$ -IFN Elispot assays for the ability to stimulate the two P501S-specific CTL clones, 4E5 and 4E7. Both 4E5 and 4E7 specifically recognized one 20-mer peptide (SEQ ID NO: 710; cDNA sequence provided in SEQ ID NO: 711) that spanned amino acids 453-472 of P501S. Since the minimal epitope recognized by CD8+ T cells is almost always either a 9 or 10-mer peptide sequence, 10-mer peptides that spanned the entire sequence of SEQ ID NO: 710 were synthesized that differed by 1 amino acid. Each of these 10-mer peptides was tested for the ability to stimulate two P501S-specific clones, (referred to as 1D5 and 1E12). One 10-mer peptide (SEQ ID NO: 712; cDNA sequence provided in

SEQ ID NO: 713) was identified that specifically stimulated the P501S-specific clones. This epitope spans amino acids 463-472 of P501S. This sequence defines a minimal 10-mer epitope from P501S that can be naturally processed and to which CTL responses can be identified in normal PBMC. Thus, this epitope is a candidate for use as a vaccine moiety, and as a therapeutic and/or diagnostic reagent for prostate cancer.

To identify the class I restriction element for the P501S-derived sequence of SEQ ID NO: 712, HLA blocking and mismatch analyses were performed. In  $\gamma$ -IFN Elispot assays, the specific response of clones 4A7 and 4E5 to P501S-transduced autologous fibroblasts was blocked by pre-incubation with 25ug/ml W6/32 (pan-Class I blocking antibody) and B1.23.2 (HLA-B/C blocking antibody). These results demonstrate that the SEQ ID NO: 712-specific response is restricted to an HLA-B or HLA-C allele.

For the HLA mismatch analysis, autologous B-LCL (HLA-A1,A2,B8,B51, Cw1, Cw7) and heterologous B-LCL (HLA-A2,A3,B18,B51,Cw5,Cw14) that share the HLAB51 allele were pulsed for one hour with 20ug/ml of peptide of SEQ ID NO: 712, washed, and tested in  $\gamma$ -IFN Elispot assays for the ability to stimulate clones 4A7 and 4E5. Antibody blocking assays with the B1.23.2 (HLA-B/C blocking antibody) were also performed. SEQ ID NO: 712-specific response was detected using both the autologous (D326) and heterologous (D107) B-LCL, and furthermore the responses were blocked by pre-incubation with 25ug/ml of B1.23.2 HLA-B/C blocking antibody. Together these results demonstrate that the P501S-specific response to the peptide of SEQ ID NO: 712 is restricted to the HLA-B51 class I allele. Molecular cloning and sequence analysis of the HLA-B51 allele from D3326 revealed that the HLA-B51 subtype of D326 is HLA-B51011.

Based on the 10-mer P501S-derived epitope of SEQ ID NO: 712, two 9-mers with the sequences of SEQ ID NO: 714 and 715 were synthesized and tested in Elispot assays for the ability to stimulate two P501S-specific CTL clones derived from line 2A2. The 10-mer peptide of SEQ ID NO: 712, as well as the 9-mer peptide of SEQ ID NO: 715, but not the 9-mer peptide of SEQ ID NO: 714, were capable of stimulating the P501S-specific CTL to produce IFN-gamma. These results demonstrate that the peptide of SEQ ID NO: 715 is a 9-mer P501S-derived epitope recognized by P501S-

specific CTL. The DNA sequence encoding the epitope of SEQ ID NO: 715 is provided in SEQ ID NO: 716.

To identify the class I restricting allele for the P501S-derived peptide of SEQ ID NO: 712 and 715 specific response, each of the HLA B and C alleles were  
5 cloned from the donor used in the *in vitro* priming experiment. Sequence analysis indicated that the relevant alleles were HLA-B8, HLA-B51, HLA-Cw01 and HLA-Cw07. Each of these alleles were subcloned into an expression vector and co-transfected together with the P501S gene into VA-13 cells. Transfected VA-13 cells were then tested for the ability to specifically stimulate the P501S-specific CTL in  
10 ELISPOT assays. VA-13 cells transfected with P501S and HLA-B51 were capable of stimulating the P501S-specific CTL to secrete gamma-IFN. VA-13 cells transfected with HLA-B51 alone or P501S + the other HLA-alleles were not capable of stimulating the P501S-specific CTL. These results demonstrate that the restricting allele for the P501S-specific response is the HLAB51 allele. Sequence analysis revealed that the  
15 subtype of the relevant restricting allele is HLA-B51011.

To determine if the P501S-specific CTL could recognize prostate tumor cells that express P501S, the P501S-positive lines LnCAP and CRL2422 (both expressing "moderate" amounts of P501S mRNA and protein), and PC-3 (expressing low amounts of P501S mRNA and protein), plus the P501S-negative cell line DU-145  
20 were retrovirally transduced with the HLA-B51011 allele that was cloned from the donor used to generate the P501S-specific CTL. HLA-B51011- or EGFP-transduced and selected tumor cells were treated with gamma-interferon and androgen (to upregulate stimulatory functions and P501S, respectively) and used in gamma-interferon Elispot assays with the P501S-specific CTL clones 4E5 and 4E7. Untreated  
25 cells were used as a control.

Both 4E5 and 4E7 efficiently and specifically recognized LnCAP and CRL2422 cells that were transduced with the HLA-B51011 allele, but not the same cell lines transduced with EGFP. Additionally, both CTL clones specifically recognized PC-3 cells transduced with HLA-B51011, but not the P501S-negative tumor cell line  
30 DU-145. Treatment with gamma-interferon or androgen did not enhance the ability of CTL to recognize tumor cells. These results demonstrate that P501S-specific CTL,

generated by *in vitro* whole gene priming, specifically and efficiently recognize prostate tumor cell lines that express P501S.

A naturally processed CD4 epitope of P501S was identified as follows.

CD4 cells specific for P501S were prepared as described above. A series  
5 of 16 overlapping peptides were synthesized that spanned approximately 50% of the amino terminal portion of the P501S gene (amino acids 1- 325 of SEQ ID NO: 113). For priming, peptides were combined into pools of 4 peptides, pulsed at 4  $\mu$ g/ml onto dendritic cells (DC) for 24 hours, with TNF-alpha. DC were then washed and mixed with negatively selected CD4+ T cells in 96 well U-bottom plates. Cultures were re-  
10 stimulated weekly on fresh DC loaded with peptide pools. Following a total of 4 stimulation cycles, cells were rested for an additional week and tested for specificity to APC pulsed with peptide pools using  $\gamma$ -IFN ELISA and proliferation assays. For these assays, adherent monocytes loaded with either the relevant peptide pool at 4 $\mu$ g/ml or an irrelevant peptide at  $\mu$ g/ml were used as APC. T cell lines that demonstrated either  
15 specific cytokine secretion or proliferation were then tested for recognition of individual peptides that were present in the pool. T cell lines could be identified from pools A and B that recognized individual peptides from these pools.

From pool A, lines AD9 and AE10 specifically recognized peptide 1 (SEQ ID NO: 719), and line AF5 recognized peptide 39 (SEQ ID NO: 718). From pool B, line BC6 could be identified that recognized peptide 58 (SEQ ID NO: 717). Each of these lines were stimulated on the specific peptide and tested for specific recognition of the peptide in a titration assay as well as cell lysates generated by infection of HEK 293 cells with adenovirus expressing either P501S or an irrelevant antigen. For these assays, APC-adherent monocytes were pulsed with either 10, 1, or 0.1 µg/ml individual P501S peptides, and DC were pulsed overnight with a 1:5 dilution of adenovirally infected cell lysates. Lines AD9, AE10 and AF5 retained significant recognition of the relevant P501S-derived peptides even at 0.1 mg/ml. Furthermore, line AD9 demonstrated significant (8.1 fold stimulation index) specific activity for lysates from adenovirus-P501S infected cells. These results demonstrate that high affinity CD4 T cell lines can be generated toward P501S-derived epitopes, and that at least a subset of these T cells specific for the P501S derived sequence of SEQ ID NO: 719 are specific for an epitope that is naturally processed by human cells. The DNA sequences encoding the amino acid sequences of SEQ ID NO: 717-719 are provided in SEQ ID NO: 720-722, respectively.

To further characterize the P501S-specific activity of AD9, the line was cloned using anti-CD3. Three clones, referred to as 1A1, 1A9 and 1F5, were identified that were specific for the P501S-1 peptide (SEQ ID NO: 719). To determine the HLA restriction allele for the P501S-specific response, each of these clones was tested in class II antibody blocking and HLA mismatch assays using proliferation and gamma-interferon assays. In antibody blocking assays and measuring gamma-interferon production using ELISA assays, the ability of all three clones to recognize peptide pulsed APC was specifically blocked by co-incubation with either a pan-class II blocking antibody or a HLA-DR blocking antibody, but not with a HLA-DQ or an irrelevant antibody. Proliferation assays performed simultaneously with the same cells confirmed these results. These data indicate that the P501S-specific response of the clones is restricted by an HLA-DR allele. Further studies demonstrated that the restricting allele for the P501S-specific response is HLA-DRB1501.

## EXAMPLE 13

## IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS

## BY MICROARRAY ANALYSIS

5           This Example describes the isolation of certain prostate-specific polypeptides from a prostate tumor cDNA library.

          A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to  
10 non-prostate normal tissues (not including testis). 372 clones were identified, and 319 were successfully sequenced. Table I presents a summary of these clones, which are shown in SEQ ID NOs:385-400. Of these sequences SEQ ID NOs:386, 389, 390 and 392 correspond to novel genes, and SEQ ID NOs: 393 and 396 correspond to previously identified sequences. The others (SEQ ID NOs:385, 387, 388, 391, 394, 395 and 397-  
15 400) correspond to known sequences, as shown in Table I.

Table I  
Summary of Prostate Tumor Antigens

Known Genes	Previously Identified Genes	Novel Genes
T-cell gamma chain	P504S	23379 (SEQ ID NO:389)
Kallikrein	P1000C	23399 (SEQ ID NO:392)
Vector	P501S	23320 (SEQ ID NO:386)
CGI-82 protein mRNA (23319; SEQ ID NO:385)	P503S	23381 (SEQ ID NO:390)
PSA	P510S	
Ald. 6 Dehyd.	P784P	
L-idoitol-2 dehydrogenase (23376; SEQ ID NO:388)	P502S	
Ets transcription factor PDEF (22672; SEQ ID NO:398)	P706P	
hTGR (22678; SEQ ID NO:399)	19142.2, bangur.seq (22621; SEQ ID NO:396)	
KIAA0295(22685; SEQ ID NO:400)	5566.1 Wang (23404; SEQ ID NO:393)	
Prostatic Acid Phosphatase(22655; SEQ ID NO:397)	P712P	
transglutaminase (22611; SEQ ID NO:395)	P778P	
HDLBP (23508; SEQ ID NO:394)		
CGI-69 Protein(23367; SEQ ID NO:387)		
KIAA0122(23383; SEQ ID NO:391)		
TEEG		



CGI-82 showed 4.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 43% of prostate tumors, 25% normal prostate, not detected in other normal tissues tested. L-idoitol-2 dehydrogenase showed 4.94 fold over-expression in prostate tissues as compared to  
5 other normal tissues tested. It was over-expressed in 90% of prostate tumors, 100% of normal prostate, and not detected in other normal tissues tested. Ets transcription factor PDEF showed 5.55 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% prostate tumors, 25% normal prostate and not detected in other normal tissues tested. hTGR1 showed 9.11 fold over-expression in  
10 prostate tissues as compared to other normal tissues tested. It was over-expressed in 63% of prostate tumors and is not detected in normal tissues tested including normal prostate. KIAA0295 showed 5.59 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% of prostate tumors, low to undetectable in normal tissues tested including normal prostate tissues. Prostatic acid  
15 phosphatase showed 9.14 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 67% of prostate tumors, 50% of normal prostate, and not detected in other normal tissues tested. Transglutaminase showed 14.84 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 30% of prostate tumors, 50% of normal prostate, and is  
20 not detected in other normal tissues tested. High density lipoprotein binding protein (HDLBP) showed 28.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% of normal prostate, and is undetectable in all other normal tissues tested. CGI-69 showed 3.56 fold over-expression in prostate tissues as compared to other normal tissues tested. It is  
25 a low abundant gene, detected in more than 90% of prostate tumors, and in 75% normal prostate tissues. The expression of this gene in normal tissues was very low. KIAA0122 showed 4.24 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 57% of prostate tumors, it was undetectable in all normal tissues tested including normal prostate tissues. 19142.2  
30 bangur showed 23.25 fold over-expression in prostate tissues as compared to other

normal tissues tested. It was over-expressed in 97% of prostate tumors and 100% of normal prostate. It was undetectable in other normal tissues tested. .5566.1 Wang showed 3.31 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% normal prostate and was also over-expressed in normal bone marrow, pancreas, and activated PBMC. Novel clone 23379 (also referred to as P553S) showed 4.86 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in 97% of prostate tumors and 75% normal prostate and is undetectable in all other normal tissues tested. Novel clone 23399 showed 4.09 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 27% of prostate tumors and was undetectable in all normal tissues tested including normal prostate tissues. Novel clone 23320 showed 3.15 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in all prostate tumors and 50% of normal prostate tissues. It was also expressed in normal colon and trachea. Other normal tissues do not express this gene at high level.

Subsequent full-length cloning studies on P553S, using standard techniques, revealed that this clone is an incomplete spliced form of P501S. The determined cDNA sequences for four splice variants of P553S are provided in SEQ ID NO: 623-626. An amino acid sequence encoded by SEQ ID NO: 626 is provided in SEQ ID NO: 627. The cDNA sequence of SEQ ID NO: 623 was found to contain two open reading frames (ORFs). The amino acid sequences encoded by these two ORFs are provided in SEQ ID NO: 628 and 629.

#### EXAMPLE 14

##### IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY ELECTRONIC SUBTRACTION

This Example describes the use of an electronic subtraction technique to identify prostate-specific antigens.

Potential prostate-specific genes present in the GenBank human EST database were identified by electronic subtraction (similar to that described by Vasmatizis et al., *Proc. Natl. Acad. Sci. USA* 95:300-304, 1998). The sequences of EST clones (43,482) derived from various prostate libraries were obtained from the GenBank public human EST database. Each prostate EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (length of matching sequence >100 base pairs, density of identical matches over this region > 70%) were grouped (aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 4,345 prostate superclusters.

Records for the 479 human cDNA libraries represented in the GenBank release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups: Plus (normal prostate and prostate tumor libraries, and breast cell line libraries, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other (libraries from fetal tissue, infant tissue, tissues found only in women, non-prostate tumors and cell lines other than prostate cell lines, in which expression was considered to be irrelevant). A summary of these library groups is presented in Table II.

Table IIProstate cDNA Libraries and ESTs

Library	# of Libraries	# of ESTs
Plus	25	43,482
Normal	11	18,875
Tumor	11	21,769
Cell lines	3	2,838
Minus	166	
Other	287	

5                Each supercluster was analyzed in terms of the ESTs within the supercluster. The tissue source of each EST clone was noted and used to classify the superclusters into four groups: Type 1- EST clones found in the Plus group libraries only; no expression detected in Minus or Other group libraries; Type 2- EST clones derived from the Plus and Other group libraries only; no expression detected in the

10 Minus group; Type 3- EST clones derived from the Plus, Minus and Other group libraries, but the number of ESTs derived from the Plus group is higher than in either the Minus or Other groups; and Type 4- EST clones derived from Plus, Minus and Other group libraries, but the number derived from the Plus group is higher than the number derived from the Minus group. This analysis identified 4,345 breast clusters

15 (see Table III). From these clusters, 3,172 EST clones were ordered from Research Genetics, Inc., and were received as frozen glycerol stocks in 96-well plates.

Table III  
Prostate Cluster Summary

Type	# of Superclusters	# of ESTs Ordered
1	688	677
2	2899	2484
3	85	11
4	673	0
Total	4345	3172

5           The EST clone inserts were PCR-amplified using amino-linked PCR primers for Synteni microarray analysis. When more than one PCR product was obtained for a particular clone, that PCR product was not used for expression analysis. In total, 2,528 clones from the electronic subtraction method were analyzed by microarray analysis to identify electronic subtraction breast clones that had high levels of tumor vs. normal tissue mRNA. Such screens were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Within these analyses, the clones were arrayed on the chip, which was then probed with fluorescent probes generated from normal and tumor prostate cDNA, as well as various other normal tissues. The slides were scanned and the fluorescence intensity was measured.

15           Clones with an expression ratio greater than 3 (*i.e.*, the level in prostate tumor and normal prostate mRNA was at least three times the level in other normal tissue mRNA) were identified as prostate tumor-specific sequences (Table IV). The sequences of these clones are provided in SEQ ID NO: 401-453, with certain novel sequences shown in SEQ ID NO: 407, 413, 416-419, 422, 426, 427 and 450.

Table IV

Prostate-tumor Specific Clones

SEQ ID NO.	Sequence Designation	Comments
401	22545	previously identified P1000C
402	22547	previously identified P704P
403	22548	known
404	22550	known
405	22551	PSA
406	22552	prostate secretory protein 94
407	22553	novel
408	22558	previously identified P509S
409	22562	glandular kallikrein
410	22565	previously identified P1000C
411	22567	PAP
412	22568	B1006C (breast tumor antigen)
413	22570	novel
414	22571	PSA
415	22572	previously identified P706P
416	22573	novel
417	22574	novel
418	22575	novel
419	22580	novel
420	22581	PAP
421	22582	prostatic secretory protein 94
422	22583	novel
423	22584	prostatic secretory protein 94
424	22585	prostatic secretory protein 94
425	22586	known
426	22587	novel
427	22588	novel
428	22589	PAP
429	22590	known
430	22591	PSA
431	22592	known
432	22593	Previously identified P777P
433	22594	T cell receptor gamma chain
434	22595	Previously identified P705P
435	22596	Previously identified P707P
436	22847	PAP
437	22848	known
438	22849	prostatic secretory protein 57

439	22851	PAP
440	22852	PAP
441	22853	PAP
442	22854	previously identified P509S
443	22855	previously identified P705P
444	22856	previously identified P774P
445	22857	PSA
446	23601	previously identified P777P
447	23602	PSA
448	23605	PSA
449	23606	PSA
450	23612	novel
451	23614	PSA
452	23618	previously identified P1000C
453	23622	previously identified P705P

Further studies on the clone of SEQ ID NO: 407 (also referred to as P1020C) led to the isolation of an extended cDNA sequence provided in SEQ ID NO: 591. This extended cDNA sequence was found to contain an open reading frame that  
5 encodes the predicted amino acid sequence of SEQ ID NO: 592. The P1020C cDNA and amino acid sequences were found to show some similarity to the human endogenous retroviral HERV-K pol gene and protein.

#### EXAMPLE 15

##### 10 FURTHER IDENTIFICATION OF PROSTATE-SPECIFIC ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of additional prostate-specific polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above  
15 was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 142 clones were identified and sequenced. Certain of these clones are shown in SEQ ID NO: 454-467. Of these sequences, SEQ ID NO: 459-460 represent novel genes. The others (SEQ ID NO: 454-  
20 458 and 461-467) correspond to known sequences. Comparison of the determined

cDNA sequence of SEQ ID NO: 461 with sequences in the Genbank database using the BLAST program revealed homology to the previously identified transmembrane protease serine 2 (TMPRSS2). The full-length cDNA sequence for this clone is provided in SEQ ID NO: 751, with the corresponding amino acid sequence being provided in SEQ ID NO: 752. The cDNA sequence encoding the first 209 amino acids of TMPRSS2 is provided in SEQ ID NO: 753, with the first 209 amino acids being provided in SEQ ID NO: 754.

The sequence of SEQ ID NO: 462 (referred to as P835P) was found to correspond to the previously identified clone FLJ13518 (Accession AK023643; SEQ ID NO: 774), which had no associated open reading frame (ORF). This clone was used to search the Geneseq DNA database and matched a clone previously identified as a G protein-coupled receptor protein (DNA Geneseq Accession A09351; amino acid Geneseq Accession Y92365), that is characterized by the presence of seven transmembrane domains. The sequences of fragments between these domains are provided in SEQ ID NO: 778-785, with SEQ ID NO: 778, 780, 782 and 784 representing extracellular domains and SEQ ID NO: 779, 781, 783 and 785 representing intracellular domains. SEQ ID NO: 778-785 represent amino acids 1-28, 53-61, 83-103, 124-143, 165-201, 226-238, 263-272 and 297-381, respectively, of P835P. The full-length cDNA sequence for P835P is provided in SEQ ID NO: 773. The cDNA sequence of the open reading frame for P835P, including stop codon, is provided in SEQ ID NO: 775, with the open reading frame without stop codon being provided in SEQ ID NO: 776 and the corresponding amino acid sequence being provided in SEQ ID NO: 777.

25

## EXAMPLE 16

## FURTHER CHARACTERIZATION OF PROSTATE-SPECIFIC ANTIGEN P710P

This Example describes the full length cloning of P710P.

The prostate cDNA library described above was screened with the P710P fragment described above. One million colonies were plated on LB/Ampicillin plates.

30



Nylon membrane filters were used to lift these colonies, and the cDNAs picked up by these filters were then denatured and cross-linked to the filters by UV light. The P710P fragment was radiolabeled and used to hybridize with the filters. Positive cDNA clones were selected and their cDNAs recovered and sequenced by an automatic Perkin Elmer/Applied Biosystems Division Sequencer. Four sequences were obtained, and are presented in SEQ ID NO: 468-471. These sequences appear to represent different splice variants of the P710P gene. Subsequent comparison of the cDNA sequences of P710P with those in Genbank revealed homology to the DD3 gene (Genbank accession numbers AF103907 & AF103908). The cDNA sequence of DD3 is provided in SEQ ID NO: 618.

## EXAMPLE 17

### PROTEIN EXPRESSION OF PROSTATE-SPECIFIC ANTIGENS

This example describes the expression and purification of prostate-specific antigens in *E. coli*, baculovirus, mammalian and yeast cells.

#### a) Expression of P501S in *E. coli*

Expression of the full-length form of P501S was attempted by first cloning P501S without the leader sequence (amino acids 36-553 of SEQ ID NO: 113) downstream of the first 30 amino acids of the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 484) in pET17b. Specifically, P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW003 (SEQ ID NO: 486). AW025 is a sense cloning primer that contains a HindIII site. AW003 is an antisense cloning primer that contains an EcoRI site. DNA amplification was performed using 5 µl 10X Pfu buffer, 1 µl 20 mM dNTPs, 1 µl each of the PCR primers at 10 µM concentration, 40 µl water, 1 µl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 µl DNA at 100 ng/µl. Denaturation at 95°C was performed for 30 sec, followed by 10 cycles of 95°C for 30 sec, 60°C for 1 min and by 72°C for 3 min. 20 cycles of 95°C for 30 sec, 65°C for 1 min and by 72°C for 3 min, and lastly by 1 cycle of 72°C for 10 min. The PCR product was

cloned to Ra12m/pET17b using HindIII and EcoRI. The sequence of the resulting fusion construct (referred to as Ra12-P501S-F) was confirmed by DNA sequencing.

The fusion construct was transformed into BL21(DE3)pLysE, pLysS and CodonPlus *E. coli* (Stratagene) and grown overnight in LB broth with kanamycin. The resulting culture was induced with IPTG. Protein was transferred to PVDF membrane and blocked with 5% non-fat milk (in PBS-Tween buffer), washed three times and incubated with mouse anti-His tag antibody (Clontech) for 1 hour. The membrane was washed 3 times and probed with HRP-Protein A (Zymed) for 30 min. Finally, the membrane was washed 3 times and developed with ECL (Amersham). No expression was detected by Western blot. Similarly, no expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage (Invitrogen).

An N-terminal fragment of P501S (amino acids 36-325 of SEQ ID NO: 113) was cloned down-stream of the first 30 amino acids of the *M. tuberculosis* antigen Ra12 in pET17b as follows. P501S DNA was used to perform PCR using the primers AW025 (SEQ ID NO: 485) and AW027 (SEQ ID NO: 487). AW027 is an antisense cloning primer that contains an EcoRI site and a stop codon. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The fusion construct (referred to as Ra12-P501S-N) was confirmed by DNA sequencing.

The Ra12-P501S-N fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, essentially as described above. Using Western blot analysis, protein bands were observed at the expected molecular weight of 36 kDa. Some high molecular weight bands were also observed, probably due to aggregation of the recombinant protein. No expression was detected by Western blot when the Ra12-P501S-F fusion was used for expression in BL21CodonPlus by CE6 phage.

A fusion construct comprising a C-terminal portion of P501S (amino acids 257-553 of SEQ ID NO: 113) located down-stream of the first 30 amino acids of the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 484) was prepared as follows. P501S

DNA was used to perform PCR using the primers AW026 (SEQ ID NO: 488) and AW003 (SEQ ID NO: 486). AW026 is a sense cloning primer that contains a HindIII site. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the HindIII and EcoRI sites. The  
5 sequence for the fusion construct (referred to as Ra12-P501S-C) was confirmed.

The Ra12-P501S-C fusion construct was used for expression in BL21(DE3)pLysE, pLysS and CodonPlus, as described above. A small amount of protein was detected by Western blot, with some molecular weight aggregates also being observed. Expression was also detected by Western blot when the Ra12-P501S-C  
10 fusion was used for expression in BL21CodonPlus induced by CE6 phage.

A fusion construct comprising a fragment of P501S (amino acids 36-298 of SEQ ID NO: 113) located down-stream of the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 705) was prepared as follows. P501S DNA was used to perform PCR using the primers AW042 (SEQ ID NO: 706) and AW053 (SEQ ID NO: 707). AW042 is a sense  
15 cloning primer that contains a EcoRI site. AW053 is an antisense primer with stop and Xho I sites. DNA amplification was performed essentially as described above. The resulting PCR product was cloned to Ra12 in pET17b at the EcoRI and Xho I sites. The resulting fusion construct (referred to as Ra12-P501S-E2) was expressed in B834 (DE3) pLys S *E. coli* host cells in TB media for 2 h at room temperature. Expressed protein  
20 was purified by washing the inclusion bodies and running on a Ni-NTA column. The purified protein stayed soluble in buffer containing 20 mM Tris-HCl (pH 8), 100 mM NaCl, 10 mM  $\beta$ -Me and 5% glycerol. The determined cDNA and amino acid sequences for the expressed fusion protein are provided in SEQ ID NO: 708 and 709, respectfully.

#### 25 b) Expression of P501S in Baculovirus

The Bac-to-Bac baculovirus expression system (BRL Life Technologies, Inc.) was used to express P501S protein in insect cells. Full-length P501S (SEQ ID NO: 113) was amplified by PCR and cloned into the XbaI site of the donor plasmid pFastBacI. The recombinant bacmid and baculovirus were prepared according to the

manufacturer's instructions. The recombinant baculovirus was amplified in Sf9 cells and the high titer viral stocks were utilized to infect High Five cells (Invitrogen) to make the recombinant protein. The identity of the full-length protein was confirmed by N-terminal sequencing of the recombinant protein and by Western blot analysis (Figure 5 7). Specifically, 0.6 million High Five cells in 6-well plates were infected with either the unrelated control virus BV/ECD\_PD (lane 2), with recombinant baculovirus for P501S at different amounts or MOIs (lanes 4-8), or were uninfected (lane 3). Cell lysates were run on SDS-PAGE under reducing conditions and analyzed by Western blot with the anti-P501S monoclonal antibody P501S-10E3-G4D3 (prepared as 10 described below). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

The localization of recombinant P501S in the insect cells was investigated as follows. The insect cells overexpressing P501S were fractionated into fractions of nucleus, mitochondria, membrane and cytosol. Equal amounts of protein from each fraction were analyzed by Western blot with a monoclonal antibody against 15 P501S. Due to the scheme of fractionation, both nucleus and mitochondria fractions contain some plasma membrane components. However, the membrane fraction is basically free from mitochondria and nucleus. P501S was found to be present in all fractions that contain the membrane component, suggesting that P501S may be associated with plasma membrane of the insect cells expressing the recombinant 20 protein.

#### c) Expression of P501S in Mammalian Cells

Full-length P501S (553 amino acids; SEQ ID NO: 113) was cloned into various mammalian expression vectors, including pCEP4 (Invitrogen), pVR1012 (Vical, San Diego, CA) and a modified form of the retroviral vector pBMN, referred to 25 as pBIB. Transfection of P501S/pCEP4 and P501S/pVR1012 into HEK293 fibroblasts was carried out using the Fugene transfection reagent (Boehringer Mannheim). Briefly, 2 ul of Fugene reagent was diluted into 100 ul of serum-free media and incubated at room temperature for 5-10 min. This mixture was added to 1 ug of P501S plasmid DNA, mixed briefly and incubated for 30 minutes at room temperature. The

Fugene/DNA mixture was added to cells and incubated for 24-48 hours. Expression of recombinant P501S in transfected HEK293 fibroblasts was detected by means of Western blot employing a monoclonal antibody to P501S.

Transfection of p501S/pCEP4 into CHO-K cells (American Type Culture Collection, Rockville, MD) was carried out using GenePorter transfection reagent (Gene Therapy Systems, San Diego, CA). Briefly, 15 µl of GenePorter was diluted in 500 µl of serum-free media and incubated at room temperature for 10 min. The GenePorter/media mixture was added to 2 µg of plasmid DNA that was diluted in 500 µl of serum-free media, mixed briefly and incubated for 30 min at room temperature. CHO-K cells were rinsed in PBS to remove serum proteins, and the GenePorter/DNA mix was added and incubated for 5 hours. The transfected cells were then fed an equal volume of 2x media and incubated for 24-48 hours.

FACS analysis of P501S transiently infected CHO-K cells, demonstrated surface expression of P501S. Expression was detected using rabbit polyclonal antiserum raised against a P501S peptide, as described below. Flow cytometric analysis was performed using a FaCScan (Becton Dickinson), and the data were analyzed using the Cell Quest program.

d) Expression of P501S in *S. cerevisiae*

P501S was expressed in yeast, directed in membranes, using the yeast  $\alpha$  prepro signal sequence. The natural signal sequence and first luminal domain of P501S was deleted in order to conserve the natural positioning of the expressed P501S protein.

Specifically, the  $\alpha$  prepro signal sequence of *S. cerevisiae* linked to amino acids 55-553 of SEQ ID NO: 113 with a His tag tail was cloned into the plasmid pRIT15068 with the CUP1 promoter and transfected into *S. cerevisiae* strain Y1790. The Y1790 strain is Leu<sup>+</sup> and His<sup>-</sup>. Expression of protein was induced by addition of either 500 µM or 250 µM of CuSO<sub>4</sub> at 30 °C in minimal medium supplemented with histidine. Cells were harvested 24 hours after induction. Extracts were prepared by growing cells to a concentration of OD<sub>600</sub> 5.0 in 50 mM citrate phosphate buffer (pH 4.0) plus 130 mM NaCl supplemented with protease inhibitors. Cells were disrupted

using glass beads and centrifuged for 20 min at 15,000 g. The recombinant protein was found to be 100% pellet associated.

Expression of the recombinant protein (molecular weight 63 kD) was demonstrated by Western blot analysis, using the anti-P501S monoclonal antibody 10E-D4-G3 described below. The amino acid sequence of the expressed protein is provided in SEQ ID NO: 792.

Fermentation processes for the production of the  $\alpha$  prepro-P501S-His tag recombinant protein in *S. cerevisiae* (strain Y1790 – CUP1 inducible promoter) were evaluated as follows. One hundred  $\mu$ l of a master seed containing  $2.5 \times 10^8$  cells/ml of transformed *S. cerevisiae* Y1790 were spread on FSC004AA solid medium. The composition of the FSC004AA medium is as follows: glucose 10 g/l;  $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$  0.0002 g/l; folic acid 0.000064 g/l;  $\text{KH}_2\text{PO}_4$  1 g/l;  $\text{MnSO}_4 \cdot \text{H}_2\text{O}$  0.0004 g/l; Inositol 0.064 g/l;  $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$  0.5 g/l;  $\text{H}_3\text{BO}_3$  0.0005 g/l; Pyridoxine 0.008 g/l;  $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$  0.1 g/l; KI 0.0001 g/l; Thiamine 0.008 g/l; NaCl 0.1 g/l;  $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$  0.00009 g/l; Niacin 0.000032 g/l;  $\text{FeCl}_3 \cdot 6\text{H}_2\text{O}$  0.0002 g/l; Riboflavin 0.000016 g/l; Panthotenate Ca 0.008 g/l;  $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$  0.00004 g/l; Biotin 0.000064 g/l; para-aminobenzoic acid 0.000016 g/l;  $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$  0.0004 g/l;  $(\text{NH}_4)_2\text{SO}_4$  5 g/l; agar 18 g/l; Histidine 0.1 g/l.

Two plates were incubated for 26 h at 30 °C. These solid pre-cultures were harvested in 5 ml of liquid medium FSC007AA and 0.5 ml (or  $9.3 \times 10^7$  cells) of this suspension was used to inoculate 2 liquid pre-cultures.

The composition of the FSC007AA medium is as follows: Glucose 10 g/l;  $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$  0.0002 g/l; folic acid 0.000064 g/l;  $\text{KH}_2\text{PO}_4$  1 g/l;  $\text{MnSO}_4 \cdot \text{H}_2\text{O}$  0.0004 g/l; Inositol 0.064 g/l;  $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$  0.5 g/l;  $\text{H}_3\text{BO}_3$  0.0005 g/l; Pyridoxine 0.008 g/l;  $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$  0.1 g/l; KI 0.0001 g/l; Thiamine 0.008 g/l; NaCl 0.1 g/l;  $\text{CoCl}_2 \cdot 6\text{H}_2\text{O}$  0.00009 g/l; Niacine 0.000032 g/l;  $\text{FeCl}_3 \cdot 6\text{H}_2\text{O}$  0.0002 g/l; Riboflavin 0.000016 g/l; Panthotenate Ca 0.008 g/l;  $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$  0.00004 g/l; Biotin 0.000064 g/l; para-aminobenzoic acid 0.000016 g/l;  $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$  0.0004 g/l;  $(\text{NH}_4)_2\text{SO}_4$  5 g/l; Histidine 0.1 g/l.

These pre-cultures were run for 20 hours in 2L flasks containing 400 ml of medium FSC007AA in order to obtain an OD of 1.8. The other characteristics of these pre-cultures are as follows: pH 2.8; glucose 2.3 g/L; ethanol 3.4 g/L.

The best timing for liquid pre-cultures for strain Y1790 was determined in preliminary experiments. Liquid pre-cultures containing 400 ml of medium and inoculated with various volumes of Master Seed (0.25, 0.5, 1 or 2 ml) were monitored in order to identify the best inoculum size and timing. Glucose, ethanol, pH, OD and  
5 cell number (determined by flow cytometry) were followed between 16 and 23 hours of culture. Glucose exhaustion and maximal biomass were obtained after 20 hour incubation with 0.5 inoculum. These conditions were adopted for transferring the pre-culture into fermentation.

In total, 800ml of pre-culture were used to inoculate a 20 L fermenter  
10 containing 5L of medium FSC002AA. Three ml of irradiated antifoam were added before inoculation. The composition of the FSC002AA medium is as follows:  
(NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub> 6.4 g/l; Na<sub>2</sub>MoO<sub>4</sub>·2H<sub>2</sub>O 2.05 mg/l; folic acid 0.54 mg/l; KH<sub>2</sub>PO<sub>4</sub> 8.25 g/l;  
MnSO<sub>4</sub>·H<sub>2</sub>O 4.1 mg/l; inositol 540 mg/l; MgSO<sub>4</sub>·7H<sub>2</sub>O 4.69 g/l; H<sub>3</sub>BO<sub>3</sub> 5.17 mg/l;  
pyridoxine 68 mg/l; CaCl<sub>2</sub>·2H<sub>2</sub>O 0.92 g/l; KI 1.03 mg/l; thiamine 68 mg/l; NaCl 0.06g/l;  
15 CoCl<sub>2</sub>·6H<sub>2</sub>O 0.92 mg/l; Niacine 0.27 mg/l; HCl 1 ml/l; FeCl<sub>3</sub>·6H<sub>2</sub>O 9.92 mg/l;  
Riboflavin 0.13 mg/l; CuSO<sub>4</sub>·5H<sub>2</sub>O 0.41 mg/l; Glucose 0.14 g/l; Panthotenate Ca 68  
mg/l; ZnSO<sub>4</sub>·7H<sub>2</sub>O 4.1 mg/l; Biotin 0.54 mg/l; para-aminobenzoic acid 0.13 mg/l;  
Histidine 0.3 g/l

The carbon source (glucose) was supplemented by a continuous feeding  
20 of FFB004AA medium. The composition of the FFB004AA medium is as follows:  
glucose 350 g/l; Na<sub>2</sub>MoO<sub>4</sub>·2H<sub>2</sub>O 5.15 mg/l; folic acid 1.36 mg/l; KH<sub>2</sub>PO<sub>4</sub> 20.6 g/l;  
MnSO<sub>4</sub>·H<sub>2</sub>O 10.3 mg/l; inositol 1350 mg/l; MgSO<sub>4</sub>·7H<sub>2</sub>O 11.7 g/l; H<sub>3</sub>BO<sub>3</sub> 12.9 mg/l;  
pyridoxine 170 mg/l; CaCl<sub>2</sub>·2H<sub>2</sub>O 2.35 g/l; KI 2.6 mg/l; thiamine 170 mg/l; NaCl 0.15 g/l;  
CoCl<sub>2</sub>·6H<sub>2</sub>O 2.3 mg/l; niacine 0.67 mg/l; HCl 2.5 ml/l; FeCl<sub>3</sub>·6H<sub>2</sub>O 24.8 mg/l;  
25 riboflavin; 0.33 mg/l; CuSO<sub>4</sub>·5H<sub>2</sub>O 1.03 mg/l; biotin 1.36 mg/l; panthotenate Ca 170  
mg/l; ZnSO<sub>4</sub>·7H<sub>2</sub>O 10.3 mg/l; para-aminobenzoic acid: 0.33 mg/l; histidine 5.35 g/l.

The residual glucose concentration was maintained very low (□50 mg/L)  
in order to minimize ethanol production by fermentation. This was achieved by limiting  
the development of the microorganism using a limited glucose feed rate. The Standard  
30 biomass content (OD 80-90) was reached in fermentation after 44 hour growth phase.

CUP1 promoter was then induced by adding 500μM CuSO<sub>4</sub> in order to

produce P501S antigen. CuSO<sub>4</sub> addition was followed by ethanol accumulation (up to 6 g/L), and the glucose feeding rate was then reduced in order to consume the ethanol. The copper available for the microorganism was monitored by testing Cu ion concentration in the broth supernatant using a spectrophotometric copper assay (DETC  
5 method). The fermentation was then supplemented by CuSO<sub>4</sub> throughout the induction phase in order to maintain its concentration between 150 and 250 µM in the supernatant. The biomass reached an OD of 100 at the end of induction. Cells were harvested after 8 hours of induction.

Cell homogenate was prepared and analysed by SDS-PAGE and Western  
10 Blot using standard protocols. A major protein band with the expected molecular weight of 62KD was detected by Western blot using anti-P501S monoclonal antibodies. Western blot analysis also showed that the major 62KD band was progressively produced from 30 minutes of induction on, and reached a maximum after 3 hours. No more antigen seemed to be produced between 3 and 12 hours of induction.

15 The number of passages through a French Press necessary to extract all the antigen from the cells was evaluated. One, three and five passages were tested and total cell lysates, supernatants and pellets of cell lysates were analysed by Western blot. Three passages through a French Press were sufficient to completely extract the antigen. The antigen was present in the insoluble fraction.

20

#### e) Expression of P703P in Baculovirus

The cDNA for full-length P703P-DE5 (SEQ ID NO: 326), together with several flanking restriction sites, was obtained by digesting the plasmid pCDNA703 with restriction endonucleases Xba I and Hind III. The resulting restriction fragment  
25 (approx. 800 base pairs) was ligated into the transfer plasmid pFastBacI which was digested with the same restriction enzymes. The sequence of the insert was confirmed by DNA sequencing. The recombinant transfer plasmid pFBP703 was used to make recombinant bacmid DNA and baculovirus using the Bac-To-Bac Baculovirus expression system (BRL Life Technologies). High Five cells were infected with the  
30 recombinant virus BVP703, as described above, to obtain recombinant P703P protein.



e) Expression of P788P in *E. Coli*

A truncated, N-terminal portion, of P788P (residues 1-644 of SEQ ID NO: 777; referred to as P788P-N) fused with a C-terminal 6xHis Tag was expressed in *E. coli* as follows. P788P cDNA was amplified using the primers AW080 and AW081 (SEQ ID NO: 672 and 673). AW080 is a sense cloning primer with an NdeI site. AW081 is an antisense cloning primer with a XhoI site. The PCR-amplified P788P, as well as the vector pCRX1, were digested with NdeI and XhoI. Vector and insert were ligated and transformed into NovaBlue cells. Colonies were randomly screened for insert and then sequenced. P788P-N clone #6 was confirmed to be identical to the designed construct. The expression construct P788P-N #6/pCRX1 was transformed into *E. coli* BL21 CodonPlus-RIL competent cells. After induction, most of the cells grew well, achieving OD600 of greater than 2.0 after 3 hr. Coomassie stained SDS-PAGE showed an over-expressed band at about 75 kD. Western blot analysis using a 6xHisTag antibody confirmed the band was P788P-N. The determined cDNA sequence for P788P-N is provided in SEQ ID NO: 674, with the corresponding amino acid sequence being provided in SEQ ID NO: 675.

f) Expression of P510S in *E. Coli*

The P510S protein has 9 potential transmembrane domains and is predicted to be located at the plasma membrane. The C-terminal protein of this protein, as well as the predicted third extracellular domain of P510S were expressed in *E. coli* as follows.

The expression construct referred to as Ra12-P501S-C was designed to have a 6 HisTag at the N-terminal end, followed by the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 676) and then the C-terminal portion of P510S (amino residues 1176-1261 of SEQ ID NO: 538). Full-length P510S was used to amplify the P510S-C fragment by PCR using the primers AW056 and AW057 (SEQ ID NO: 677 and 678, respectively). AW056 is a sense cloning primer with an EcoRI site. AW057 is an antisense primer with stop and XhoI sites. The amplified P501S fragment and Ra12/pCRX1 were digested with EcoRI and XhoI and then purified. The insert and

vector were ligated together and transformed into NovaBlue. Colonies were randomly screened for insert and sequences. For protein expression, the expression construct was transformed into *E. coli* BL21 (DE3) CodonPlus-RIL competent cells. A mini-induction screen was performed to optimize the expression conditions. After induction  
5 the cells grew well, achieving OD 600 nm greater than 2.0 after 3 hours. Coomassie stain SDS-PAGE showed a highly over-expressed band at approx. 30 kD. Though this is higher than the expected molecular weight, western blot analysis was positive, showing this band to be the His tag-containing protein. The optimized culture conditions are as follows. Dilute overnight culture/daytime culture (LB + kanamycin +  
10 chloramphenicol) into 2xYT (with kanamycin and chloramphenicol) at a ratio of 25 ml culture to 1 liter 2xYT. Allow to grow at 37 °C until OD600 = 0.6. Take an aliquot out as T0 sample. Add 1 mM IPTG and allow to grow at 30 °C for 3 hours. Take out a T3 sample, spin down cells and store at -80 °C. The determined cDNA and amino acid sequences for the Ra12-P510S-C construct are provided in SEQ ID NO: 679 and 682,  
15 respectively.

The expression construct P510S-C was designed to have a 5' added start codon and a glycine (GGA) codon and then the P510S C terminal fragment followed by the in frame 6x histidine tag and stop codon from the pET28b vector. The cloning strategy is similar to that used for Ra12-P510S-C, except that the PCR primers employed were  
20 those shown in SEQ ID NO: 685 and 686, respectively and the NcoI/XhoI cut in pET28b was used. The primer of SEQ ID NO: 685 created a 5' NcoI site and added a start codon. The antisense primer of SEQ ID NO: 686 creates a XhoI site on P510S C terminal fragment. Clones were confirmed by sequencing. For protein expression, the expression construct was transformed into *E. coli* BL21 (DE3) CodonPlus-RIL  
25 competent cells. An OD600 of greater than 2.0 was obtained 30 hours after induction. Coomassie stained SDS-PAGE showed an over-expressed band at about 11 kD. Western blot analysis confirmed that the band was P510S-C, as did N-terminal protein sequencing. The optimized culture conditions are as follows: dilute overnight culture/daytime culture (LB + kanamycin + chloramphenicol) into 2x YT (+ kanamycin  
30 and chloramphenicol) at a ratio of 25 mL culture to 1 liter 2x YT, and allow to grow at

37 °C until an OD 600 of about 0.5 is reached. Take out an aliquot as T0 sample. Add 1 mM IPTG and allow to grow at 30 °C for 3 hours. Spin down the cells and store at -80 °C until purification. The determined cDNA and amino acid sequences for the P510S-C construct are shown in SEQ ID NO: 680 and 683, respectively.

- 5                   The predicted third extracellular domain of P510S (P510S-E3; residues 328-676 of SEQ ID NO: 538) was expressed in *E. coli* as follows. The P510S fragment was amplified by PCR using the primers shown in SEQ ID NO: 687 and 688. The primer of SEQ ID NO: 687 is a sense primer with an NdeI site for use in ligating into pPDM. The primer of SEQ ID NO: 688 is an antisense primer with an added XhoI site  
10 for use in ligating into pPDM. The resulting fragment was cloned to pPDM at the NdeI and XhoI sites. Clones were confirmed by sequencing. For protein expression, the clone was transformed into *E. coli* BL21 (DE3) CodonPlus-RIL competent cells. After induction, an OD600 of greater than 2.0 was achieved after 3 hours. Coomassie stained SDS-PAGE showed an over-expressed band at about 39 kD, and N-terminal sequencing  
15 confirmed the N-terminal to be that of P510S-E3. Optimized culture conditions are as follows: dilute overnight culture/daytime culture (LB + kanamycin + chloramphenicol) into 2x YT (kanamycin and chloramphenicol) at a ratio of 25 ml culture to 1 liter 2x YT. Allow to grow at 37 °C until OD 600 equals 0.6. Take out an aliquot as T0 sample. Add 1 mM IPTG and allow to grow at 30 °C for 3 hours. Take out a T3  
20 sample, spin down the cells and store at -80 °C until purification. The determined cDNA and amino acid sequences for the P501S-E3 construct are provided in SEQ ID NO: 681 and 684, respectively.

g) Expression of P775S in *E. Coli*

- 25                   The antigen P775P contains multiple open reading frames (ORF). The third ORF, encoding the protein of SEQ ID NO: 483, has the best emotif score. An expression fusion construct containing the *M. tuberculosis* antigen Ra12 (SEQ ID NO: 676) and P775P-ORF3 with an N-terminal 6x HisTag was prepared as follows. P775P-ORF3 was amplified using the sense PCR primers of SEQ ID NO: 689 and the anti-sense PCR primer of SEQ ID NO: 690. The PCR amplified fragment of P775P and

Ra12/pCRX1 were digested with the restriction enzymes EcoRI and XhoI. Vector and insert were ligated and then transformed into NovaBlue cells. Colonies were randomly screened for insert and then sequenced. A clone having the desired sequence was transformed into *E. coli* BL21 (DE3) CodonPlus-RIL competent cells. Two hours after  
5 induction, the cell density peaked at OD600 of approximately 1.8. Coomassie stained SDS-PAGE showed an over-expressed band at about 31 kD. Western blot using 6x HisTag antibody confirmed that the band was Ra12-P775P-ORF3. The determined cDNA and amino acid sequences for the fusion construct are provided in SEQ ID NO: 691 and 692, respectively.

10

#### **H) EXPRESSION OF A P703P HIS TAG FUSION PROTEIN IN *E. COLI***

The cDNA for the coding region of P703P was prepared by PCR using the primers of SEQ ID NO: 693 and 694. The PCR product was digested with EcoRI restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag  
15 in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into *E. coli* BL21 (DE3) pLys S expression host cells. The determined amino acid and cDNA sequences for the expressed recombinant P703P are provided in SEQ ID NO: 695 and 696, respectively.

20

#### **I) EXPRESSION OF A P705P HIS TAG FUSION PROTEIN IN *E. COLI***

The cDNA for the coding region of P705P was prepared by PCR using the primers of SEQ ID NO: 697 and 698. The PCR product was digested with EcoRI restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag  
25 in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into *E. coli* BL21 (DE3) pLys S and BL21 (DE3) CodonPlus expression host cells. The determined amino acid and cDNA sequences for the expressed recombinant P705P are provided in SEQ ID NO: 699 and 700, respectively.

30

#### J) EXPRESSION OF A P711P HIS TAG FUSION PROTEIN IN *E. COLI*

The cDNA for the coding region of P711P was prepared by PCR using the primers of SEQ ID NO: 701 and 702. The PCR product was digested with EcoRI restriction enzyme, gel purified and cloned into a modified pET28 vector with a His tag in frame, which had been digested with Eco72I and EcoRI restriction enzymes. The correct construct was confirmed by DNA sequence analysis and then transformed into *E. coli* BL21 (DE3) pLys S and BL21 (DE3) CodonPlus expression host cells. The determined amino acid and cDNA sequences for the expressed recombinant P711P are provided in SEQ ID NO: 703 and 704, respectively.

10

#### EXAMPLE 18

##### PREPARATION AND CHARACTERIZATION OF ANTIBODIES AGAINST PROSTATE-SPECIFIC POLYPEPTIDES

15

##### a) Preparation and Characterization of Polyclonal Antibodies against P703P, P504S and P509S

Polyclonal antibodies against P703P, P504S and P509S were prepared as follows.

Each prostate tumor antigen expressed in an *E. coli* recombinant expression system was grown overnight in LB broth with the appropriate antibiotics at 37°C in a shaking incubator. The next morning, 10 ml of the overnight culture was added to 500 ml to 2x YT plus appropriate antibiotics in a 2L-baffled Erlenmeyer flask. When the Optical Density (at 560 nm) of the culture reached 0.4-0.6, the cells were induced with IPTG (1 mM). Four hours after induction with IPTG, the cells were harvested by centrifugation. The cells were then washed with phosphate buffered saline and centrifuged again. The supernatant was discarded and the cells were either frozen for future use or immediately processed. Twenty ml of lysis buffer was added to the cell pellets and vortexed. To break open the *E. coli* cells, this mixture was then run

20

25

through the French Press at a pressure of 16,000 psi. The cells were then centrifuged again and the supernatant and pellet were checked by SDS-PAGE for the partitioning of the recombinant protein. For proteins that localized to the cell pellet, the pellet was resuspended in 10 mM Tris pH 8.0, 1% CHAPS and the inclusion body pellet was washed and centrifuged again. This procedure was repeated twice more. The washed inclusion body pellet was solubilized with either 8 M urea or 6 M guanidine HCl containing 10 mM Tris pH 8.0 plus 10 mM imidazole. The solubilized protein was added to 5 ml of nickel-chelate resin (Qiagen) and incubated for 45 min to 1 hour at room temperature with continuous agitation. After incubation, the resin and protein mixture were poured through a disposable column and the flow through was collected. The column was then washed with 10-20 column volumes of the solubilization buffer. The antigen was then eluted from the column using 8M urea, 10 mM Tris pH 8.0 and 300 mM imidazole and collected in 3 ml fractions. A SDS-PAGE gel was run to determine which fractions to pool for further purification.

As a final purification step, a strong anion exchange resin such as HiPrepQ (Biorad) was equilibrated with the appropriate buffer and the pooled fractions from above were loaded onto the column. Each antigen was eluted off the column with a increasing salt gradient. Fractions were collected as the column was run and another SDS-PAGE gel was run to determine which fractions from the column to pool. The pooled fractions were dialyzed against 10 mM Tris pH 8.0. The proteins were then vialled after filtration through a 0.22 micron filter and the antigens were frozen until needed for immunization.

Four hundred micrograms of each prostate antigen was combined with 100 micrograms of muramyl dipeptide (MDP). Every four weeks rabbits were boosted with 100 micrograms mixed with an equal volume of Incomplete Freund's Adjuvant (IFA). Seven days following each boost, the animal was bled. Sera was generated by incubating the blood at 4°C for 12-4 hours followed by centrifugation.

Ninety-six well plates were coated with antigen by incubating with 50 microliters (typically 1 microgram) of recombinant protein at 4 °C for 20 hours. 250 microliters of BSA blocking buffer was added to the wells and incubated at room

temperature for 2 hours. Plates were washed 6 times with PBS/0.01% Tween. Rabbit sera was diluted in PBS. Fifty microliters of diluted sera was added to each well and incubated at room temperature for 30 min. Plates were washed as described above before 50 microliters of goat anti-rabbit horse radish peroxidase (HRP) at a 1:10000  
5 dilution was added and incubated at room temperature for 30 min. Plates were again washed as described above and 100 microliters of TMB microwell peroxidase substrate was added to each well. Following a 15 min incubation in the dark at room temperature, the colorimetric reaction was stopped with 100 microliters of 1N H<sub>2</sub>SO<sub>4</sub> and read immediately at 450 nm. All polyclonal antibodies showed immunoreactivity  
10 to the appropriate antigen.

b) Preparation and Characterization of Antibodies against P501S

A murine monoclonal antibody directed against the carboxy-terminus of the prostate-specific antigen P501S was prepared as follows.

A truncated fragment of P501S (amino acids 355-526 of SEQ ID NO:  
15 113) was generated and cloned into the pET28b vector (Novagen) and expressed in *E. coli* as a thioredoxin fusion protein with a histidine tag. The trx-P501S fusion protein was purified by nickel chromatography, digested with thrombin to remove the trx fragment and further purified by an acid precipitation procedure followed by reverse phase HPLC.

20 Mice were immunized with truncated P501S protein. Serum bleeds from mice that potentially contained anti-P501S polyclonal sera were tested for P501S-specific reactivity using ELISA assays with purified P501S and trx-P501S proteins. Serum bleeds that appeared to react specifically with P501S were then screened for P501S reactivity by Western analysis. Mice that contained a P501S-specific antibody  
25 component were sacrificed and spleen cells were used to generate anti-P501S antibody producing hybridomas using standard techniques. Hybridoma supernatants were tested for P501S-specific reactivity initially by ELISA, and subsequently by FACS analysis of reactivity with P501S transduced cells. Based on these results, a monoclonal hybridoma referred to as 10E3 was chosen for further subcloning. A number of subclones were

generated, tested for specific reactivity to P501S using ELISA and typed for IgG isotype. The results of this analysis are shown below in Table V. Of the 16 subclones tested, the monoclonal antibody 10E3-G4-D3 was selected for further study.

5

Table V

Isotype analysis of murine anti-P501S monoclonal antibodies

Hybridoma clone	Isotype	Estimated [Ig] in supernatant ( $\mu\text{g/ml}$ )
4D11	IgG1	14.6
1G1	IgG1	0.6
4F6	IgG1	72
4H5	IgG1	13.8
4H5-E12	IgG1	10.7
4H5-EH2	IgG1	9.2
4H5-H2-A10	IgG1	10
4H5-H2-A3	IgG1	12.8
4H5-H2-A10-G6	IgG1	13.6
4H5-H2-B11	IgG1	12.3
10E3	IgG2a	3.4
10E3-D4	IgG2a	3.8
10E3-D4-G3	IgG2a	9.5
10E3-D4-G6	IgG2a	10.4
10E3-E7	IgG2a	6.5
8H12	IgG2a	0.6

The specificity of 10E3-G4-D3 for P501S was examined by FACS analysis. Specifically, cells were fixed (2% formaldehyde, 10 minutes), permeabilized (0.1% saponin, 10 minutes) and stained with 10E3-G4-D3 at 0.5 – 1  $\mu\text{g/ml}$ , followed by incubation with a secondary, FITC-conjugated goat anti-mouse Ig antibody (Pharmingen, San Diego, CA). Cells were then analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. For analysis of infected cells, B-LCL were infected with a vaccinia vector that expresses P501S. To demonstrate specificity in these assays, B-LCL transduced with a different antigen (P703P) and uninfected B-LCL vectors were utilized. 10E3-G4-D3 was shown to bind with P501S-transduced B-



LCL and also with P501S-infected B-LCL, but not with either uninfected cells or P703P-transduced cells.

To determine whether the epitope recognized by 10E3-G4-D3 was found on the surface or in an intracellular compartment of cells, B-LCL were transduced with  
5 P501S or HLA-B8' as a control antigen and either fixed and permeabilized as described above or directly stained with 10E3-G4-D3 and analyzed as above. Specific recognition of P501S by 10E3-G4-D3 was found to require permeabilization, suggesting that the epitope recognized by this antibody is intracellular.

The reactivity of 10E3-G4-D3 with the three prostate tumor cell lines  
10 Lncap, PC-3 and DU-145, which are known to express high, medium and very low levels of P501S, respectively, was examined by permeabilizing the cells and treating them as described above. Higher reactivity of 10E3-G4-D3 was seen with Lncap than with PC-3, which in turn showed higher reactivity than DU-145. These results are in agreement with the real time PCR and demonstrate that the antibody specifically  
15 recognizes P501S in these tumor cell lines and that the epitope recognized in prostate tumor cell lines is also intracellular.

Specificity of 10E3-G4-D3 for P501S was also demonstrated by Western blot analysis. Lysates from the prostate tumor cell lines Lncap, DU-145 and PC-3, from P501S-transiently transfected HEK293 cells, and from non-transfected HEK293 cells  
20 were generated. Western blot analysis of these lysates with 10E3-G4-D3 revealed a 46 kDa immunoreactive band in Lncap, PC-3 and P501S-transfected HEK cells, but not in DU-145 cells or non-transfected HEK293 cells. P501S mRNA expression is consistent with these results since semi-quantitative PCR analysis revealed that P501S mRNA is expressed in Lncap, to a lesser but detectable level in PC-3 and not at all in DU-145  
25 cells. Bacterially expressed and purified recombinant P501S (referred to as P501SStr2) was recognized by 10E3-G4-D3 (24 kDa), as was full-length P501S that was transiently expressed in HEK293 cells using either the expression vector VR1012 or pCEP4. Although the predicted molecular weight of P501S is 60.5 kDa, both transfected and "native" P501S run at a slightly lower mobility due to its hydrophobic nature.

Immunohistochemical analysis was performed on prostate tumor and a panel of normal tissue sections (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder, ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). Tissue samples were fixed in formalin solution for 24 hours and embedded in paraffin before being sliced into 10 micron sections. Tissue sections were permeabilized and incubated with 10E3-G4-D3 antibody for 1 hr. HRP-labeled anti-mouse followed by incubation with DAB chromogen was used to visualize P501S immunoreactivity. P501S was found to be highly expressed in both normal prostate and prostate tumor tissue but was not detected in any of the other tissues tested.

To identify the epitope recognized by 10E3-G4-D3, an epitope mapping approach was pursued. A series of 13 overlapping 20-21 mers (5 amino acid overlap; SEQ ID NO: 489-501) was synthesized that spanned the fragment of P501S used to generate 10E3-G4-D3. Flat bottom 96 well microtiter plates were coated with either the peptides or the P501S fragment used to immunize mice, at 1 microgram/ml for 2 hours at 37 °C. Wells were then aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature, and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified antibody 10E3-G4-D3 was added at 2 fold dilutions (1000 ng – 16 ng) in PBST and incubated for 30 minutes at room temperature. This was followed by washing 6 times with PBST and subsequently incubating with HRP-conjugated donkey anti-mouse IgG (H+L)Affinipure F(ab') fragment (Jackson Immunoresearch, West Grove, PA) at 1:20000 for 30 minutes. Plates were then washed and incubated for 15 minutes in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As shown in Fig. 8, reactivity was seen with the peptide of SEQ ID NO: 496 (corresponding to amino acids 439-459 of P501S) and with the P501S fragment but not with the remaining peptides, demonstrating that the epitope recognized by 10E3-G4-D3 is localized to amino acids 439-459 of SEQ ID NO: 113.

In order to further evaluate the tissue specificity of P501S, multi-array immunohistochemical analysis was performed on approximately 4700 different human tissues encompassing all the major normal organs as well as neoplasias derived from

these tissues. Sixty-five of these human tissue samples were of prostate origin. Tissue sections 0.6 mm in diameter were formalin-fixed and paraffin embedded. Samples were pretreated with HIER using 10 mM citrate buffer pH 6.0 and boiling for 10 min. Sections were stained with 10E3-G4-D3 and P501S immunoreactivity was visualized with HRP. All the 65 prostate tissues samples (5 normal, 55 untreated prostate tumors, 5 hormone refractory prostate tumors) were positive, showing distinct perinuclear staining. All other tissues examined were negative for P501S expression.

c) Preparation and Characterization of Antibodies against P503S

A fragment of P503S (amino acids 113-241 of SEQ ID NO: 114) was expressed and purified from bacteria essentially as described above for P501S and used to immunize both rabbits and mice. Mouse monoclonal antibodies were isolated using standard hybridoma technology as described above. Rabbit monoclonal antibodies were isolated using Selected Lymphocyte Antibody Method (SLAM) technology at Immgenics Pharmaceuticals (Vancouver, BC, Canada). Table VI, below, lists the monoclonal antibodies that were developed against P503S.

Table VI

Antibody	Species
20D4	Rabbit
JA1	Rabbit
1A4	Mouse
1C3	Mouse
1C9	Mouse
1D12	Mouse
2A11	Mouse
2H9	Mouse
4H7	Mouse
8A8	Mouse
8D10	Mouse
9C12	Mouse
6D12	Mouse

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 20D4 and JA1 were determined and are provided in SEQ ID NO: 502 and 503, respectively.

5           In order to better define the epitope binding region of each of the antibodies, a series of overlapping peptides were generated that span amino acids 109-213 of SEQ ID NO: 114. These peptides were used to epitope map the anti-P503S monoclonal antibodies by ELISA as follows. The recombinant fragment of P503S that was employed as the immunogen was used as a positive control. Ninety-six well  
10 microtiter plates were coated with either peptide or recombinant antigen at 20 ng/well overnight at 4 °C. Plates were aspirated and blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature then washed in PBS containing 0.1% Tween 20 (PBST). Purified rabbit monoclonal antibodies diluted in PBST were added to the wells and incubated for 30 min at room temperature. This was  
15 followed by washing 6 times with PBST and incubation with Protein-A HRP conjugate at a 1:2000 dilution for a further 30 min. Plates were washed six times in PBST and incubated with tetramethylbenzidine (TMB) substrate for a further 15 min. The reaction was stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using at ELISA plate reader. ELISA with the mouse monoclonal antibodies was performed with  
20 supernatants from tissue culture run neat in the assay.

All of the antibodies bound to the recombinant P503S fragment, with the exception of the negative control SP2 supernatant. 20D4, JA1 and 1D12 bound strictly to peptide #2101 (SEQ ID NO: 504), which corresponds to amino acids 151-169 of SEQ ID NO: 114. 1C3 bound to peptide #2102 (SEQ ID NO: 505), which corresponds  
25 to amino acids 165-184 of SEQ ID NO: 114. 9C12 bound to peptide #2099 (SEQ ID NO: 522), which corresponds to amino acids 120-139 of SEQ ID NO: 114. The other antibodies bind to regions that were not examined in these studies.

Subsequent to epitope mapping, the antibodies were tested by FACS analysis on a cell line that stably expressed P503S to confirm that the antibodies bind to  
30 cell surface epitopes. Cells stably transfected with a control plasmid were employed as

a negative control. Cells were stained live with no fixative. 0.5 ug of anti-P503S monoclonal antibody was added and cells were incubated on ice for 30 min before being washed twice and incubated with a FITC-labelled goat anti-rabbit or mouse secondary antibody for 20 min. After being washed twice, cells were analyzed with an Excalibur  
5 fluorescent activated cell sorter. The monoclonal antibodies 1C3, 1D12, 9C12, 20D4 and JA1, but not 8D3, were found to bind to a cell surface epitope of P503S.

In order to determine which tissues express P503S, immunohistochemical analysis was performed, essentially as described above, on a panel of normal tissues (prostate, adrenal, breast, cervix, colon, duodenum, gall bladder,  
10 ileum, kidney, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis). HRP-labeled anti-mouse or anti-rabbit antibody followed by incubation with TMB was used to visualize P503S immunoreactivity. P503S was found to be highly expressed in prostate tissue, with lower levels of expression being observed in cervix, colon, ileum and kidney, and no expression being observed in adrenal, breast, duodenum, gall  
15 bladder, ovary, pancreas, parotid gland, skeletal muscle, spleen and testis.

Western blot analysis was used to characterize anti-P503S monoclonal antibody specificity. SDS-PAGE was performed on recombinant (rec) P503S expressed in and purified from bacteria and on lysates from HEK293 cells transfected with full length P503S. Protein was transferred to nitrocellulose and then Western blotted with  
20 each of the anti-P503S monoclonal antibodies (20D4, JA1, 1D12, 6D12 and 9C12) at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to either a goat anti-mouse monoclonal antibody or to protein A-sepharose. The monoclonal antibody 20D4 detected the appropriate molecular weight 14 kDa recombinant P503S (amino acids 113-241) and the 23.5 kDa  
25 species in the HEK293 cell lysates transfected with full length P503S. Other anti-P503S monoclonal antibodies displayed similar specificity by Western blot.

#### d) Preparation and Characterization of Antibodies against P703P

Rabbits were immunized with either a truncated (P703Ptr1; SEQ ID NO: 172) or full-length mature form (P703Pfl; SEQ ID NO: 523) of recombinant P703P

protein was expressed in and purified from bacteria as described above. Affinity purified polyclonal antibody was generated using immunogen P703Pfl or P703Ptrl attached to a solid support. Rabbit monoclonal antibodies were isolated using SLAM technology at Immgenics Pharmaceuticals. Table VII below lists both the polyclonal and monoclonal antibodies that were generated against P703P.

Table VII

Antibody	Immunogen	Species/type
Aff. Purif. P703P (truncated); #2594	P703Ptrl	Rabbit polyclonal
Aff. Purif. P703P (full length); #9245	P703Pfl	Rabbit polyclonal
2D4	P703Ptrl	Rabbit monoclonal
8H2	P703Ptrl	Rabbit monoclonal
7H8	P703Ptrl	Rabbit monoclonal

The DNA sequences encoding the complementarity determining regions (CDRs) for the rabbit monoclonal antibodies 8H2, 7H8 and 2D4 were determined and are provided in SEQ ID NO: 506-508, respectively.

Epitope mapping studies were performed as described above. Monoclonal antibodies 2D4 and 7H8 were found to specifically bind to the peptides of SEQ ID NO: 509 (corresponding to amino acids 145-159 of SEQ ID NO: 172) and SEQ ID NO: 510 (corresponding to amino acids 11-25 of SEQ ID NO: 172), respectively. The polyclonal antibody 2594 was found to bind to the peptides of SEQ ID NO: 511-514, with the polyclonal antibody 9427 binding to the peptides of SEQ ID NO: 515-517.

The specificity of the anti-P703P antibodies was determined by Western blot analysis as follows. SDS-PAGE was performed on (1) bacterially expressed recombinant antigen; (2) lysates of HEK293 cells and Ltk<sup>-/-</sup> cells either untransfected or transfected with a plasmid expressing full length P703P; and (3) supernatant isolated from these cell cultures. Protein was transferred to nitrocellulose and then Western blotted using the anti-P703P polyclonal antibody #2594 at an antibody concentration of 1 ug/ml. Protein was detected using horse radish peroxidase (HRP) conjugated to an anti-rabbit antibody. A 35 kDa immunoreactive band could be observed with

recombinant P703P. Recombinant P703P runs at a slightly higher molecular weight since it is epitope tagged. In lysates and supernatants from cells transfected with full length P703P, a 30 kDa band corresponding to P703P was observed. To assure specificity, lysates from HEK293 cells stably transfected with a control plasmid were  
5 also tested and were negative for P703P expression. Other anti-P703P antibodies showed similar results.

Immunohistochemical studies were performed as described above, using anti-P703P monoclonal antibody. P703P was found to be expressed at high levels in normal prostate and prostate tumor tissue but was not detectable in all other tissues  
10 tested (breast tumor, lung tumor and normal kidney).

e) Preparation and Characterization of Antibodies against P504S

Full-length P504S (SEQ ID NO: 108) was expressed and purified from bacteria essentially as described above for P501S and employed to raise rabbit monoclonal antibodies using Selected Lymphocyte Antibody Method (SLAM)  
15 technology at Immgenics Pharmaceuticals (Vancouver, BC, Canada). The anti-P504S monoclonal antibody 13H4 was shown by Western blot to bind to both expressed recombinant P504S and to native P504S in tumor cells.

Immunohistochemical studies using 13H4 to assess P504S expression in various prostate tissues were performed as described above. A total of 104 cases,  
20 including 65 cases of radical prostatectomies with prostate cancer (PC), 26 cases of prostate biopsies and 13 cases of benign prostate hyperplasia (BPH), were stained with the anti-P504S monoclonal antibody 13H4. P504S showed strongly cytoplasmic granular staining in 64/65 (98.5%) of PCs in prostatectomies and 26/26 (100%) of PCs in prostatic biopsies. P504S was stained strongly and diffusely in carcinomas (4+ in  
25 91.2% of cases of PC; 3+ in 5.5%; 2+ in 2.2% and 1+ in 1.1%) and high grade prostatic intraepithelial neoplasia (4+ in all cases). The expression of P504S did not vary with Gleason score. Only 17/91 (18.7%) of cases of NP/BPH around PC and 2/13 (15.4%) of BPH cases were focally (1+, no 2+ to 4+ in all cases) and weakly positive for P504S in large glands. Expression of P504S was not found in small atrophic glands, postatrophic  
30 hyperplasia, basal cell hyperplasia and transitional cell metaplasia in either biopsies or

prostatectomies. P504S was thus found to be over-expressed in all Gleason scores of prostate cancer (98.5 to 100% of sensitivity) and exhibited only focal positivities in large normal glands in 19/104 of cases (82.3% of specificity). These findings indicate that P504S may be usefully employed for the diagnosis of prostate cancer.

5

## EXAMPLE 19

### CHARACTERIZATION OF CELL SURFACE EXPRESSION AND CHROMOSOME LOCALIZATION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

10 This example describes studies demonstrating that the prostate-specific antigen P501S is expressed on the surface of cells, together with studies to determine the probable chromosomal location of P501S.

The protein P501S (SEQ ID NO: 113) is predicted to have 11 transmembrane domains. Based on the discovery that the epitope recognized by the anti-  
15 P501S monoclonal antibody 10E3-G4-D3 (described above in Example 17) is intracellular, it was predicted that following transmembrane determinants would allow the prediction of extracellular domains of P501S. Fig. 9 is a schematic representation of the P501S protein showing the predicted location of the transmembrane domains and the intracellular epitope described in Example 17. Underlined sequence represents the  
20 predicted transmembrane domains, bold sequence represents the predicted extracellular domains, and italicized sequence represents the predicted intracellular domains. Sequence that is both bold and underlined represents sequence employed to generate polyclonal rabbit serum. The location of the transmembrane domains was predicted using HHMTOP as described by Tusnady and Simon (Principles Governing Amino  
25 Acid Composition of Integral Membrane Proteins: Applications to Topology Prediction, *J. Mol. Biol.* 283:489-506, 1998).

Based on Fig. 9, the P501S domain flanked by the transmembrane domains corresponding to amino acids 274-295 and 323-342 is predicted to be extracellular. The peptide of SEQ ID NO: 518 corresponds to amino acids 306-320 of  
30 P501S and lies in the predicted extracellular domain. The peptide of SEQ ID NO: 519,



which is identical to the peptide of SEQ ID NO: 518 with the exception of the substitution of the histidine with an asparagine, was synthesized as described above. A Cys-Gly was added to the C-terminus of the peptide to facilitate conjugation to the carrier protein. Cleavage of the peptide from the solid support was carried out using the  
5 following cleavage mixture: trifluoroacetic acid:ethanediol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for two hours, the peptide was precipitated in cold ether. The peptide pellet was then dissolved in 10% v/v acetic acid and lyophilized prior to purification by C18 reverse phase hplc. A gradient of 5-60% acetonitrile (containing 0.05% TFA) in water (containing 0.05% TFA) was used to elute the peptide. The purity  
10 of the peptide was verified by hplc and mass spectrometry, and was determined to be >95%. The purified peptide was used to generate rabbit polyclonal antisera as described above.

Surface expression of P501S was examined by FACS analysis. Cells were stained with the polyclonal anti-P501S peptide serum at 10 µg/ml, washed,  
15 incubated with a secondary FITC-conjugated goat anti-rabbit Ig antibody (ICN), washed and analyzed for FITC fluorescence using an Excalibur fluorescence activated cell sorter. For FACS analysis of transduced cells, B-LCL were retrovirally transduced with P501S. To demonstrate specificity in these assays, B-LCL transduced with an irrelevant antigen (P703P) or nontransduced were stained in parallel. For FACS analysis of  
20 prostate tumor cell lines, Lncap, PC-3 and DU-145 were utilized. Prostate tumor cell lines were dissociated from tissue culture plates using cell dissociation medium and stained as above. All samples were treated with propidium iodide (PI) prior to FACS analysis, and data was obtained from PI-excluding (*i.e.*, intact and non-permeabilized) cells. The rabbit polyclonal serum generated against the peptide of SEQ ID NO: 519  
25 was shown to specifically recognize the surface of cells transduced to express P501S, demonstrating that the epitope recognized by the polyclonal serum is extracellular.

To determine biochemically if P501S is expressed on the cell surface, peripheral membranes from Lncap cells were isolated and subjected to Western blot analysis. Specifically, Lncap cells were lysed using a dounce homogenizer in 5 ml of  
30 homogenization buffer (250 mM sucrose, 10 mM HEPES, 1mM EDTA, pH 8.0, 1

complete protease inhibitor tablet (Boehringer Mannheim)). Lysate samples were spun at 1000 g for 5 min at 4 °C. The supernatant was then spun at 8000g for 10 min at 4 °C. Supernatant from the 8000g spin was recovered and subjected to a 100,000g spin for 30 min at 4 °C to recover peripheral membrane. Samples were then separated by SDS-  
5 PAGE and Western blotted with the mouse monoclonal antibody 10E3-G4-D3 (described above in Example 17) using conditions described above. Recombinant purified P501S, as well as HEK293 cells transfected with and over-expressing P501S were included as positive controls for P501S detection. LCL cell lysate was included as a negative control. P501S could be detected in Lncap total cell lysate, the 8000g  
10 (internal membrane) fraction and also in the 100,000g (plasma membrane) fraction. These results indicate that P501S is expressed at, and localizes to, the peripheral membrane.

To demonstrate that the rabbit polyclonal antiserum generated to the peptide of SEQ ID NO: 519 specifically recognizes this peptide as well as the  
15 corresponding native peptide of SEQ ID NO: 518, ELISA analyses were performed. For these analyses, flat-bottomed 96 well microtiter plates were coated with either the peptide of SEQ ID NO: 519, the longer peptide of SEQ ID NO: 520 that spans the entire predicted extracellular domain, the peptide of SEQ ID NO: 521 which represents the epitope recognized by the P501S-specific antibody 10E3-G4-D3, or a P501S fragment  
20 (corresponding to amino acids 355-526 of SEQ ID NO: 113) that does not include the immunizing peptide sequence, at 1 µg/ml for 2 hours at 37 °C. Wells were aspirated, blocked with phosphate buffered saline containing 1% (w/v) BSA for 2 hours at room temperature and subsequently washed in PBS containing 0.1% Tween 20 (PBST). Purified anti-P501S polyclonal rabbit serum was added at 2 fold dilutions (1000 ng -  
25 125 ng) in PBST and incubated for 30 min at room temperature. This was followed by washing 6 times with PBST and incubating with HRP-conjugated goat anti-rabbit IgG (H+L) Affinipure F(ab') fragment at 1:20000 for 30 min. Plates were then washed and incubated for 15 min in tetramethyl benzidine. Reactions were stopped by the addition of 1N sulfuric acid and plates were read at 450 nm using an ELISA plate reader. As  
30 shown in Fig. 11, the anti-P501S polyclonal rabbit serum specifically recognized the

peptide of SEQ ID NO: 519 used in the immunization as well as the longer peptide of SEQ ID NO: 520, but did not recognize the irrelevant P501S-derived peptides and fragments.

In further studies, rabbits were immunized with peptides derived from the P501S sequence and predicted to be either extracellular or intracellular, as shown in Fig. 9. Polyclonal rabbit sera were isolated and polyclonal antibodies in the serum were purified, as described above. To determine specific reactivity with P501S, FACS analysis was employed, utilizing either B-LCL transduced with P501S or the irrelevant antigen P703P, of B-LCL infected with vaccinia virus-expressing P501S. For surface expression, dead and non-intact cells were excluded from the analysis as described above. For intracellular staining, cells were fixed and permeabilized as described above. Rabbit polyclonal serum generated against the peptide of SEQ ID NO: 548, which corresponds to amino acids 181-198 of P501S, was found to recognize a surface epitope of P501S. Rabbit polyclonal serum generated against the peptide SEQ ID NO: 551, which corresponds to amino acids 543-553 of P501S, was found to recognize an epitope that was either potentially extracellular or intracellular since in different experiments intact or permeabilized cells were recognized by the polyclonal sera. Based on similar deductive reasoning, the sequences of SEQ ID NO: 541-547, 549 and 550, which correspond to amino acids 109-122, 539-553, 509-520, 37-54, 342-359, 295-323, 217-274, 143-160 and 75-88, respectively, of P501S, can be considered to be potential surface epitopes of P501S recognized by antibodies.

In further studies, mouse monoclonal antibodies were raised against amino acids 296 to 322 to P501S, which are predicted to be in an extracellular domain. A/J mice were immunized with P501S/adenovirus, followed by subsequent boosts with an *E. coli* recombinant protein, referred to as P501N, that contains amino acids 296 to 322 of P501S, and with peptide 296-322 (SEQ ID NO: 755) coupled with KLH. The mice were subsequently used for splenic B cell fusions to generate anti-peptide hybridomas. The resulting 3 clones, referred to as 4F4 (IgG1,kappa), 4G5 (IgG2a,kappa) and 9B9 (IgG1,kappa), were grown for antibody production. The 4G5 mAb was purified by passing the supernatant over a Protein A-sepharose column,

followed by antibody elution using 0.2M glycine, pH 2.3. Purified antibody was neutralized by the addition of 1M Tris, pH 8, and buffer exchanged into PBS.

For ELISA analysis, 96 well plates were coated with P501S peptide 296-322 (referred to as P501-long), an irrelevant P775 peptide, P501S-N, P501TR2, P501S-long-KLH, P501S peptide 306-319 (referred to as P501-short)-KLH, or the irrelevant peptide 2073-KLH, all at a concentration of 2 ug/ml and allowed to incubate for 60 minutes at 37 °C. After coating, plates were washed 5X with PBS + 0.1% Tween and then blocked with PBS, 0.5% BSA, 0.4% Tween20 for 2 hours at room temperature. Following the addition of supernatants or purified mAb, the plates were incubated for 60 minutes at room temperature. Plates were washed as above and donkey anti-mouse IgHRP-linked secondary antibody was added and incubated for 30 minutes at room temperature, followed by a final washing as above. TMB peroxidase substrate was added and incubated 15 minutes at room temperature in the dark. The reaction was stopped by the addition of 1N H<sub>2</sub>SO<sub>4</sub> and the OD was read at 450 nM. All three hybrid clones secreted mAb that recognized peptide 296-322 and the recombinant protein P501N.

For FACS analysis, HEK293 cells were transiently transfected with a P501S/VR1012 expression constructs using Fugene 6 reagent. After 2 days of culture, cells were harvested and washed, then incubated with purified 4G5 mAb for 30 minutes on ice. After several washes in PBS, 0.5% BSA, 0.01% azide, goat anti-mouse Ig-FITC was added to the cells and incubated for 30 minutes on ice. Cells were washed and resuspended in wash buffer including 1% propidium iodide and subjected to FACS analysis. The FACS analysis confirmed that amino acids 296-322 of P501S are in an extracellular domain and are cell surface expressed.

The chromosomal location of P501S was determined using the GeneBridge 4 Radiation Hybrid panel (Research Genetics). The PCR primers of SEQ ID NO: 528 and 529 were employed in PCR with DNA pools from the hybrid panel according to the manufacturer's directions. After 38 cycles of amplification, the reaction products were separated on a 1.2% agarose gel, and the results were analyzed through the Whitehead Institute/MIT Center for Genome Research web server

(<http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl>) to determine the probable chromosomal location. Using this approach, P501S was mapped to the long arm of chromosome 1 at WI-9641 between q32 and q42. This region of chromosome 1 has been linked to prostate cancer susceptibility in hereditary prostate cancer (Smith *et al.* *Science* 274:1371-1374, 1996 and Berthon *et al.* *Am. J. Hum. Genet.* 62:1416-1424, 1998). These results suggest that P501S may play a role in prostate cancer malignancy.

## EXAMPLE 20

### REGULATION OF EXPRESSION OF THE PROSTATE-SPECIFIC ANTIGEN P501S

10

Steroid (androgen) hormone modulation is a common treatment modality in prostate cancer. The expression of a number of prostate tissue-specific antigens have previously been demonstrated to respond to androgen. The responsiveness of the prostate-specific antigen P501S to androgen treatment was examined in a tissue culture system as follows.

15

Cells from the prostate tumor cell line LNCaP were plated at  $1.5 \times 10^6$  cells/T75 flask (for RNA isolation) or  $3 \times 10^5$  cells/well of a 6-well plate (for FACS analysis) and grown overnight in RPMI 1640 media containing 10% charcoal-stripped fetal calf serum (BRL Life Technologies, Gaithersburg, MD). Cell culture was continued for an additional 72 hours in RPMI 1640 media containing 10% charcoal-stripped fetal calf serum, with 1 nM of the synthetic androgen Methyltrienolone (R1881; New England Nuclear) added at various time points. Cells were then harvested for RNA isolation and FACS analysis at 0, 1, 2, 4, 8, 16, 24, 28 and 72-hours post androgen addition. FACS analysis was performed using the anti-P501S antibody 10E3-G4-D3 and permeabilized cells.

25

For Northern analysis, 5-10 micrograms of total RNA was run on a formaldehyde denaturing gel, transferred to Hybond-N nylon membrane (Amersham Pharmacia Biotech, Piscataway, NJ), cross-linked and stained with methylene blue. The filter was then prehybridized with Church's Buffer (250 mM  $\text{Na}_2\text{HPO}_4$ , 70 mM  $\text{H}_3\text{PO}_4$ , 1 mM EDTA, 1% SDS, 1% BSA in pH 7.2) at 65 °C for 1 hour. P501S DNA was

30

labeled with  $^{32}\text{P}$  using High Prime random-primed DNA labeling kit (Boehringer Mannheim). Unincorporated label was removed using MicroSpin S300-HR columns (Amersham Pharmacia Biotech). The RNA filter was then hybridized with fresh Church's Buffer containing labeled cDNA overnight, washed with 1X SCP (0.1 M NaCl, 0.03 M  $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$ , 0.001 M  $\text{Na}_2\text{EDTA}$ ), 1% sarkosyl (n-lauroylsarcosine) and exposed to X-ray film.

Using both FACS and Northern analysis, P501S message and protein levels were found in increase in response to androgen treatment.

10

## EXAMPLE 20

## PREPARATION OF FUSION PROTEINS OF PROSTATE-SPECIFIC ANTIGENS

The example describes the preparation of a fusion protein of the prostate-specific antigen P703P and a truncated form of the known prostate antigen PSA. The truncated form of PSA has a 21 amino acid deletion around the active serine site. The expression construct for the fusion protein also has a restriction site at 3' end, immediately prior to the termination codon, to aid in adding cDNA for additional antigens.

The full-length cDNA for PSA was obtained by RT-PCR from a pool of RNA from human prostate tumor tissues using the primers of SEQ ID NO: 607 and 608, and cloned in the vector pCR-Blunt II-TOPO. The resulting cDNA was employed as a template to make two different fragments of PSA by PCR with two sets of primers (SEQ ID NO: 609 and 610; and SEQ ID NO: 611 and 612). The PCR products having the expected size were used as templates to make truncated forms of PSA by PCR with the primers of SEQ ID NO: 611 and 613, which generated PSA (delta 208-218 in amino acids). The cDNA for the mature form of P703P with a 6X histidine tag at the 5' end, was prepared by PCR with P703P and the primers of SEQ ID NO: 614 and 615. The cDNA for the fusion of P703P with the truncated form of PSA (referred to as FOPP) was then obtained by PCR using the modified P703P cDNA and the truncated form of PSA cDNA as templates and the primers of SEQ ID NO: 614 and 615. The FOPP

cDNA was cloned into the NdeI site and XhoI site of the expression vector pCRX1, and confirmed by DNA sequencing. The determined cDNA sequence for the fusion construct FOPP is provided in SEQ ID NO: 616, with the amino acid sequence being provided in SEQ ID NO: 617.

- 5                   The fusion FOPP was expressed as a single recombinant protein in *E. coli* as follows. The expression plasmid pCRX1FOPP was transformed into the *E. coli* strain BL21-CodonPlus RIL. The transformant was shown to express FOPP protein upon induction with 1 mM IPTG. The culture of the corresponding expression clone was inoculated into 25 ml LB broth containing 50 ug/ml kanamycin and 34 ug/ml
- 10 chloramphenicol, grown at 37 °C to OD600 of about 1, and stored at 4 °C overnight. The culture was diluted into 1 liter of TB LB containing 50 ug/ml kanamycin and 34 ug/ml chloramphenicol, and grown at 37 °C to OD600 of 0.4. IPTG was added to a final concentration of 1 mM, and the culture was incubated at 30 °C for 3 hours. The cells were pelleted by centrifugation at 5,000 RPM for 8 min. To purify the protein, the
- 15 cell pellet was suspended in 25 ml of 10 mM Tris-Cl pH 8.0, 2mM PMSF, complete protease inhibitor and 15 ug lysozyme. The cells were lysed at 4 °C for 30 minutes, sonicated several times and the lysate centrifuged for 30 minutes at 10,000 x g. The precipitate, which contained the inclusion body, was washed twice with 10 mM Tris-Cl pH 8.0 and 1% CHAPS. The inclusion body was dissolved in 40 ml of 10 mM Tris-Cl
- 20 pH 8.0, 100 mM sodium phosphate and 8 M urea. The solution was bound to 8 ml Ni-NTA (Qiagen) for one hour at room temperature. The mixture was poured into a 25 ml column and washed with 50 ml of 10 mM Tris-Cl pH 6.3, 100 mM sodium phosphate, 0.5% DOC and 8M urea. The bound protein was eluted with 350 mM imidazole, 10 mM Tris-Cl pH 8.0, 100 mM sodium phosphate and 8 M urea. The fractions containing
- 25 FOPP proteins were combined and dialyzed extensively against 10 mM Tris-Cl pH 4.6, aliquoted and stored at - 70 °C.

## EXAMPLE 21

REAL-TIME PCR CHARACTERIZATION OF THE PROSTATE-SPECIFIC ANTIGEN P501S IN  
PERIPHERAL BLOOD OF PROSTATE CANCER PATIENTS

5                   Circulating epithelial cells were isolated from fresh blood of normal individuals and metastatic prostate cancer patients, mRNA isolated and cDNA prepared using real-time PCR procedures. Real-time PCR was performed with the Taqman<sup>TM</sup> procedure using both gene specific primers and probes to determine the levels of gene expression.

10                   Epithelial cells were enriched from blood samples using an immunomagnetic bead separation method (Dynal A.S., Oslo, Norway). Isolated cells were lysed and the magnetic beads removed. The lysate was then processed for poly A+ mRNA isolation using magnetic beads coated with Oligo(dT)25. After washing the beads in buffer, bead/poly A+ RNA samples were suspended in 10 mM Tris HCl pH 8.0

15                   and subjected to reversed transcription. The resulting cDNA was subjected to real-time PCR using gene specific primers. Beta-actin content was also determined and used for normalization. Samples with P501S copies greater than the mean of the normal samples + 3 standard deviations were considered positive. Real time PCR on blood samples was performed using the Taqman<sup>TM</sup> procedure but extending to 50 cycles using

20                   forward and reverse primers and probes specific for P501S. Of the eight samples tested, 6 were positive for P501S and  $\beta$ -actin signal. The remaining 2 samples had no detectable  $\beta$ -actin or P501S. No P501S signal was observed in the four normal blood samples tested.

25

## EXAMPLE 22

EXPRESSION OF THE PROSTATE-SPECIFIC ANTIGENS P703P AND P501S IN  
SCID MOUSE-PASSAGED PROSTATE TUMORS

When considering the effectiveness of antigens in the treatment of

30   prostate cancer, the continued presence of the antigens in tumors during androgen



ablation therapy is important. The presence of the prostate-specific antigens P703P and P501S in prostate tumor samples grown in SCID mice in the presence of testosterone was evaluated as follows.

Two prostate tumors that had metastasized to the bone were removed from patients, implanted into SCID mice and grown in the presence of testosterone. Tumors were evaluated for mRNA expression of P703P, P501S and PSA using quantitative real time PCR with the SYBR green assay method. Expression of P703P and P501S in a prostate tumor was used as a positive control and the absence in normal intestine and normal heart as negative controls. In both cases, the specific mRNA was present in late passage tumors. Since the bone metastases were grown in the presence of testosterone, this implies that the presence of these genes would not be lost during androgen ablation therapy.

#### EXAMPLE 23

##### ANTI-P503S MONOCLONAL ANTIBODY INHIBITS TUMOR GROWTH *IN VIVO*

The ability of the anti-P503S monoclonal antibody 20D4 to suppress tumor formation in mice was examined as follows.

Ten SCID mice were injected subcutaneously with HEK293 cells that expressed P503S. Five mice received 150 micrograms of 20D4 intravenously at day 0 (time of tumor cell injection), day 5 and day 9. Tumor size was measured for 50 days. Of the five animals that received no 20D4, three formed detectable tumors after about 2 weeks which continued to enlarge throughout the study. In contrast, none of the five mice that received 20D4 formed tumors. These results demonstrate that the anti-P503S Mab 20D4 displays potent anti-tumor activity *in vivo*.

#### EXAMPLE 24

##### CHARACTERIZATION OF A T CELL RECEPTOR CLONE FROM A P501S-SPECIFIC T CELL CLONE

T cells have a limited lifespan. However, cloning of T cell receptor (TCR) chains and subsequent transfer essentially enables infinite propagation of the T

cell specificity. Cloning of tumor-antigen TCR chains allows the transfer of the specificity into T cells isolated from patients that share the TCR MHC-restricting allele. Such T cells could then be expanded and used in adoptive transfer settings to introduce the tumor antigen specificity into patients carrying tumors that express the antigen. T  
5 cell receptor alpha and beta chains from a CD8 T cell clone specific for the prostate-specific antigen P501S were isolated and sequenced as follows.

Total mRNA from  $2 \times 10^6$  cells from CTL clone 4E5 (described above in Example 12) was isolated using Trizol reagent and cDNA was synthesized. To determine Va and Vb sequences in this clone, a panel of Va and Vb subtype-specific  
10 primers was synthesized and used in RT-PCR reactions with cDNA generated from each of the clones. The RT-PCR reactions demonstrated that each of the clones expressed a common Vb sequence that corresponded to the Vb7 subfamily. Furthermore, using cDNA generated from the clone, the Va sequence expressed was determined to be Va6. To clone the full TCR alpha and beta chains from clone 4E5,  
15 primers were designed that spanned the initiator and terminator-coding TCR nucleotides. The primers were as follows: TCR Valpha-6 5'(sense): GGATCC---GCCGCCACC---ATGTCACCTTCTAGCCTGCT (SEQ ID NO: 756) BamHI site Kozak TCR alpha sequence TCR alpha 3' (antisense): GTCGAC---TCAGCTGGACCACAGCCGCAG (SEQ ID NO: 757) Sall site TCR alpha constant  
20 sequence TCR Vbeta-7. 5'(sense): GGATCC---GCCGCCACC--ATGGGCTGCAGGCTGCTCT (SEQ ID NO: 758) BamHI site Kozak TCR alpha sequence TCR beta 3' (antisense): GTCGAC---TCAGAAATCCTTTCTCTTGAC (SEQ ID NO: 759) Sall site TCR beta constant sequence. Standard 35 cycle RT-PCR reactions were established using cDNA synthesized from the CTL clone and the above  
25 primers, employing the proofreading thermostable polymerase PWO (Roche, Nutley, NJ).

The resultant specific bands (approx. 850 bp for alpha and approx. 950 for beta) were ligated into the PCR blunt vector (Invitrogen) and transformed into *E. coli*. *E. coli* transformed with plasmids containing full-length alpha and beta chains  
30 were identified, and large scale preparations of the corresponding plasmids were generated. Plasmids containing full-length TCR alpha and beta chains were submitted

for sequencing. The sequencing reactions demonstrated the cloning of full-length TCR alpha and beta chains with the determined cDNA sequences for the Vb and Va chains being shown in SEQ ID NO: 760 and 761, respectively. The corresponding amino acid sequences are shown in SEQ ID NO: 762 and 763, respectively. The Va sequence was  
5 shown by nucleotide sequence alignment to be 99% identical (347/348) to Va6.2, and the Vb to be 99% identical to Vb7 (336/338).

From the foregoing it will be appreciated that, although specific embodiments of the invention have been described herein for purposes of illustration,  
10 various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

## CLAIMS

## What is Claimed:

1. An isolated polynucleotide comprising a sequence selected from the group consisting of:
  - (a) sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788;
  - (b) complements of the sequences provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788;
  - (c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788;
  - (d) sequences that hybridize to a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788 under moderately stringent conditions;
  - (e) sequences having at least 75% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-

375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788;

(f) sequences having at least 90% identity to a sequence of SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788; and

(g) degenerate variants of a sequence provided in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 and 786-788.

2. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) sequences recited in SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 627-629, 632, 633, 635, 637, 638, 656-671, 675, 683, 684, 710, 712, 714, 715, 717-719, 723-734, 736, 740-750, 752, 754, 755, 766-772, 777-785 and 789-791;

(b) sequences having at least 70% identity to a sequence of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 627-629, 632, 633, 635, 637, 638, 656-671, 675, 683, 684, 710, 712, 714, 715, 717-719, 723-734, 736, 740-750, 752, 754, 755, 766-772, 777-785 and 789-791;

(c) sequences having at least 90% identity to a sequence of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380, 383, 477-483, 496, 504, 505, 519, 520, 522, 525, 527, 532, 534, 537-551, 553-568, 573-586, 588-590, 592, 627-

629, 632, 633, 635, 637, 638, 656-671, 675, 683, 684, 710, 712, 714, 715, 717-719, 723-734, 736, 740-750, 752, 754, 755, 766-772, 777-785 and 789-791;

- (d) sequences encoded by a polynucleotide of claim 1;
- (e) sequences having at least 70% identity to a sequence encoded by a polynucleotide of claim 1; and
- (f) sequences having at least 90% identity to a sequence encoded by a polynucleotide of claim 1.

3. An expression vector comprising a polynucleotide of claim 1 operably linked to an expression control sequence.

4. A host cell transformed or transfected with an expression vector according to claim 3.

5. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 2.

6. A method for detecting the presence of a cancer in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with a binding agent that binds to a polypeptide of claim 2;
- (c) detecting in the sample an amount of polypeptide that binds to the binding agent; and
- (d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of a cancer in the patient.

7. A fusion protein comprising at least one polypeptide according to claim 2.

8. The fusion protein of claim 7, wherein the fusion protein comprises a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO: 682, 692, 695, 699, 703 and 709; and

(b) sequences encoded by SEQ ID NO: 679, 691, 696, 700, 704 and 708.

9. An oligonucleotide that hybridizes to a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 and 384-476, 524, 526, 530, 531, 533, 535, 536, 552, 569-572, 587, 591, 593-606, 618-626, 630, 631, 634, 636, 639-655, 674, 680, 681, 711, 713, 716, 720-722, 735, 737-739, 751, 753, 764, 765, 773-776 or 786-788 under moderately stringent conditions.

10. A method for stimulating and/or expanding T cells specific for a tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

(a) polypeptides according to claim 2;  
(b) polynucleotides according to claim 1; and  
(c) antigen-presenting cells that express a polypeptide according to claim 1,

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

11. An isolated T cell population, comprising T cells prepared according to the method of claim 10.

12. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

- (a) polypeptides according to claim 2;
- (b) polynucleotides according to claim 1;
- (c) antibodies according to claim 5;
- (d) fusion proteins according to claim 7;
- (e) T cell populations according to claim 11; and
- (f) antigen presenting cells that express a polypeptide according to claim 2.

13. A method for stimulating an immune response in a patient, comprising administering to the patient a composition of claim 12.

14. A method for the treatment of a cancer in a patient, comprising administering to the patient a composition of claim 12.

15. A method for determining the presence of a cancer in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide according to claim 9;
- (c) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and
- (d) compare the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence of the cancer in the patient.

16. A diagnostic kit comprising at least one oligonucleotide according to claim 9.



17. A diagnostic kit comprising at least one antibody according to claim 5 and a detection reagent, wherein the detection reagent comprises a reporter group.

18. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with at least one component selected from the group consisting of: (i) polypeptides according to claim 2; (ii) polynucleotides according to claim 1; and (iii) antigen presenting cells that express a polypeptide of claim 2, such that T cell proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells,

thereby inhibiting the development of a cancer in the patient.

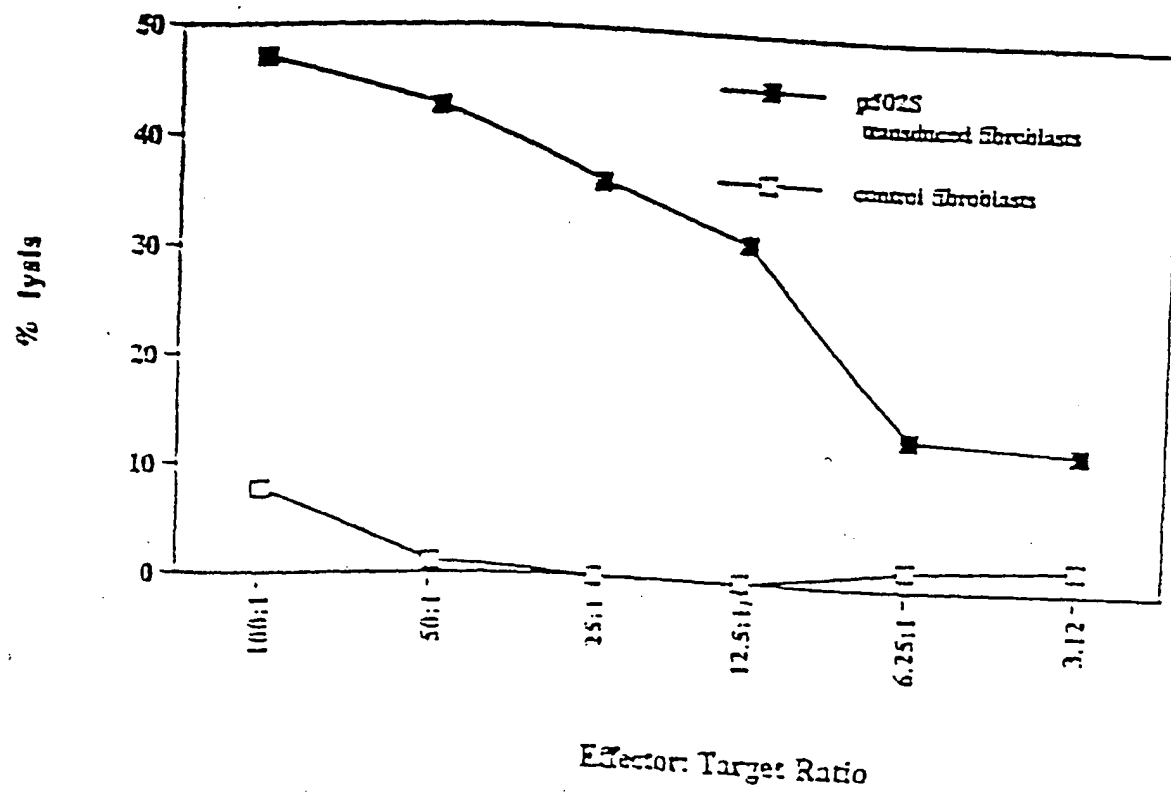


Fig. 1

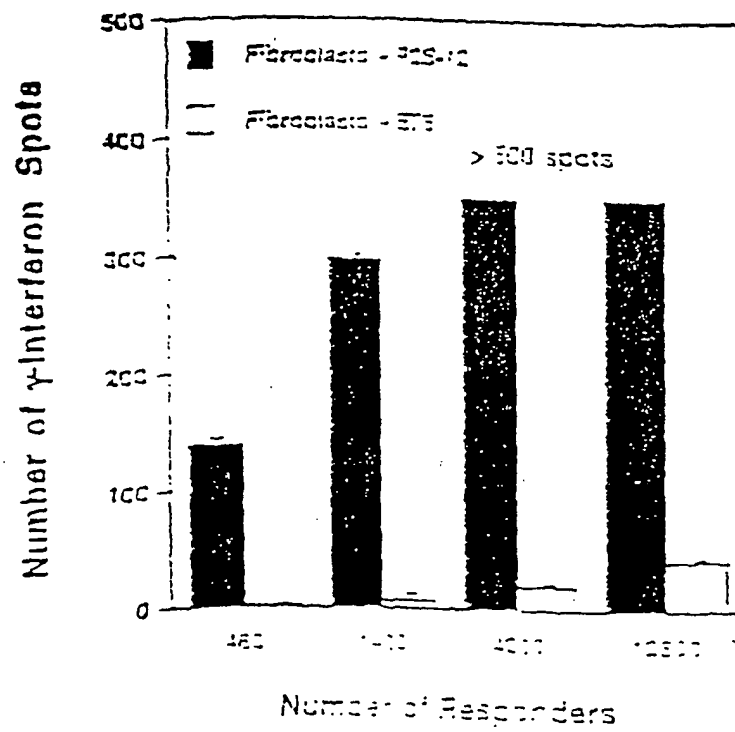


FIG. 2A

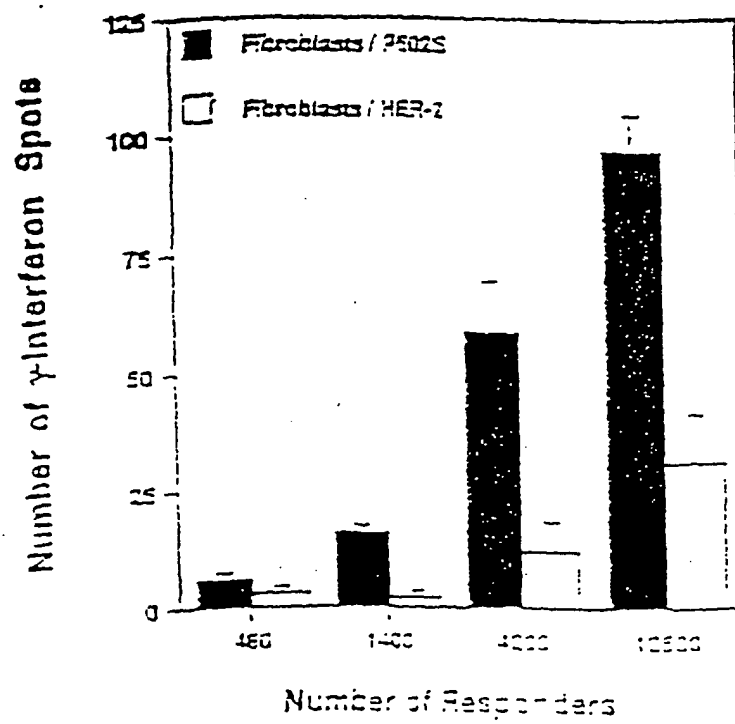


Fig. 25

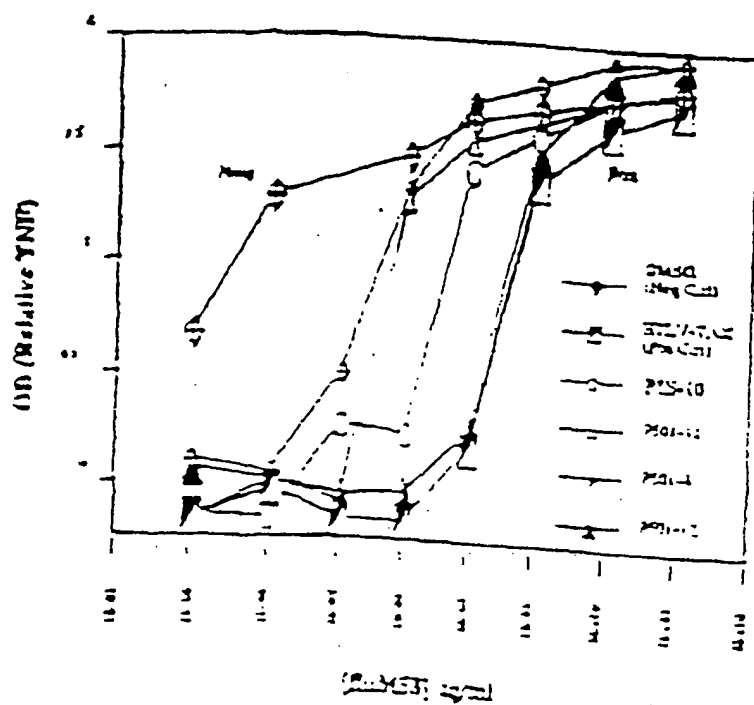


Fig. 3

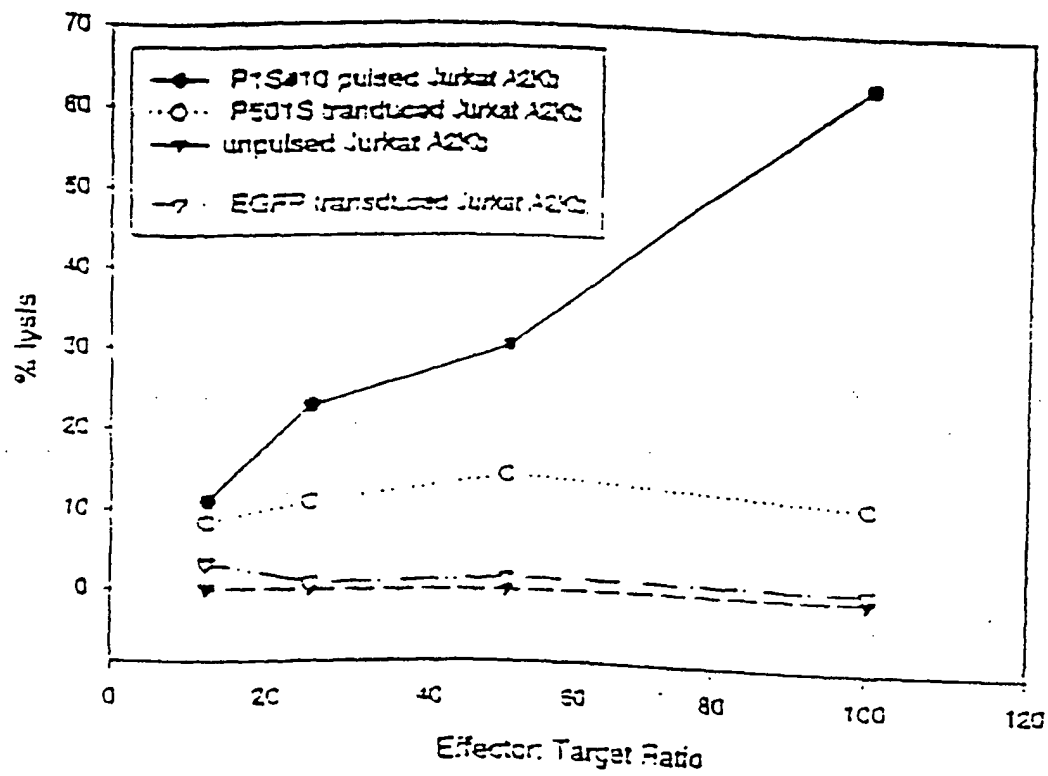


Fig. 4

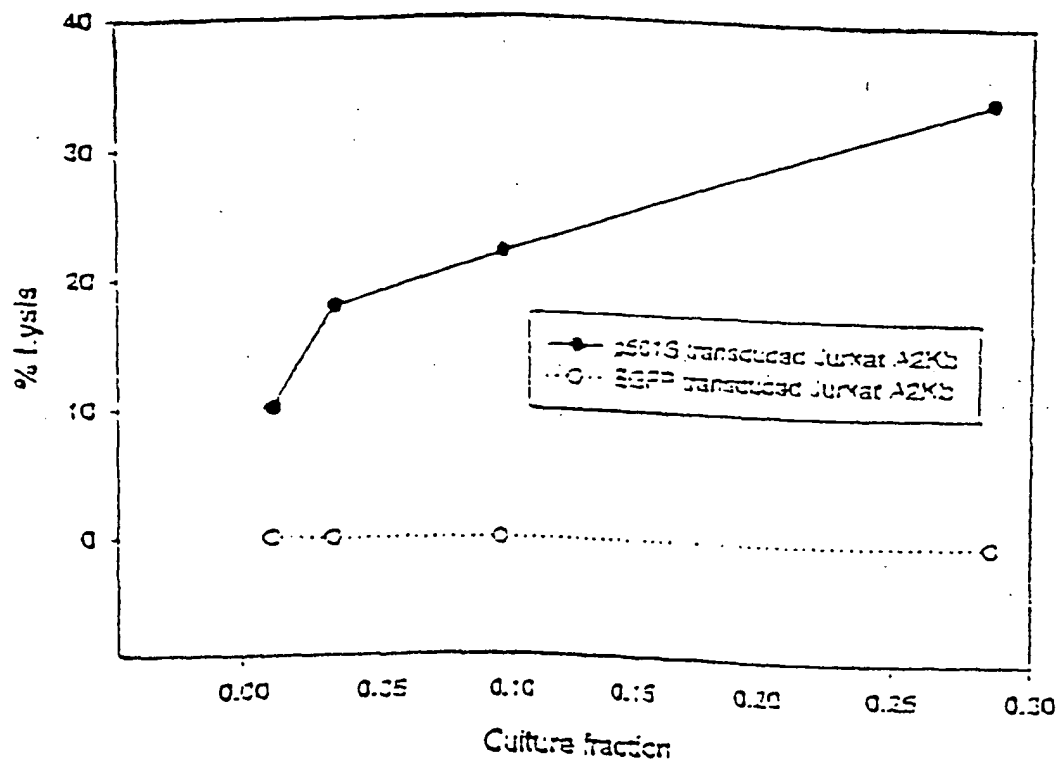


Fig. 5

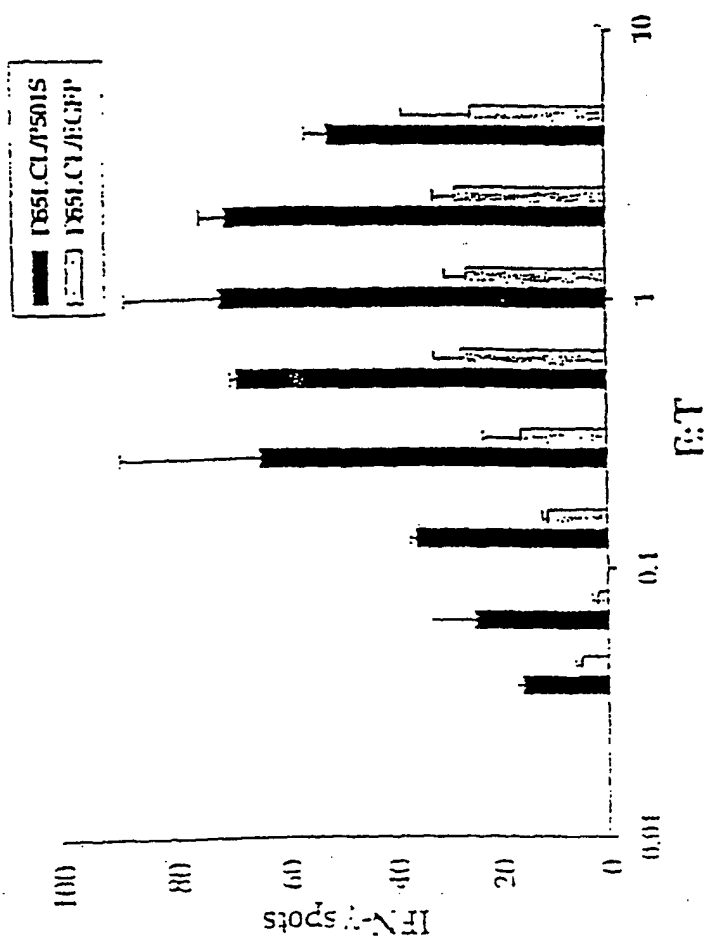


Fig. 6B

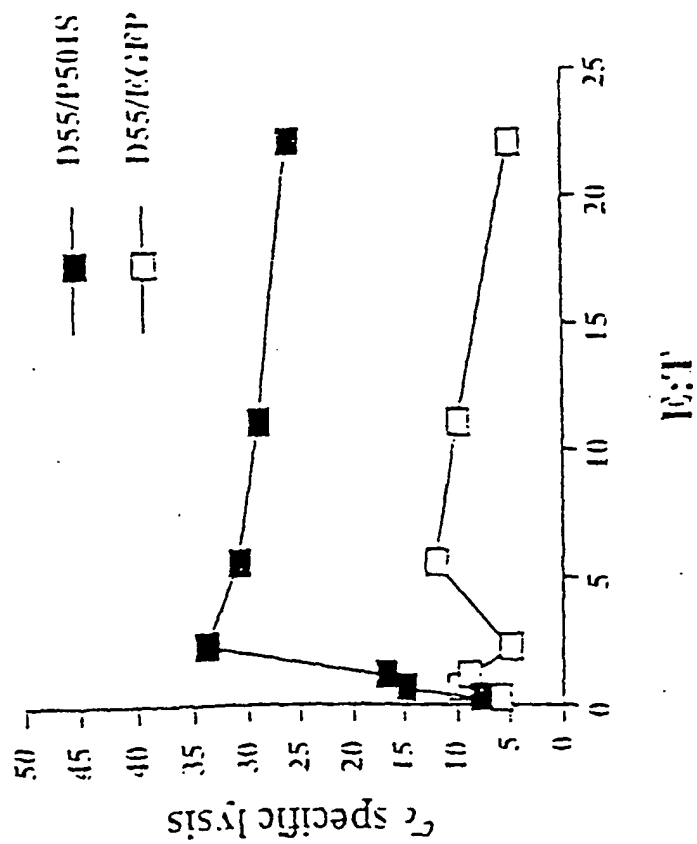
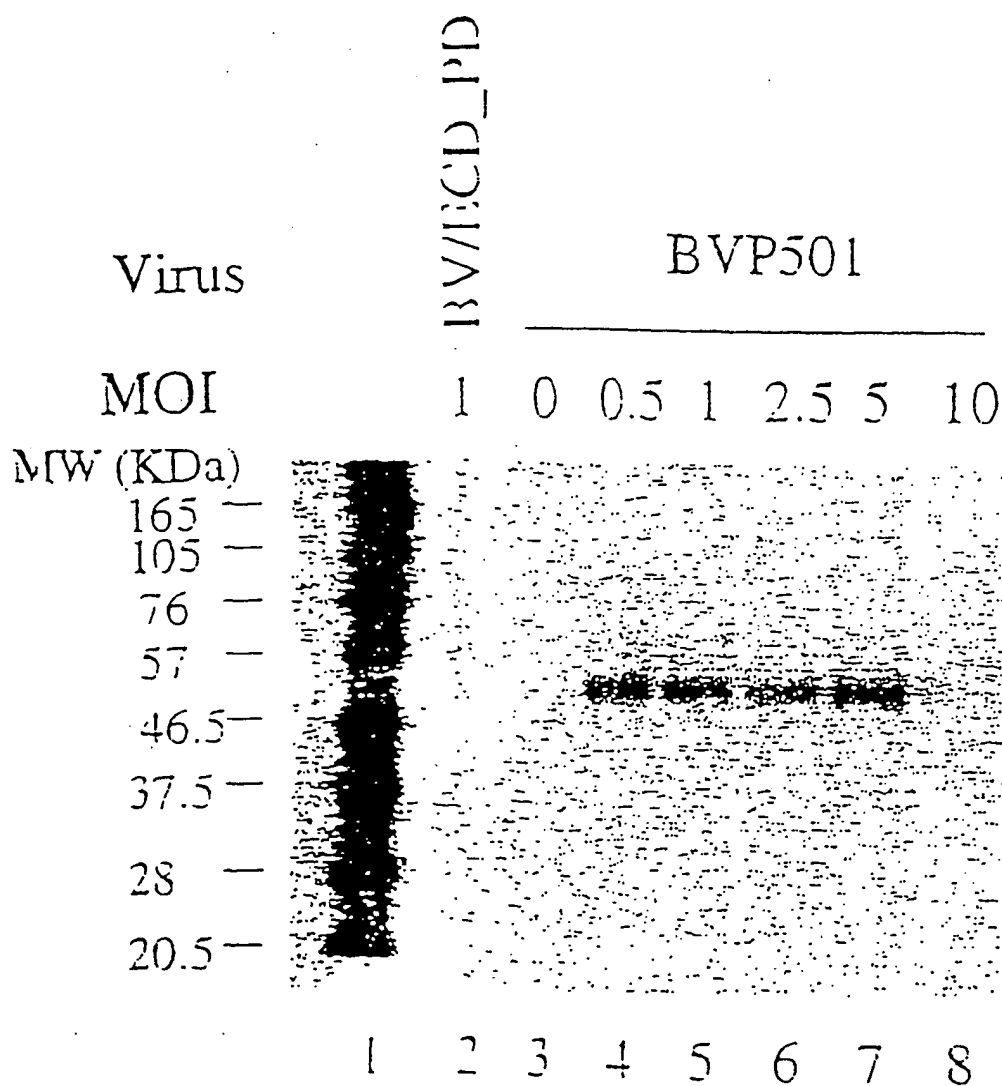


Fig. 6A



# Expression of P501S by the Baculovirus Expression System



0.6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD\_PD (lane 2), without virus (lane 3), or with recombinant baculovirus for P501 at different MOIs (lane 4-8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E9-G4D3). Lane 1 is the biotinylated protein molecular weight marker (BioLabs).

Fig. 7



# Figure 1. Schematic of P501S with predicted transmembrane, cytoplasmic, and extracellular regions

MVQRLWYSRLRHK AQLILVNLITTEGLEVCLAAQIT VVPPIILLEVGVREKENI TMVLGICPVILGVCYPLLGSAS  
 DHWRGRYGRRRP FIWALSGLILSLFIPRAGWL AGLCTDDPRPLE LAIIILGVGLIDFCGQVCFITPL  
 FALISILFRDPDHCRQ AYSVYAFMHSLSGGCTGYLIPAI DWDTSAMAPYLCTQEE  
 CLPGLITLFLTCVAAATLY AFEAMGPTEPAEGHSAPSLPHCTPCRARIAFRNLGALLPRL  
 HOLCCRAMPTLRR LPVAFICSWMAI NITFTTYTIP VGEGLYOGVPPRAIRPGTLEARRHIYDEGVYR  
 MGSLGLFLQCAISLYESLYM DRIVQRECTRAVYLAS VAAFPVAAGATCLSHSVAAVVTA SAA  
 LTGETFSALQILPYTLASLY HREKQVFLPKYRGDTGGASSEDSIATSEFILPGPKPGAPFPNGIIVGAGGSGL  
 LPPPPALCGASACDVSVRVVVGEPTEARVVVPGRG ICILDLAULDSAPILLSQVAPSLF MGSIVQLSQS  
 VTAYMVSAAAGLILVAIFYAT QVVFDKSDIAXYSA

Underlined sequence: Predicted transmembrane domain; **Bold sequence**: Predicted extracellular domain;

*Italic sequence*: Predicted intracellular domain. Sequence in bold/underlined: used to generate polyclonal rabbit serum

Localization of domains predicted using IMMTPP (G.E. Tusnady and I. Simon (1998) Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology Prediction. J.Mol Biol. 283, 489-506.

# Genomic Map of (5) Corixa Candidate Genes

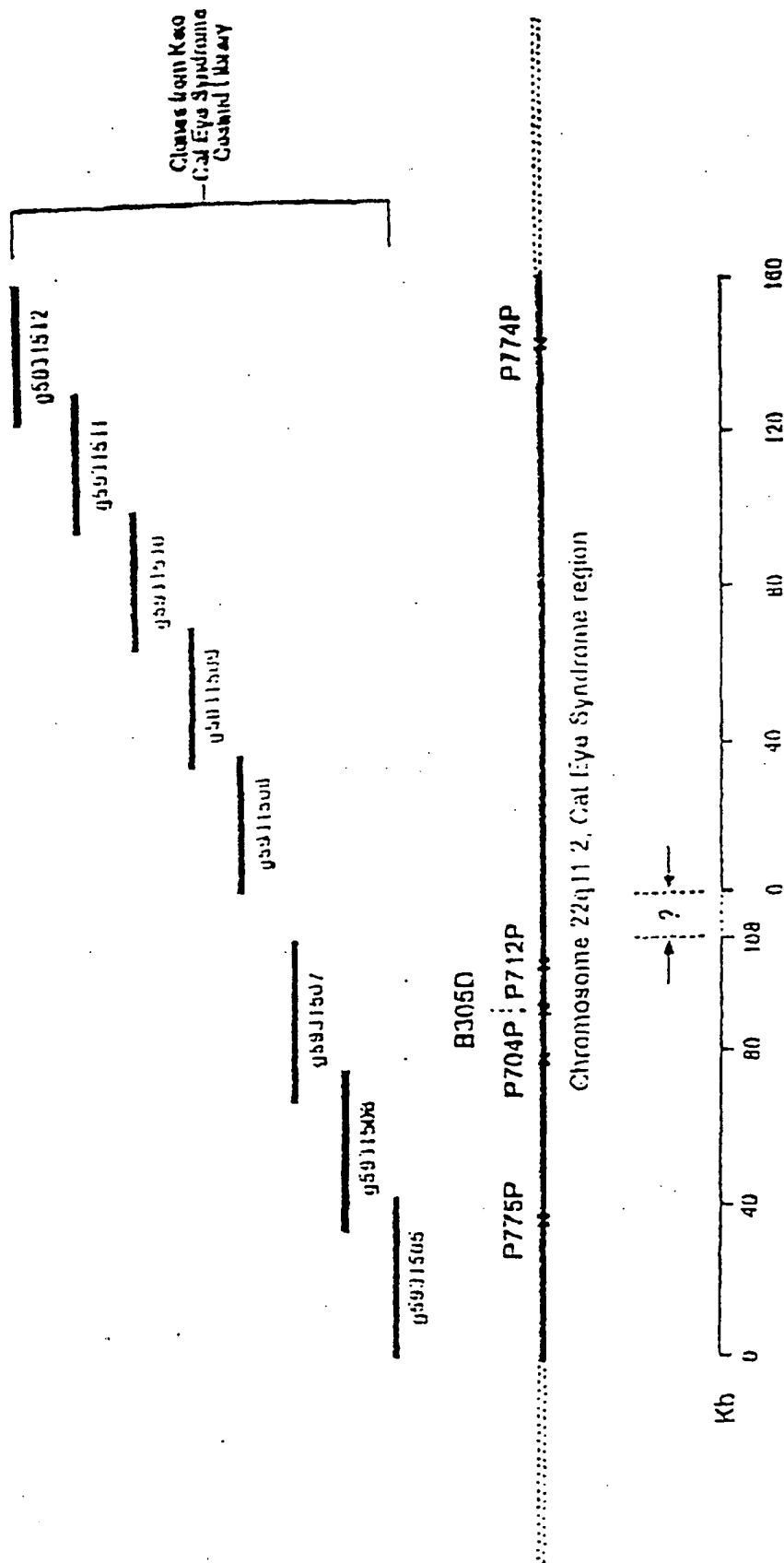


Fig. 10

**FIGURE 4. Elisa assay of rabbit polyclonal antibody specificity**

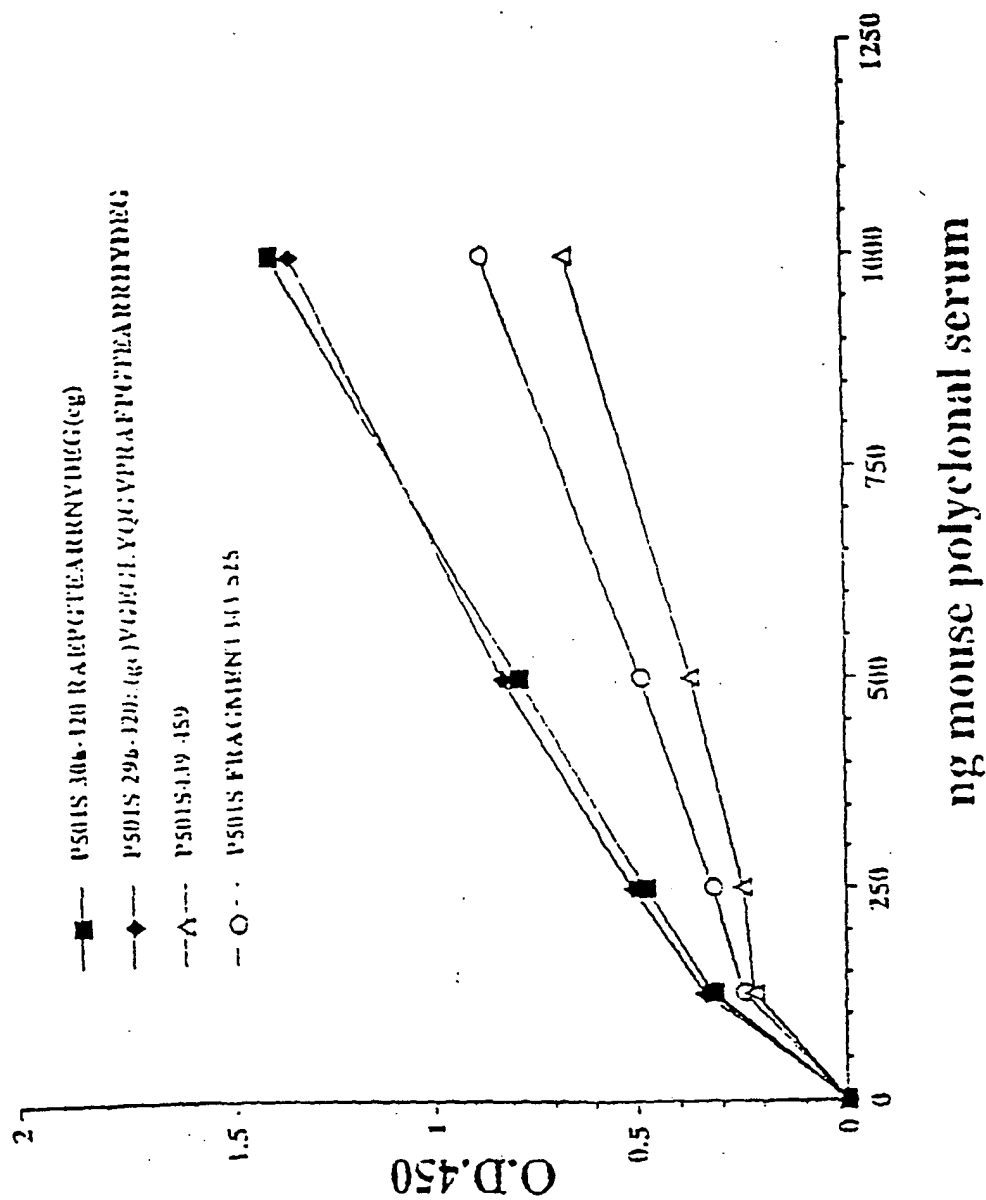


Fig. 11

## SEQUENCE LISTING

<110> Corixa Corporation  
 Smithkline Beechan Biologicals S.A.  
 Xu, Jiangchun  
 Dillon, Davin C.  
 Mitcham, Jennifer L.  
 Harlocker, Susan L.  
 Jiang, Yuqui  
 Reed, Steven G.  
 Kalos, Michael D.  
 Fanger, Gary R.  
 Retter, Marc W.  
 Stolk, John A.  
 Day, Craig H.  
 Skeiky, Yasir A.W.  
 Wang, Aijun  
 Meagher, Medeleine Joy  
 Vanderbrugge, Didier  
 Dewerchin, Marianne  
 Dehottay, Ph.  
 de Rop, Philippe

<120> COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 DIAGNOSIS OF PROSTATE CANCER

<130> 210121.42722PC

<140> PCT

<141> 2001-01-16

<160> 792

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 814

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(814)

<223> n = A, T, C or G

<400> 1

tttttttttt	tttttcacag	tataacagct	ctttatttct	gtgagttcta	ctaggaaatc	60
atcaaactctg	agggttgtct	ggaggacttc	aatacacctc	cccccatagt	gaatcagctt	120
ccaggggggtc	cagtccctct	ccttacttca	tccccatccc	atgccaaagg	aagaccctcc	180
ctccttggtc	cacagccttc	tctaggcttc	ccagtgcctc	caggacagag	tgggttatgt	240
tttcagctcc	atccttgctg	tgagtgtctg	gtgcgttgtg	cctccagctt	ctgctcagtg	300
cttcatggac	agtgtccagc	acatgtcact	ctccactctc	tcagtgtgga	tccactagtt	360
ctagagcggc	cgccaccgcg	gtggagctcc	agcttttggt	cccttttagtg	agggttaatt	420
gcgcgcttgg	cgtaaatcatg	gtcataactg	tttcctgtgt	gaaattgtta	tccgctcaca	480
attccacaca	acatacgagc	cggaagcata	aagtgtaaag	cctgggggtgc	ctaatgagtg	540
anctaactca	cattaattgc	gttgcgctca	ctgnccgctt	tccagtcngg	aaaactgtcg	600
tgccagctgc	attaatgaat	cggccaacgc	ncggggaaaa	gcgggtttgcg	ttttgggggc	660

tcttccgctt ctcgctcact nantcctgcg ctöggctcntt cggtcgcggg gaacgggtatc	720
actcctcaaa ggnggtatta cggttatccn naaatcnggg gatacccnngg aaaaaanttt	780
aacaaaaggg cancaaaggg cngaaacgta aaaa	814

<210> 2  
 <211> 816  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(816)  
 <223> n = A,T,C or G

<400> 2							
acagaaatgt tggatggtgg agcacctttc tatacgactt acaggacagc agatggggaa							60
ttcatggctg ttggagcaat agaaccccag ttctacgagc tgctgatcaa aggacttggg							120
ctaaagtctg atgaacttcc caatcagatg agcatggatg attggccaga aatgaagaag							180
aagtttgacg atgtatttgc aaagaagacg aaggcagagt ggtgtcaaatt ctttgacggc							240
acagatgcct gtgtgactcc ggttctgact tttgaggagg ttgttcatca tgatcacaa							300
aaggaacggg gctcgtttat caccagttag gagcaggacg tgagcccccg cctgcacct							360
ctgctgttaa acaccccagc catcccttct ttcaaaaggg atccactagt tctagaagcg							420
gccgcaccgg cgggtggagct ccagcttttg ttcccttttag tgagggttaa ttgcgcgctt							480
ggcgtaataca tgggtcatagc tgtttcctgt gtgaaattgt tatccgctca caattcccc							540
aacatacgag ccggaacata aagtgttaag cctgggggtgc ctaatgantg agctaactcn							600
cattaattgc gttgcgctca ctgcccgctt tccagtcggg aaaactgtcg tgccactgcn							660
ttantgaatc ngccaccccc cgggaaaagg cgggtgcntt ttgggcctct tccgctttcc							720
tcgctcattg atcctngcnc ccggtcttcg gctgcggnga acggttcact cctcaaaggc							780
ggtntnccgg ttatcccaa acnnggggata cccnga							816

<210> 3  
 <211> 773  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(773)  
 <223> n = A,T,C or G

<400> 3							
cttttgaaaag aagggatggc tgggggtgttt aacagcagag gtgcagggcg ggggctcacg							60
tcttgctcct cactggtgat aaacgagccc cgttccttgt tgtgatcatg atgaacaacc							120
tctcaaaaag tcagaaccgg agtcacacag gcatctgtgc cgtcaaagat ttgacaccac							180
tctgccttcg tcttctttgc aaatacatct gcaaacttct tcttcatttc tggccaatca							240
tccatgctca tctgattggg aagttcatca gacttttagtc canntccttt gatcagcagc							300
tcgtagaact ggggttctat tgctccaaca gccatgaatt ccccatctgc tgtcctgtaa							360
gtcgtataga aagggtgctcc accatccaac atgtttctgtc ctgagggggg ggcccgggtac							420
ccaattcgcc ctatantgag tcgtattacg cgcgctcact ggccgtcgtt ttacaacgtc							480
gtgactggga aaaccctggg cgttaccaac ttaatgcct tgcagcacat ccccttttcg							540
ccagctgggc gtaatanega aaaggccgc acogatgcc cttccaacag ttgogcacct							600
gaatgggnaa atgggacccc cctgttacgg cgcattnaac ccccgnggg tttngttggt							660
accccacnt nnaccgctta cactttgcc ggccttanc gccgctccc tttcncttt							720
cttcccttcc tttcnncnccn ctttcccccg gggtttcccc cntcaaacc cna							773

<210> 4  
 <211> 828  
 <212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(828)

<223> n = A,T,C or G

<400> 4

cctcctgagt	cctactgacc	tgtgctttct	ggtgtggagt	ccagggctgc	taggaaaagg	60
aatgggcaga	cacaggtgta	tgccaatgtt	tctgaaatgg	gtataatttc	gtcctctcct	120
tcggaacact	ggctgtctct	gaagacttct	cgctcagttt	cagtgaggac	acacacaaag	180
acgtgggtga	ccatgtttgt	tgtgggggtgc	agagatggga	gggggtggggc	ccaccctgga	240
agagtggaca	gtgacacaag	gtggacactc	tctacagatc	actgaggata	agctggagcc	300
acaatgcatg	aggcacacac	acagcaagga	tgacnctgta	aacatagccc	acgctgtcct	360
gnngggcactg	ggaagcctan	atnaggccgt	gagcanaaaag	aaggggagga	tccactagtt	420
ctanagcggc	cgccaccgcg	gtgganctcc	ancctttgtt	cccttttagtg	agggttaatt	480
gcgcgcttgg	cntaatcatg	gtcatanctn	tttcctgtgt	gaaattgtta	tccgctcaca	540
attccacaca	acatacganc	cggaaacata	aantgtaaac	ctggggtgcc	taatgantga	600
ctaactcaca	ttaattgcgt	tgcgctcact	gcccgccttc	caatcnggaa	acctgtcttg	660
ccncttgcat	tnatgaatcn	gccaaacccc	ggggaaaagc	gtttgcgttt	tgggcgctct	720
tccgcttcct	cntctantta	ntccctnenc	tcggtcattc	cggctgcngc	aaaccggttc	780
accnctcca	aaggggggtat	tccggtttcc	ccnaatccgg	gganancc		828

<210> 5

<211> 834

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(834)

<223> n = A,T,C or G

<400> 5

tttttttttt	tttttactga	tagatggaat	ttattaagct	tttcacatgt	gatagcacat	60
agttttaatt	gcatccaaag	tactaacaaa	aactctagca	atcaagaatg	gcagcatgtt	120
attttataac	aatcaacacc	tgtggctttt	aaaatttggt	tttcataaga	taatttatac	180
tgaagtaaat	ctagccatgc	ttttaaaaaa	tgcttttaggt	cactccaagc	ttggcagtta	240
acatttgga	taaaacaata	taaaacaatc	acaatttaat	aaataacaaa	tacaacattg	300
taggccataa	tcatatacac	tataaggaaa	aggtggtagt	gttgagtaag	cagttattag	360
aatagaatac	cttggcctct	atgcaaatat	gtctagacac	tttgattcac	tcagccctga	420
cattcagttt	tcaaagtagg	agacagggtc	tacagtatca	ttttacagtt	tccaacacat	480
tgaaaacaag	tagaaaatga	tgagttgatt	tttattaatg	cattacatcc	tcaagagtta	540
tcaccaaccc	ctcagttata	aaaaattttc	aagttatatt	agtcataata	cttgggtgtgc	600
ttatttttaa	ttagtgtctaa	atggattaag	tgaagacaac	aatgggtccc	taatgtgatt	660
gatattggtc	atttttacca	gcttctaaat	ctnaactttc	aggcttttga	actggaacat	720
tgnatnacag	tgttccanag	ttncaaccta	ctggaacatt	acagtgtgct	tgattcaaaa	780
tgttattttg	ttaaaaatta	aattttaacc	tggtggaaaa	ataatttgaa	atna	834

<210> 6

<211> 818

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(818)

<223> n = A,T,C or G



&lt;400&gt; 6

tttttttttt	tttttttttt	aagaccctca	tcaatagatg	gagacatata	gaaatagtca	60
aaccacatct	acaaaatgcc	agtatcaggc	ggcggttcg	aagccaaagt	gatgtttgga	120
tgtaaagtga	aatattagtt	ggcggatgaa	gcagatagtg	aggaaagttg	agccaataat	180
gacgtgaagt	ccgtggaagc	ctgtggctac	aaaaaatgtt	gagccgtaga	tgccgtcgga	240
aatggtgaag	ggagactcga	agtactctga	ggcttgtagg	agggtaaaat	agagaccag	300
taaaattgta	ataagcagtg	cttgaattat	ttggtttcgg	ttgttttcta	ttagactatg	360
gtgagctcag	gtgattgata	ctcctgatgc	gagtaatacg	gatgtgttta	ggagtgggac	420
ttctagggga	tttagcgggg	tgatgcctgt	tggggggccag	tgccctocta	gttggggggg	480
aggggctagg	ctggagtggg	aaaaggctca	gaaaaatcct	gcgaagaaaa	aaacttctga	540
ggtaataaat	aggattatcc	cgtatcgaag	gccttttttg	acaggtgggt	tgtggtggcc	600
ttggtatgtg	ctttctcgtg	ttacatcgcg	ccatcattgg	tatatgggta	gtgtgttggg	660
ttantangg	ctantatgaa	gaacttttgg	antggaatta	aatcaatngc	ttggccggaa	720
gtcattanga	nggctnaaaa	ggccctgtta	ngggtctggg	ctnggtttta	cccnacccat	780
ggaatncnc	ccccggacna	ntgnatccct	attcttaa			818

&lt;210&gt; 7

&lt;211&gt; 817

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(817)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 7

tttttttttt	tttttttttt	tggctctaga	gggggtagag	gggtgctat	agggtaaata	60
cgggccctat	ttcaaagatt	tttaggggaa	ttaattctag	gacgatgggt	atgaaactgt	120
ggtttgctcc	acagatttca	gagcattgac	cgtagtatac	ccccggtcgt	gtagcgggta	180
aagtggtttg	gttttagacgt	ccgggaattg	catctgtttt	taagcctaata	gtggggacag	240
ctcatgagt	caagacgtct	tgtgatgtaa	ttattatacn	aatgggggct	tcaatcgga	300
gtactactcg	attgtcaacg	tcaaggagtc	gcaggtcgcc	tggttctagg	aataatgggg	360
gaagtatgta	ggaattgaag	attaatccgc	cgtagtcggt	gttctcctag	gttcaatacc	420
attggtggcc	aattgatttg	atggtaagg	gaggatcgt	tgaactcgtc	tgttatgtaa	480
aggatncctt	ngggatggga	aggcnatnaa	ggactangga	tnaatggcgg	gcangatatt	540
tcaaacngtc	tctanttcct	gaaacgtctg	aaatgttaat	aanaattaan	tttngttatt	600
gaatnttnng	gaaaagggct	tacaggacta	gaaaccaa	angaaaanta	atnntaangg	660
cnttatcntn	aaaggtnata	accnctccta	tnatcccacc	caatngnatt	ccccacnenn	720
acnattggat	nccccanttc	canaaanggc	cncctcccg	tgnannccnc	cttttgttcc	780
cttnantgan	ggttattcnc	ccctngcntt	atcance			817

&lt;210&gt; 8

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(799)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 8

catttccggg	tttactttct	aaggaaagcc	gagcggaagc	tgctaacgtg	ggaatcgggtg	60
cataaggaga	actttctgct	ggcacgcgct	agggacaagc	gggagagcga	ctccgagcgt	120
ctgaagcgca	cgtcccagaa	ggtggacttg	gcactgaaac	agctgggaca	catccgcgag	180
tacgaacagc	gcctgaaagt	gctggagcgg	gaggtccagc	agtgtagccg	cgtcctgggg	240

tgggtggcgcg	angcctganc	cgtcttgcct	tgctgcccc	angtgggcgcg	ccacccccctg	300
acctgcctg	gtccaaacac	tgagccctgc	tggcggactt	caagganaac	ccccacangg	360
ggattttgct	cctanantaa	ggctcatctg	ggcctcggcc	ccccacactg	gttggccttg	420
tctttgagt	gagcccatg	tccatctggg	ccactgtcng	gaccaccttt	ngggagtgtt	480
ctccttaaaa	ccacannatg	cccggctcct	cccggaaacc	antcccancc	tgngaaggat	540
caagnccctgn	atccactnnt	netanaaccg	gcncncnccg	cngtggaacc	cnccttntgt	600
tccttttctnt	tnagggttaa	tnnccgcttg	gccttnccan	ngtcctncnc	nttttccnnt	660
gttnaaattg	ttangcnccc	nccntcccn	cnnnnnnan	cccgaaccnn	annttnnann	720
ncttgggggt	nccnnccgat	tgaccnnc	nccctntant	tgcnttnggg	nncnntgccc	780
ctttccctct	nggganncg					799

&lt;210&gt; 9

&lt;211&gt; 801

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(801)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 9

acgccttgat	cctcccaggc	tgggactggt	tctgggagga	gccgggcatg	ctgtgggttg	60
taangatgac	actcccaaag	gtggtcctga	cagtggccca	gatggacatg	gggctcacct	120
caaggacaag	gccaccaggt	gcgggggccc	aagccacat	gaccttact	ctatgagcaa	180
aatccctgt	gggggcttct	ccttgaagtc	cgccancagg	gctcagtctt	tggacccang	240
caggtcatgg	ggttgtngnc	caactggggg	ccncaacgca	aaanggcnc	gggctcngn	300
cacccatccc	angacgcggc	tacactnctg	gacctccnc	tccaccactt	tcatgcgctg	360
ttontacccg	cgnatntgtc	ccanctgttt	cngtgconac	tccancttct	nggacgtgcg	420
ctacatacgc	ccggantcnc	ntcccgcctt	tgccctatc	cacgtncan	caacaaattt	480
cncctantg	caccnattcc	cacttttnc	agntttccnc	nncnggcttc	cttntaaaag	540
ggttganccc	cggaaaatnc	cccaaagggg	gggggcccng	tacccaactn	ccccctnata	600
getgaantcc	ccatnaccnn	gnctcnatgg	ancntccnt	tttaannacn	ttctnaactt	660
gggaanance	ctcgnccntn	ccccnttaa	tccncccttg	cnangnnct	cccccnntcc	720
ncccnntng	gcntntnann	cnaaaaaggc	ccnnancaa	tctcctnncn	cctcanttgc	780
ccanccctcg	aatcgcccn	c				801

&lt;210&gt; 10

&lt;211&gt; 789

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(789)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 10

cagtctatnt	ggccagtgtg	gcagctttcc	ctgtggctgc	cggtgccaca	tgctgtccc	60
acagtgtggc	cgtggtgaca	gcttcagccg	ccctcaccgg	gttcaccttc	tcagccctgc	120
agatcctgcc	ctacacactg	gcctccctct	accaccggga	gaagcaggtg	ttcctgccca	180
aataccgagg	ggacactgga	ggtgctagca	gtgaggacag	cctgatgacc	agcttcctgc	240
caggccctaa	gcctggagct	cccttcccta	atggacacgt	gggtgctgga	ggcagtggcc	300
tgctcccacc	tccaccgcg	ctctgcgggg	cctctgcctg	tgatgtctcc	gtacgtgtgg	360
tggtgggtga	gcccaccgan	gccaggggtg	ttccggggccg	gggcatctgc	ctggacctcg	420
ccatcctgga	tagtgcttcc	tgctgtccca	ngtggcccca	tccctgttta	tgggctccat	480
tgtccagctc	agccagtctg	tactgccta	tatggtgtct	gccgcaggcc	tgggtctggt	540
cccatttact	ttgtacaca	ggtantattt	gacaagaacg	anttgcccaa	atactcagcg	600

ttaaaaaatt	ccagcaacat	tgggggtgga	aggcctgcct	cactgggtcc	aactccccgc	660
tcctgttaac	cccatggggc	tgccggcttg	gccgccaaat	tctgttgctg	ccaaantnat	720
gtggtctctc	gctgccacct	gttgctggct	gaagtgcnta	cngcncanct	nggggggtng	780
gnggttccc						789

<210> 11  
 <211> 772  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(772)  
 <223> n = A,T,C or G

<400> 11						
cccaccctac	ccaaatatta	gacaccaaca	cagaaaagct	agcaatggat	tcccttctac	60
tttggttaa	aaataagtta	aataatttaa	tgccctgtgc	tctgtgatgg	caacagaagg	120
accaacaggc	cacatcctga	taaaaggtaa	gaggggggtg	gatcagcaaa	aagacagtgc	180
tgtgggctga	ggggacctgg	ttcttgtgtg	ttgccctca	ggactcttcc	cctacaaata	240
actttcatat	gttcaaatac	catggaggag	tgtttcatcc	tagaaactcc	catgcaagag	300
ctacattaaa	cgaagctgca	ggttaagggg	cttanagatg	ggaaaccagg	tgactgagtt	360
tattcagctc	ccaaaaaccc	ttctctaggt	gtgtctcaac	taggaggcta	gctgttaacc	420
ctgagcctgg	gtaatccacc	tgacagatcc	ccgcattcca	gtgcatggaa	cccttctggc	480
ctccctgtat	aagtccagac	tgaaaccccc	ttggaaggnc	tccagtcagg	cagccctana	540
aactggggaa	aaaagaaaag	gacgccccan	ccccagctg	tgcanctacg	cacctcaaca	600
gcacagggtg	gcagcaaaaa	aaccacttta	ctttggcaca	aacaaaaact	ngggggggca	660
accccggcac	cccnangggg	gttaacagga	ancngggnaa	cntggaaccc	aattnaggca	720
ggcccnccac	ccnnaatntt	gctggggaat	ttttcctccc	ctaaattntt	tc	772

<210> 12  
 <211> 751  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(751)  
 <223> n = A,T,C or G

<400> 12						
gccccaatc	cagctgccac	accacccaag	gtgactgcat	tagttcggat	gtcatacaaa	60
agctgattga	agcaaccctc	tacttttttg	tcgtgagcct	tttgcttggt	gcaggtttca	120
ttggctgtgt	tggtgacgtt	gtcattgcaa	cagaatgggg	gaaaggcact	gttctctttg	180
aagtanggtg	agtcctcaaa	atccgtatag	ttggtgaagc	cacagcactt	gagccctttc	240
atggtggtgt	tccacacttg	agtgaagtct	tcctgggaac	cataatcttt	cttgatggca	300
ggcactacca	gcaacgtcag	ggaagtgtct	agccattgtg	gtgtacacca	aggcgaccac	360
agcagctgcn	acctcagcaa	tgaagatgan	gaggangatg	aagaagaacg	tcncgagggc	420
acacttgctc	tcagtcttan	caccatanca	gcccntgaaa	accaananca	aagaccacna	480
cnccggctgc	gatgaagaaa	tnaccccncg	ttgacaaact	tgcatggcac	tggganccac	540
agtggccnna	aaaatcttca	aaaaggatgc	cccatcnatt	gaccccccaa	atgccactg	600
ccaacagggg	ctgccccacn	cncnnaacga	tgancnatt	gnacaagatc	tncntggtct	660
tnatnaacnt	gaaccctgcn	tngtggctcc	tgttcaggnc	cnnggcctga	cttctnaann	720
aangaactcn	gaagncccca	cngganannc	g			751

<210> 13  
 <211> 729  
 <212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(729)

<223> n = A,T,C or G

<400> 13

gagccaggcg	tcctctgcc	tgccactca	gtggcaacac	ccgggagctg	ttttgtcctt	60
tgtggancct	cagcagtncc	ctctttcaga	actcantgcc	aaganccctg	aacaggagcc	120
accatgcagt	gcttcagctt	cattaagacc	atgatgatcc	tcttcaattt	gctcatcttt	180
ctgtgtggtg	cagccctggt	ggcagtgggc	atctgggtgt	caatcgatgg	ggcatccttt	240
ctgaagatct	tcggggccact	gtcgtccagt	gccatgcagt	ttgtcaacgt	gggctacttc	300
ctcatcgag	ccggcggttg	ggtcttagct	ctaggtttcc	tgggctgcta	tggtgctaag	360
actgagagca	agtgtgccct	cgtgacgttc	ttcttcaccc	tcctcctcat	cttcattgct	420
gaggttgcaa	tgctgtggtc	gccttggtgt	acaccacaat	ggctgagcac	ttcctgacgt	480
tgtgtgtaat	gcctgccatc	aanaaaagat	tatgggttcc	caggaanact	tactcaagt	540
gttggaacac	caccatgaaa	gggctcaagt	gctgtggctt	cnnccaacta	tacggatttt	600
gaagantcac	ctacttcaaa	gaaaanagt	cctttccccc	atttctgttg	caattgacaa	660
acgtcccaaa	cacagccaat	tgaaaacctg	caccaacccc	aaanggggtc	ccaaccanaa	720
attnaaggg						729

<210> 14

<211> 816

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(816)

<223> n = A,T,C or G

<400> 14

tgctcttcc	caaagttgtt	cttggtgcc	taacaaccac	cataggtaaa	gcgggcgcag	60
tgcttgcctga	aggggttgta	gtaccagcgc	gggatgctct	ccttgacagag	tcctgtgtct	120
ggcaggtcca	cgcagtgccc	tttgtcactg	gggaaatgga	tgcgtggag	ctcgtcaaag	180
ccactcgtgt	atttttcaca	ggcagcctcg	tcogacgcgt	cggggcagtt	gggggtgtct	240
tcacactcca	ggaaactgtc	natgcagcag	ccattgctgc	agcggaaactg	gggtggctga	300
cangtgccag	agcacactgg	atggcgcctt	tccatgnnan	gggccctgng	ggaaagtccc	360
tganccccc	anctgcctct	caaangcccc	accttgacac	ccccgacagg	ctagaatgga	420
atcttcttcc	cgaaaggtag	ttnttcttgt	tgcccaancc	ancccntaa	acaaactctt	480
gcanatctgc	tcgngggggg	tentantacc	ancgtgggaa	aagaacccca	ggcngcgaac	540
caancttggt	tggatncgaa	gcnataatct	ncntttctgc	ttggtggaca	gcaccantna	600
ctgtnnanct	ttagnccntg	gtcctcntgg	gttgnncttg	aacctaatcn	ccnntcaact	660
gggacaaggt	aantngccnt	cctttnaatt	cccnanctn	ccccctggtt	tgggggtttt	720
cncnctcta	ccccagaaan	nccgtgttcc	cccccaacta	ggggccnaaa	ccnnttnttc	780
cacaacctn	ccccaccac	gggttcngnt	ggttng			816

<210> 15

<211> 783

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(783)

<223> n = A,T,C or G

<400> 15  
 ccaaggcctg ggcaggcata nacttgaagg tacaacccca ggaacccctg gtgctgaagg 60  
 atgtggaaaa cacagattgg cgcctactgc ggggtgacac ggatgtcagg gtagagagga 120  
 aagacccaaa ccaggtggaa ctgtggggac tcaaggaang cacctacctg ttccagctga 180  
 cagtgactag ctacagaccac ccagaggaca cggccaacgt cacagtcaact gtgctgtcca 240  
 ccaagcagac agaagactac tgcctcgcat ccaacaangt gggtcgctgc cggggctctt 300  
 tcccacgctg gtactatgac cccacggagc agatctgcaa gagtttcgtt tatggaggct 360  
 gcttgggcaa caagaacaac taccttcggg aagaagagt cattctancc tgtcnggggtg 420  
 tgcaagggtg gcccttgana ngcanctctg gggtcangc gactttcccc cagggccctt 480  
 ccatggaaag ggcctatcca ntgttctctg gcacctgtca gccacccag ttccgctgca 540  
 ncaatggctg ctgcatcnac antttcctng aattgtgaca acacccccca ntgccccaa 600  
 cctcccaac aaagcttccc tgttnaaaaa tacnccantt ggcttttnac aaacncccg 660  
 cncctccntt tccccnntn aacaaagggc nctngcnttt gaactgccc n aacccnggaa 720  
 tctnccnngg aaaaantncc cccctggtt cctnnaanc cctccncaa anctncccc 780  
 ccc 783

<210> 16  
 <211> 801  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(801)  
 <223> n = A,T,C or G

<400> 16  
 gcccgaattc cagctgccac accacccacg gtgactgcat tagttcggat gtcatacaaa 60  
 agctgattga agcaaccctc tacttttttg tegttagcct tttgcttggg gcaggtttca 120  
 ttggctgtgt tggtagcgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg 180  
 aagtaggggt agtcctcaaa atccgtatag ttggtagaag cacagcactt gagccctttc 240  
 atggtggtgt tccacacttg agtgaagtct tcctgggaac cataatcttt cttgatggca 300  
 ggcactacca gcaacgtcag gaagtgtca gccattgttg tgtacaccaa ggcgaccaca 360  
 gcagctgcaa cctcagcaat gaagatgagg aggaggatga agaagaacgt cncgagggca 420  
 cacttgctct cgtcttagc accatagcag cccangaaac caagagcaaa gaccacaacg 480  
 ccngctgcga atgaaagaaa ntaccacgt tgacaaactg catggccact ggacgacagt 540  
 tggccgaan atcttcagaa aaggatgcc ccacogattg aacaccana tgccactgc 600  
 cncaggggt gcnccnccn gaaagaatga gccattgaag aaggatcntc ntggctttaa 660  
 tgaactgaaa cctgcatgg tggccctgt tcagggtct tggcagtga ttctganaaa 720  
 aaggaacngc ntnagcccc ccaaangana aaacaccccc ggggtgttgc ctgaattggc 780  
 ggccaaggan ccctgccccn g 801

<210> 17  
 <211> 740  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(740)  
 <223> n = A,T,C or G

<400> 17  
 gtgagagcca ggcgtccctc tgcctgccca ctacgtggca acacccggga gctgttttgt 60  
 cctttgtgga gcctcagcag ttccctcttt cagaactcac tgccaagagc cctgaacagg 120  
 agccaccatg cagtgttca gcttcattaa gaccatgatg atcctcttca atttgctcat 180  
 ctttctgtgt ggtgcagccc tgttggcagt gggcatctgg gtgtcaatcg atggggcatc 240  
 ctttctgaag atcttcgggc cactgtcgtc cagtgccatg cagtttgtca acgtgggcta 300

cttccctcatc	gcagccggcg	ttgtggtctt	tgtctttggt	ttcctgggct	gctatgggtgc	360
taagacggag	agcaagtgtg	ccctcgtgac	gttctttctt	atcctcctcc	tcattcttcat	420
tgctgaagtt	gcagctgctg	tggtcgctt	ggtgtacacc	acaatggctg	aaccattcct	480
gacgttgctg	gtantgcctg	ccatcaanaa	agattatggg	ttcccaggaa	aaattcactc	540
aannttgtaa	caccnccatg	aaaagggctc	caattttctgn	tggtttcccc	aactataccg	600
gaattttgaa	agantcnccc	tacttccaaa	aaaaaanant	tgcttttnc	ccntttctgt	660
tgcaatgaaa	acntcccaan	acngccaatn	aaaacctgcc	cnnncaaaaa	ggntcncaaa	720
caaaaaaant	nnaagggttn					740

<210> 18  
 <211> 802  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1) ... (802)  
 <223> n = A,T,C or G

<400> 18						
ccgctggttg	cgctgggtcca	gngnagccac	gaagcacgtc	agcatacaca	gcctcaatca	60
caaggtcttc	cagctgccgc	acattacgca	gggcaagagc	ctccagcaac	actgcatatg	120
ggatacactt	tacttttagca	gccagggtga	caactgagag	gtgtcgaagc	ttattcttct	180
gagcctctgt	tagtggagga	agattccggg	cttcagctaa	gtagtcagcg	tatgtcccat	240
aagcaaacac	tgtgagcagc	cggaggttag	aggcaaagtc	actctcagcc	agctctctaa	300
cattgggcat	gtccagcagt	tctccaaaca	cgtagacacc	agnggcctcc	agcacctgat	360
ggatgagtgt	ggccagcgct	gcccccttgg	ccgacttggc	taggagcaga	aattgctcct	420
ggtttctgcc	tgtcaccttc	acttccgcac	tcatactgct	actgagtgtg	ggggacttgg	480
gctcaggatg	tccagagacg	tggttccgcc	ccctcnctta	atgacaccgn	ccanncaacc	540
gtcggctccc	gccgantgng	ttcgtcgtnc	ctgggtcagg	gtctgctggc	cnctacttgc	600
aancttcgtc	nggcccatgg	aattcacnc	accggaactn	gtangatcca	ctnnttctat	660
aaccgngcgc	caccgcnnnt	ggaactccac	tcttnttnc	tttacttgag	ggttaaggtc	720
acccttnncc	ttactttggt	ccaaacntn	cctgtgtctg	anatngtnaa	tcnggncna	780
tnccancnc	atangaagcc	ng				802

<210> 19  
 <211> 731  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1) ... (731)  
 <223> n = A,T,C or G

<400> 19						
cnaagcttcc	aggtnacggg	ccgcnaance	tgaccnagg	tancanaang	cagnncgcgg	60
gagcccaccg	tcacngngng	gngtctttat	nggagggggc	ggagccacat	cnetggacnt	120
cntgacccca	actccccncc	ncncantgca	gtgatgagtg	cagaactgaa	ggtnacgtgg	180
caggaaccaa	gancaaannc	tgtccnntc	caagtcggcn	nagggggcgg	ggctggccac	240
gcncatccnt	cnagtgtctg	aaagccccnn	cctgtctact	tgtttgagga	acngcnnnga	300
catgccccagn	gttanataac	nggengagag	tnantttgcc	tctcccttcc	ggctgcgcan	360
cgngtntgct	tagnggacat	aacctgacta	cttaactgaa	cccnngaate	tnccnccct	420
ccactaagct	cagaacaaaa	aacttcgaca	ccactcantt	gtcacctgnc	tgctcaagta	480
aagtgtaccc	catncccaat	gtntgctnga	ngctctgncc	tgcnttangt	tcggctctgg	540
gaagacctat	caattnaagc	tatgtttctg	actgcctctt	gctccctgna	acaancnacc	600
cnnccntcca	agggggggnc	ggcccccaat	cccccaacc	ntnaattnan	tttancccn	660
ccccngggc	oggcctttta	cnancntcnn	nnacngggna	aaaccnnngc	tttncccaac	720

nnaatccncc t

731

<210> 20  
 <211> 754  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(754)  
 <223> n = A,T,C or G

<400> 20  
 tttttttttt tttttttttt taaaaacccc ctccattnaa tgnaaacttc cgaaattgtc 60  
 caacccctc ntccaaatnn ccntttccgg gnggggggtc caaacccaan ttanntttgg 120  
 annntaaatt aaatnttntt tgngngnnna anccnaatgt nangaaagt naaccanta 180  
 tnancttnaa tncctggaaa ccngtngntt ccaaaaatnt ttaaccctta antccctccg 240  
 aaatngttna nggaaaaccc aanttctcnt aaggttggtt gaaggntnaa tnaaaanccc 300  
 nnccaattgt ttttngccac gcctgaatta attggnttcc gntgttttcc nttaaaanaa 360  
 ggnnancccc ggttantnaa tcccccnnc cccaattata ccgantttt ttngaattgg 420  
 ganccncgg gaattaacgg ggnnntccc tnttgggggg cnggnncccc cccntcggg 480  
 ggttngggnc aggnccnaat tgtttaaggg tccgaaaaat ccctccnaga aaaaaanctc 540  
 ccagntgag nntnggggtt ncccccccc cangggccct ctcgnanagt tgggggttgg 600  
 ggggcctggg atttntttt cctnttncc tcccccccc ccngganag aggttngnt 660  
 tttgntcnc ggccccnccn aagantttt ccganttnan ttaaaccnt gcctnggcga 720  
 agtcnttgn agggntaaan ggccccctnn cggg 754

<210> 21  
 <211> 755  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(755)  
 <223> n = A,T,C or G

<400> 21  
 atcanccat gacccnaac nngggaccnc tcancggnc nnncnaccnc cgccnatca 60  
 nngtnagnnc actncnttn natcacnccc cncnactac gccncnanc cnacgnccta 120  
 nncanatncc actganngcg cgangtngan ngagaaanct nataccanag ncaccanacn 180  
 ccagctgtcc nanaangcct nnnatacngg nnnatccaat ntgnancctc cnaagtattt 240  
 nncnncanat gattttcctn anccgattac ccntncccc tanccctcc cccccaacna 300  
 cgaaggcnct ggncnaagg nngcgnccc ccgctagntc ccnncaagt cncnnccta 360  
 aactcanccn nattacnccg ttcttgagta tcaactcccc aatctcacc tactcaactc 420  
 aaaaanatcn gatacaaat aatncaagcc tgnttatnac actntgactg ggtctctatt 480  
 ttagnggtcc ntnaanctc ctaatactc cagtctncc tcnccaattt ccnaangget 540  
 ctttngaca gcatnttttg gttccnntt ggggtcttan ngaattgcc ttctnngaac 600  
 gggctcntct tttccttcgg ttancctggn ttcnccggc cagttattat ttccntttt 660  
 aaattcntc cntttanttt tggcntttna aacccccggc cttgaaaacg gccccctgg 720  
 aaaagttgt tttganaaaa tttttgtttt gttcc 754

<210> 22  
 <211> 849  
 <212> DNA  
 <213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(849)

<223> n = A,T,C or G

<400> 22

tttttttttt	tttttangtg	tngtctgtgca	ggtagagggt	tactacaant	gtgaanacgt	60
acgtnggan	taangcgacc	cgantttctag	gannncct	aaaatcanac	tgtgaagatn	120
atcctgnna	cggaanggtc	accggnngat	nntgctaggg	tgncnctcc	cannncnttn	180
cataactng	nggccctgcc	caccaccttc	ggcgggccng	ngnccgggcc	cgggtcattn	240
gnnttaaccn	cactnngcna	ncggtttccn	nccccnng	accnggcga	tccggggtnc	300
tctgtcttc	cctgnagncn	anaaantggg	cnccggncce	ctttaccct	nnacaagcca	360
cngccteta	ncnngcgc	cccctccant	nngggggact	gcnanngct	ccgttnctng	420
nnacccnnn	gggtncctcg	gttgtcgant	cnaccgnang	ccanggatc	cnaaggaagg	480
tgcgttnttg	gccctaccc	ttcgctncgg	nnaccccttc	ccgacnanga	nccgtcccg	540
cncnncgng	cctcncctcg	caacacccgc	ntctctngt	ncggnnnccc	ccccaccgc	600
nccctcncnc	ngnccgnancn	ctccnccncc	gtctcannca	ccaccccgcc	ccgccaggcc	660
ntcanccaen	ggngacnng	nagcncntc	gcncgcgcg	gcgncnccct	cgcncngaa	720
ctnctcngg	ccantnncgc	teaancnna	cnaaacgcg	ctgcgcggcc	cgnagcgncc	780
ncctccnca	gtcctcccg	cttcnacc	angnttccn	cgaggacacn	nnaccccgcc	840
nncangcgg						849

<210> 23

<211> 872

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(872)

<223> n = A,T,C or G

<400> 23

gcgcaaacta	tacttcgctc	gnactcgtgc	gcctcgtcnc	tcttttctc	cgcaaccatg	60
tctgacnanc	ccgattnggc	ngatatchan	aagntcganc	agtccaaact	gantaacaca	120
cacacnncan	aganaaatcc	nctgccttc	anagtanacn	attgaacnng	agaaccangc	180
nggcgaatcg	taatnaggcg	tgcgcgcga	atntgtcncc	gtttattntn	ccagcctcnc	240
ctnccnacc	tacntcttcn	nagctgtcnn	accctngtn	cgnaccccc	naggctggga	300
tccgggtttn	nntgaccng	cnnccctcc	ccccntccat	nacganccnc	ccgcaccacc	360
nanngcncgc	ncccggnct	cttcgccncc	ctgtcctntn	ccccgtngc	ctggcncngn	420
accgcattga	ccccgcgnn	ctnccngaaa	ncgnanacgt	ccgggttggn	annancgctg	480
tgggnnngcg	tctgcncgc	gttccttcen	ncncttcca	ccatcttcnt	taenggtct	540
ccnccctc	tcnnncaenc	cctgggacgc	tntcctntgc	cccccttnac	ccccccctt	600
cgnctgncc	cgnccccacc	ntcatttnca	nacgntcttc	acaannncct	ggntnctcc	660
cnancngncn	gtcanccnag	ggaagggngg	ggnnccnntg	nttgacgttg	ngngngangtc	720
cgaanantcc	tcnccntcan	cctaccct	cgggcgnct	ctcngttncc	aacttancaa	780
ntctcccccg	ngngcncntc	tcagcctcnc	ccncccnct	ctctgcantg	tnctctgctc	840
tnaccnntac	gantnttcgn	cncctcttt	cc			872

<210> 24

<211> 815

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(815)

<223> n = A,T,C or G



## &lt;400&gt; 24

gcattgcaagc	ttgagtattc	tatagngtca	cctaaatanc	ttggcntaat	catggctcnta	60
nctgncttcc	tgtgtcaaat	gtatacnaan	tanatatgaa	tctnatntga	caagannnga	120
tctntcatta	gtaacaantg	tnntgtccat	cctgtcngan	canattccca	tnnattnnng	180
cgcattcncn	gncantatn	taatngggaa	ntcnntnnn	ncaccnncat	ctatcntncc	240
gncacctgac	tggnagagat	ggatnanttc	tnntntgacc	nacatgttca	tcttggattn	300
aanancccc	cgcngnccac	cggtnngng	cnagcncntc	ccaagacctc	ctgtggagggt	360
aacctgcgtc	aganncatca	aacntgggaa	acccgcnncc	angtnnaagt	ngnnncanan	420
gatcccggtc	agnttnnacc	atcccttcnc	agcgccccct	ttngtgcctt	anagnnagc	480
gtgtccnanc	cncctcaacat	ganacgcgcc	agnccanccg	caattnggca	caatgtcgnc	540
gaaccccccta	gggggantna	tncaaanc	caggattgtc	cncncangaa	atcccnanc	600
ccnccctac	ccncttttg	gacngtgacc	aantcccgga	gtncaggtcc	ggcngnctc	660
ccccaccggt	nncntgggg	gggtgaanct	cngnntcanc	cngnccagg	ntcgnaagga	720
accggnccctn	ggncgaanng	ancnntcnga	agngcncnt	cgtataacc	cccctcncca	780
nccnancngnt	agntcccccc	cngggtncgg	aangg			815

## &lt;210&gt; 25

## &lt;211&gt; 775

## &lt;212&gt; DNA

## &lt;213&gt; Homo sapien

## &lt;220&gt;

## &lt;221&gt; misc\_feature

## &lt;222&gt; (1)...(775)

## &lt;223&gt; n = A,T,C or G

## &lt;400&gt; 25

ccgagatgtc	tgcctccgtg	gccttagctg	tgctcgcgt	actctctctt	tctggcctgg	60
aggctatcca	gcgtactcca	aagattcagg	tttactcacg	tcatccagca	gagaatggaa	120
agtcaaat	cctgaattgc	tatgtgtctg	ggtttcatcc	atccgacatt	gaanttgact	180
tactgaagaa	tggnagagaa	attgaaaaag	tgagacattc	agacttgtct	ttcagcaagg	240
actggtcttt	ctatctcntg	tactacactg	aattcacccc	cactgaaaaa	gatgagtatg	300
cctgccgtgt	gaaccatgtg	actttgtcac	agcccaagat	agttaagtgg	gatcgagaca	360
tgtaagcagn	cnnatggaa	gtttgaagat	gccgcatttg	gattggatga	attccaaatt	420
ctgcttgctt	gcntttta	antgatatgc	ntatacacc	taccctttat	gncccaaat	480
tgtaggggtt	acatnantgt	tcnctnngga	catgatcttc	ctttataant	ccnccnttcg	540
aattgcccgt	cncnngttn	ngaattgttc	cnaaaccacg	gttggtccc	ccaggtcncc	600
tcttacggaa	gggctgggc	cnccttncaa	ggttggggga	accnaaaatt	tcnctntngc	660
ccncccncca	cnncttngg	nncncanttt	ggaacccttc	cnattccctt	tggcctcnna	720
nccttnncta	anaaaacttn	aaancgtngc	naaannttn	acttcccccc	ttacc	775

## &lt;210&gt; 26

## &lt;211&gt; 820

## &lt;212&gt; DNA

## &lt;213&gt; Homo sapien

## &lt;220&gt;

## &lt;221&gt; misc\_feature

## &lt;222&gt; (1)...(820)

## &lt;223&gt; n = A,T,C or G

## &lt;400&gt; 26

anattantac	agtgtaatct	tttcccagag	gtgtgtanag	ggaacggggc	ctagaggcat	60
cccanagata	ncttatanca	acagtgtttt	gaccaagagc	tgctgggcac	atttcttgca	120
gaaaagggtg	cgggtcccat	cactcctcct	ctcccatagc	catcccagag	gggtgagtag	180
ccatcangcc	ttcgggtggga	gggagtcang	gaaacaacan	accacagagc	anacagacca	240
ntgatgacca	tgggcgggag	cgagcctctt	ccctgnaccg	gggtggcana	nganagccta	300
nctgaggggt	cacactataa	acgttaacga	ccnagatnan	cacctgcttc	aagtgcaccc	360

ttcctacctg	acnaccagng	accnnnaact	gngcctggg	gacagcncctg	ggancagcta	420
acnnagcaact	cacctgcccc	cccatggccg	tnccgntccc	tggtcctgnc	aagggaagct	480
ccctggttga	attncgggga	naccaaggga	nccccctcct	ccanctgtga	aggaaaaann	540
gatggaattt	tncccttccg	gccnntcccc	tcttccttta	cacgccccct	nnactcctc	600
tccctctntt	ntcctgncnc	acttttnacc	ccnnnatttc	ccttnattga	tcgannctn	660
ganattccac	tnnccgctnc	cntcnatcng	naanaaaaa	nactntctna	ccnggggat	720
gggnncctcg	ntcatcctct	ctttttcnct	accnccnntt	ctttgcctct	ccttngatca	780
tccaaccntc	gntggccntn	cccccccnnn	tccttttccc			820

&lt;210&gt; 27

&lt;211&gt; 818

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(818)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 27

tctgggtgat	ggcctcttcc	tcctcagggg	cctctgactg	ctctgggcca	aagaatctct	60
tgtttcttct	ccgagcccca	ggcagcggtg	attcagccct	gccaacctg	attctgatga	120
ctgcggatgc	tgtgacggac	ccaaggggca	aataggggtcc	cagggtccag	ggaggggagc	180
ctgctgagca	cttccgcccc	tcaccctgcc	cagccctgct	catgagctct	gggctgggtc	240
tccgcctcca	gggttctgct	cttccangca	ngccancaa	tggtgctggg	ccacactggc	300
ttcttctctg	cccttccctg	getctgantc	tctgtcttcc	tgtcctgtgc	angcnccttg	360
gatctcagtt	tccctcncct	anngaactct	gtttctgann	tcttcantta	actntgantt	420
tatnaccnan	tggnetgtnc	tgtcnnactt	taatgggcn	gaccggctaa	tccctccctc	480
nctcccttcc	anttcnnnna	accngcttnc	cntctctctc	ccntancccg	ccnggggaanc	540
ctcctttgcc	ctnaccangg	gccnnnaccg	ccctnnctn	ggggggcngg	gtnnctncnc	600
ctgntncccc	cncctcncnt	tnccctcgtc	cnnccnccg	nngcannntc	nngtcccn	660
tnnctcttct	ngntctcnaa	ngntcncntn	tnnnnnngcn	ngntnntn	tccctctcnc	720
cnnntgnang	tnnttnnnnc	nngnncccc	nnnnnnnnnn	nggnntnnnn	tctnccngc	780
ccnncccccc	ngnattaagg	cctccnntct	ccggccnc			818

&lt;210&gt; 28

&lt;211&gt; 731

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(731)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 28

aggaagggcg	gagggatatt	gtanggggatt	gagggatagg	agnataangg	gggaggtgtg	60
tccaacatg	anggtgnngt	tctcttttga	angaggggtg	ngtttttann	ccnggtgggt	120
gattnaaccc	cattgtatgg	agnnaaagg	tttnagggat	ttttcggtc	ttatcagtat	180
ntanattcct	gtnaatcgga	aaatnatntt	tcnnccggaa	aatnttgctc	ccatccgnaa	240
attntcctcg	ggtagtgc	nttngggggn	cngccangtt	tcccaggtg	ctanaatcgt	300
actaaagntt	naagtgggan	tncaaataaa	aacctnnac	agagnatccn	taccogactg	360
tnnnttncct	tgcctctntg	actctgcngg	agcccaatac	ccnngngnat	gtcncnccng	420
nnngcgncc	tgaaannnn	tcgnggctnn	gancatcang	gggtttcgca	tcaaaaagcnn	480
cgtttncat	naaggcaact	tngcctcatc	caaccnctng	ccctcnncca	tttngccgtc	540
nggttncct	acgctnnntg	cncctnnntn	ganattttnc	ccgcctnggg	naancctcct	600
gnaatgggta	gggnccttnc	tttnaccn	gnggtntact	aatcnnctnc	acgctnctt	660
tctnaccccc	ccccctttt	caatccanc	ggcnaatggg	gtctcccn	cgangggggg	720

nnncccannc c

731

<210> 29  
 <211> 822  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(822)  
 <223> n = A,T,C or G

<400> 29  
 actagtccag tgtggtggaa ttccattgtg ttggggncnc ttctatgant antnttagat 60  
 cgctcanacc tcacanccctc ccnacnangc ctataangaa nannaataga nctgtncnnt 120  
 atntntacnc tcatanncct cnnnaccac tccctcttaa cccntactgt gcctatngcn 180  
 tnnctantct ntgccgcctn cnanccaccn gtggggccnac cncnngnatt ctcnatctcc 240  
 tcnccatntn gcctananta ngtncatacc ctatacctac nccaatgcta nnnctaancn 300  
 tccatnantt annntaacta ccactgacnt ngactttcnc atnanctcct aatttgaatc 360  
 tactctgact cccacngcct annnattagc ancntcccc nacnatntct caaccaaate 420  
 ntcaacaacc tatctantctg ttcnccaacc nttncctccg atccccnnac aacccccctc 480  
 ccaaataccc nccacctgac ncctaaccn caccatcccg gcaagccnan ggncatttan 540  
 ccaactggaat cacnatngga naaaaaaac ccnaactctc tancncnnat ctccctaana 600  
 aatnctcctn naatttactn ncantnccat caancccaen tgaaacnnaa cccctgtttt 660  
 tanatccctt ctttcgaaaa ccnacccttt annncccaac ctttngggcc ccccccctnc 720  
 ccnaatgaag gncncccaat cnangaaacg nccntgaaaa ancnaggcna anannntccg 780  
 canatccctat cccttanttn ggggnccctt ncccnngggcc cc 822

<210> 30  
 <211> 787  
 <212> DNA  
 <213> Homo sapien  
  
 <220>  
 <221> misc\_feature  
 <222> (1)...(787)  
 <223> n = A,T,C or G

<400> 30  
 cggcgcgctg ctctggcaca tgcttcctga atggcatcaa aagtgatgga ctgcccattg 60  
 ctagagaaga ccttctctcc tactgtcatt atggagccct gcagactgag ggctcccctt 120  
 gtctgcagga tttgatgtct gaagtcgtgg agtgtggctt ggagctcctc atctacatna 180  
 gctggaagcc ctggagggcc tctctcgcca gcctccccct tctctccacg ctctccangg 240  
 acaccagggg ctccaggcag cccattattc ccagnangac atgggtgtttc tccacgcgga 300  
 cccatggggc ctgnaaggcc agggctctcct ttgacaccat ctctcccgtc ctgcctggca 360  
 ggccgtggga tccactantt ctanaacggg cgccaccncg gtgggagctc cagcttttgt 420  
 tccenttaat gaagggtaat tgcncgcttg gcgtaatcat nggtcanaac tntttcctgt 480  
 gtgaaattgt ttntccccctc ncnattccnc ncnacatacn aacccggaan cataaagtgt 540  
 taaagcctgg gggtngcctn nngaanaaac tnaactcaat taattgcgtt ggctcatggc 600  
 ccgctttccn ttcnngaaaa ctgtcntccc ctgcnttntt gaatcgcca cccccnngg 660  
 aaaagcgggt tgcnttttng ggggntcctt ccncttcccc cctcnctaan cctnccgct 720  
 cggtcgttnc nggtngcggg gaangggnat nnnctccnc naagggggng agnnngntat 780  
 ccccaaa 787

<210> 31  
 <211> 799  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(799)  
 <223> n = A,T,C or G

<400> 31  
 tttttttttt tttttttggc gatgctactg ttttaattgca ggaggtgggg gtgtgtgtac 60  
 catgtaccag ggctattaga agcaagaagg aaggaggag ggcagagcgc cctgctgagc 120  
 aacaaaggac tctctgcagcc ttctctgtct gtctcttggc gcaggcacat ggggaggcct 180  
 cccgcagggt gggggccacc agtccagggg tgggagcact acanggggtg ggagtgggtg 240  
 gtggctggtt cnaatggcct gncacanatc cctacgattc ttgacacctg gatttcacca 300  
 ggggaccttc tgttctccca nggnaacttc ntnnatctcn aaagaacaca actgtttctt 360  
 cngcanttct ggctgttcat ggaaagcaca ggtgtccnat ttnggctggg acttgggtaca 420  
 tatggttccg gccacactct cccntcnaan aagtaattca ccccccccn cctctnttg 480  
 cctgggcccct taantaccca caccggaact canttanta ttcatcttng gntgggcttg 540  
 ntnatncn cctgaangcg ccaagttgaa aggccacgcc gtnccnctc cccatagnan 600  
 nttttnnct canctaagc cccccnggc aacnatecaa tcccccccn tgggggcccc 660  
 agcccanggc ccccgntctg ggnnncngn cncgnantcc ccagntctc ccantcngnc 720  
 ccnnngcncc cccgcacgca gaacanaagg ntngagccnc cgcannnnnn nggtnnncac 780  
 ctcgcccccc ccnnngnng 799

<210> 32  
 <211> 789  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(789)  
 <223> n = A,T,C or G

<400> 32  
 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60  
 ttttnccnag ggcagggttta ttgacaacct cncgggacac aancaggctg gggacaggac 120  
 ggcaacaggc tccggcggcg gggcgggcg ccctacctgc ggtaccaa at ntgcagctc 180  
 cgctcccgt tgaatntcct ctgcagctgc aggatgcctt aaaacagggc ctggccntn 240  
 ggtgggcacc ctgggatttn aatttccacg ggcacaatgc ggtcgcancc cctcaccacc 300  
 nattaggaat agtggtnnta ccnccnccg ttggcncact cccntggaa accactntc 360  
 gcggctccg catctggtct taaaccttgc aaacnctggg gccctctttt tggttantnt 420  
 nccngccaca atcatnactc agactggcnc gggctggccc caaaaaancn ccccaaaacc 480  
 ggnccatgtc tttnccgggt tgcctgcnatn tncatcacct cccgggcnca ncaggncaac 540  
 ccaaaagtgc ttngggcccn caaaaaanct ccgggggnc ccagtttcaa caaagtcac 600  
 ccccttggcc cccaaatcct cccccgntt nctgggtttg ggaacccacg cctctnnctt 660  
 tggngggcaa gntggntccc ccttggggcc cccgggtggc ccnctctaa ngaaaacncc 720  
 ntctnnnca ccatcccccc nngnnacgnc tancaangna tccctttttt tanaaacggg 780  
 cccccncc 789

<210> 33  
 <211> 793  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(793)  
 <223> n = A,T,C or G

&lt;400&gt; 33

gacagaacat	ggttgatggt	ggagcacctt	tctatacgac	ttacaggaca	gcagatgggg	60
aattcatggc	tgttgagca	atanaacccc	agttctacga	gctgctgac	aaaggacttg	120
gactaaagtc	tgtgaactt	cccaatcaga	tgagcatgga	tgattggcca	gaaatgaana	180
agaagtttgc	agatgtattt	gcaaagaaga	cgaaggcaga	gtggtgtcaa	atctttgacg	240
gcacagatgc	ctgtgtgact	ccggttctga	cttttgagga	ggttgttcat	catgatcaca	300
acaangaacg	gggctcggtt	atcaccantg	aggagcagga	cgtgagcccc	cgccctgcac	360
ctctgctggt	aaacacccca	gccatccctt	ctttcaaaag	ggatccacta	cttctagagc	420
ggncgccacc	gcggtggagc	tccagctttt	gttcccttta	gtgagggtta	attgcgcgct	480
tggcgtaatc	atggtcatan	ctgtttctctg	tgtgaaattg	ttatccgctc	acaattccac	540
acaacatacg	anccggaagc	atnaaatttt	aaagcctggg	ggtngcctaa	tgantgaact	600
nactcacatt	aattggcttt	gcgctcactg	cccgttttcc	agtcgggaaa	acctgtcctt	660
gccagctgcc	nttaatgaat	cnggccaccc	cccggggaaa	aggcngtttg	cttnttgggg	720
cgcncctccc	gctttctcgc	ttcctgaant	ccttccccc	ggtctttcgg	cttgccgcna	780
acggtatcna	cct					793

&lt;210&gt; 34

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(756)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 34

gccgcgaccg	gcatgtacga	gcaactcaag	ggcgagtggg	accgtaaaag	ccccaatctt	60
ancaagtgcg	gggaanagct	gggtcgactc	aagctagtgc	ttctggagct	caacttcttg	120
ccaaccacag	ggaccaagct	gaccaaacag	cagctaattc	tggcccgtga	catactggag	180
atcggggccc	aatggagcat	cctacgcaan	gacatcccct	ccttcgagcg	ctacatggcc	240
cagctcaaat	gctactactt	tgattacaan	gagcagctcc	ccgagtcagc	ctatatgcac	300
cagctcttgg	gcctcaacct	cctcttctctg	ctgtcccaga	accgggtggc	tgantnccac	360
acgganttgg	ancggctgcc	tgcccanga	catacanacc	aatgtctaca	tcnaccacca	420
gtgtcctgga	gcaatactga	tgganggcag	ctaccncaaa	gtnttctctg	ccnagggtaa	480
catccccgcg	cgagagctac	accttcttca	ttgacatcct	gctcgacact	atcagggatg	540
aaaatcgcn	ggttgctcca	gaaaggctnc	aanaanatcc	ttttcnctga	aggccccgg	600
atncnctagt	nctagaatcg	gcccgcacgc	gcggtgganc	ctccaacctt	tcgttnccct	660
ttactgaggg	ttnattgccg	cccttggcgt	tatcatggtc	acnccngttn	cctgtgttga	720
aattnttaac	ccccacaaat	tccacgcna	cattn			756

&lt;210&gt; 35

&lt;211&gt; 834

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(834)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 35

gggatctct	anactnacct	gnatgcatgg	ttgtcggtgt	ggtcgctgtc	gatgaanatg	60
aacaggatct	tgcccttgaa	gctctcggt	gctgtnttta	agttgtctag	tctgccgtca	120
tagtcagaca	cnetcttggg	caaaaaacan	caggatntga	gtcttgattt	cacctccaat	180
aatcttcngg	gctgtctgct	cggtgaactc	gatgacnang	ggcagctggg	tgtgtntgat	240
aaantccanc	angttctcct	tggtgacctc	cccttcaaag	ttgttccggc	cttcatcaaa	300
cttctnnaan	angannancc	canctttgtc	gagctggnat	ttgganaaca	cgtcactgtt	360

```

ggaaactgat cccaaatggt atgtcatcca tgcctctgc tgcctgcaaa aaacttgctt 420
ggcncaaate cgactcccn tccttgaaag aagccnatca cccccctc cctggactcc 480
nncaangact ctnccgctnc cccntccnng caggggtggt ggcancccg gccctgccc 540
ttcttcagcc agttcacnat ntcatcagc cctctgccca gctgtntat tccttggggg 600
ggaanccgtc tctcccttcc tgaannaact ttgaccgtng gaatagccgc gctcncct 660
acntnctggg ccgggttcaa antccctccn ttgncntcn cctcgggcca ttctggattt 720
nccnaacttt ttcttcccc cncctcccg ngtttgntt ttcatnggg ccccaactct 780
gctnttggcc antccctgg gggcntntan cncctctnt ggtccctng ggcc 834

```

```

<210> 36
<211> 814
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(814)
<223> n = A,T,C or G

```

```

<400> 36
cggncgcttt ccngccgccc cccgtttcca tgacnaaggc tcccttcang ttaaatacnn 60
cctagnaaac attaatgggt tgctctacta atacatcata cnaaccagta agcctgccc 120
naacgccaac tcaggccatt cctaccaaag gaagaaaggc tggctctctc acccctgta 180
ggaaaggcct gccttgtaag acaccacaat ncggctgaat ctnaagtctt gtgttttact 240
aatggaaaaa aaaaataaac aanaggtttt gttctcatgg ctgcccaccg cagcctggca 300
ctaaaacanc ccagcgtca cttctgcttg ganaaatatt ctttgcctt ttggacatca 360
ggcttgatgg tatcactgcc acntttccac ccagctgggc ncccttcccc catntttgtc 420
antganctgg aaggcctgaa ncttagtctc caaaagtctc ngcccacaag accggccacc 480
aggggangtc ntttncagt gatctgcaa anantaccn tatcatcnn gaataaaaaag 540
gccctgaac ganatgctc cancancctt taagaccat aatcctngaa ccatggtgcc 600
cttccggtct gatccnaaag gaatgttctt gggctccant cctcctttg ttnccttacgt 660
tgtnttggac cctgctngn atnaccaan tganatcccc ngaagcacc tnccttggc 720
atttganttt cntaaattct ctgccctaen nctgaaagca cnattccctn ggcnccnaan 780
ggngaactca agaaggtctn ngaaaaacca cncn 814

```

```

<210> 37
<211> 760
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(760)
<223> n = A,T,C or G

```

```

<400> 37
gcatgctgct cttcctcaaa gttgttcttg ttgccataac aaccaccata ggtaaagcgg 60
gcgcagtgtt cgctgaagg gttgtagtac cagcgcgga tgctctcctt gcagagtct 120
gtgtctggca ggtccacgca atgcccttg tctctggga aatggatgag ctggagctcg 180
tcnaanccac tcgtgtattt ttcacangca gcctcctccg aagcctcccg gcagttgggg 240
gtgtcgtcac actccactaa actgtcgatn cancagccca ttgctgcagc ggaactgggt 300
gggctgacag gtgccagaac acactggatn ggcctttcca tggaaagggc tgggggaaat 360
cncctnancc caaactgcct ctcaaaggcc accttgaca ccccgacagg ctagaaatgc 420
actcttcttc ccaaaggtag ttgttcttgc tgcccaagca ncctccanca aaccaaanc 480
ttgcaaaatc tgctccgtgg gggcatnnn taccanggtt ggggaaanaa acccgcnng 540
ganccnctt gtttgaatgc naaggnaata atcctcctgt cttgcttggg tggaanagca 600
caattgaact gttaacnttg ggccngttc cncctnggtg gtctgaaact aatcaccgtc 660
actggaaaaa ggtangtgcc ttccttgaat tcccaaannt cccctngntt tgggtnttt 720

```

ctcctctncc ctaaaaatcg tnttcccccc centanggcg

760

<210> 38  
 <211> 724  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(724)  
 <223> n = A,T,C or G

<400> 38  
 tttttttttt tttttttttt tttttttttt tttttaaaaa cccctccat tgaatgaaaa 60  
 cttccnaaat tgtccaaccc cctcnnecaa atnnccattt ccgggggggg gttccaaacc 120  
 caaattaatt ttgganttta aattaaatnt tnattngggg aanaanccaa atgtnaagaa 180  
 aatttaaccc attatnaact taaatnccctn gaaacccttg gnttccaaaa atttttaacc 240  
 cttaaatccc tccgaaattg ntaanggaaa accaaattcn cctaaggctn tttgaagggt 300  
 ngatttaaac ccccttnant tnttttnacc cnnngctnaa ntatttngnt tccgggtgtt 360  
 tctntttaan cntnggtaac tcccgnataa gaannnccct aanccaatta aaccgaattt 420  
 tttttgaatt ggaaattccn ngggaattna ccgggggttt tcccntttgg gggccatncc 480  
 cccnctttcg ggggtttggg ntaggttgaa ttttttnang nccccaaaaa ncccccaana 540  
 aaaaaactcc caagnnttaa ttngaantnc ccccttccca ggccttttgg gaaaggnggg 600  
 tttntggggg ccngggantt cnttcccccn ttncncccc cccccnggt aaanggttat 660  
 ngnntttggt ttttgggccc cttnanggac cttccggatn gaaattaaat cccgggngcg 720  
 gccg 724

<210> 39  
 <211> 751  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(751)  
 <223> n = A,T,C or G

<400> 39  
 tttttttttt tttttctttg ctcacattta atttttattt tgattttttt taatgctgca 60  
 caacacaata tttatttcat ttgtttcttt tatttcattt tatttgtttg ctgctgctgt 120  
 tttatttatt tttactgaaa gtgagaggga acttttgttg ccttttttcc tttttctgta 180  
 ggccgcctta agcttttctaa atttggaaca tctaagcaag ctgaanggaa aaggggggtt 240  
 cgcaaaatca ctccggggaa nggaaagggt gctttgttaa tcatgcccta tgggtgggtga 300  
 ttaactgott gtacaattac ntttcacttt taattaattg tgctnaangc ttttaattana 360  
 cttgggggtt ccttccccan accaacccon ctgacaaaaa gtgccngccc tcaaattnatg 420  
 tcccgcnnt cnttgaaaca cacngcngaa ngttctcatt ntcccnccnc caggtnaaaa 480  
 tgaagggtta ccatntttta cncacctcc acntggcnnn gcctgaatcc tcnaaaancn 540  
 cctcaancn aatttctnng ccccggtcnc gentnngtcc cncccgggct ccgggaantn 600  
 cccccccnga anncnntnnc naacnaaatt ccgaaaatat tcccnntcnc tcaattcccc 660  
 cnnagactnt cctcnncnan cncaattttc ttttntcac gaacncgnnc cnnaaaatgn 720  
 nnnnncctc cncnngtcn naatcnccan c 751

<210> 40  
 <211> 753  
 <212> DNA  
 <213> Homo sapien

<220>

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(753)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 40

gtgggtatttt	ctgtaagatc	aggtgttcct	ccctcgtagg	tttagaggaa	acaccctcat	60
agatgaaaac	ccccccgaga	cagcagcact	gcaactgcc	agcagccggg	gtagggaggg	120
cgccctatgc	acagctgggc	ccttgagaca	gcagggcttc	gatgtcaggc	tcgatgtcaa	180
tggtctggaa	gcggcggctg	tacctgcgta	ggggcacacc	gtcagggccc	accaggaaact	240
tctcaaagtt	ccaggcaacn	tcgttgcgac	acaccggaga	ccaggtgatn	agcttgggggt	300
cggtcataa	cgcggtggcg	tcgtcgtctg	gagctggcag	ggcctcccgc	aggaaggcna	360
ataaaaggtg	cgccccgcga	ccgttcantc	cgcacttctc	naanaccatg	angttgggct	420
cnaaccacc	accannccgg	acttccttga	nggaattccc	aatctctctc	gntcttgggc	480
ttctnctgat	gccctantct	gttgcccnng	atgccaanca	nccccaance	ccggggctcct	540
aaancaccn	cctcctcntt	tcattctggg	tnttntcccc	ggacntgggt	tcctctcaag	600
ggancccata	tctcnaccan	tactcacent	nccccccent	gnnaccanc	cttctannng	660
ttccnccccg	ncctctggcc	cntcaaan	gcttnacna	cctgggtctg	ccttcccccc	720
tnccctatct	gnaccnncn	tttgtctcan	tnt			753

&lt;210&gt; 41

&lt;211&gt; 341

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 41

actatatcca	tcacaacaga	catgcttcat	cccatagact	tcttgacata	gcttcaaagt	60
agtgaacca	tccttgattt	atatacatat	atgttctcag	tattttggga	gcctttccac	120
ttctttaaac	cttggttcatt	atgaacactg	aaaataggaa	tttgtgaaga	gttaaaaagt	180
tatagcttgt	ttacgtagta	agtttttgaa	gtctacattc	aatccagaca	cttagttgag	240
tgttaaactg	tgatttttaa	aaaatatcat	ttgagaatat	tctttcagag	gtattttcat	300
ttttactttt	tgattaattg	tgttttatat	attagggtag	t		341

&lt;210&gt; 42

&lt;211&gt; 101

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 42

acttactgaa	tttagttctg	tgctcttcct	tatttagtgt	tgtatcataa	atactttgat	60
gtttcaaaca	ttctaaataa	ataattttca	gtggcttcat	a		101

&lt;210&gt; 43

&lt;211&gt; 305

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 43

acatctttgt	tacagtctaa	gatgtgttct	taaatcacca	ttccttcctg	gtcctcaccc	60
tccaggggtg	tctcacactg	taattagagc	tattgaggag	tctttacagc	aaattaagat	120
tcagatgcct	tgctaagtct	agagttctag	agttatgttt	cagaaagtct	aagaaacca	180
cctcttgaga	ggtcagtaaa	gaggacttaa	tatttcatat	ctacaaaatg	accacaggat	240
tgatacaga	acgagagtta	tcctggataa	ctcagagctg	agtacctgcc	cggggggccg	300
tcgaa						305

&lt;210&gt; 44

&lt;211&gt; 852

&lt;212&gt; DNA

&lt;213&gt; Homo sapien



&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(852)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 44

acataaatat	cagagaaaag	tagtctttga	aatattttacg	tccaggagtt	ctttgtttct	60
gattatttgg	tgtgtgtttt	ggtttgtgtc	caaagtattg	gcagcttcag	ttttcatttt	120
ctctccatcc	tcgggcattc	ttcccaaatt	tatataccag	tcttcgtcca	tccacacgct	180
ccagaatttc	tctttttag	taatatctca	tagctcggct	gagcttttca	taggtcatgc	240
tgctgttggt	cttcttttta	ccccatagct	gagccactgc	ctctgatttc	aagaacctga	300
agacgccctc	agatcgggtc	tcccatttta	ttaatcctgg	gttcttgtct	gggttcaaga	360
ggatgtcgcg	gatgaattcc	cataagttag	tccctctcgg	gttgtgcttt	ttggtgtggc	420
acttggcagg	ggggtcttgc	tcctttttca	tatcagggtga	ctctgcaaca	ggaagggtgac	480
tggtgggtgt	catggagatc	tgagcccggc	agaaagtttt	gctgtccaac	aaatctactg	540
tgctaccata	gttgggtgtc	tataaatagt	tctngtcttt	ccagggtgtc	atgatggaag	600
gctcagcttt	ttcagtcctg	acaatgacat	tgtgtgtgga	ctggaacagg	tactactgc	660
actggccgtt	ccacttcaga	tgctgcaagt	tgctgtagag	gagntgcccc	gccgtccctg	720
ccgcccggtt	gaactcctgc	aaactcatgc	tgcaaagggt	ctcgccgttg	atgtcgaact	780
cntggaaagg	gatacaattg	gcattccagct	ggttggtgtc	caggaggtga	tggagccact	840
cccacacctg	gt					852

&lt;210&gt; 45

&lt;211&gt; 234

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 45

acaacagacc	cttgctcgct	aacgacctca	tgctcatcaa	gttgagcgaa	tccgtgtccg	60
agtctgacac	catccggagc	atcagcattg	cttcgcagtg	ccctaccgcg	gggaactctt	120
gcctcgtttc	tggctggggt	ctgctggcga	acggcagaat	gcctaccgtg	ctgcagtgcg	180
tgaacgtgtc	ggtggtgtct	gaggaggtct	gcagtaagct	ctatgaccgg	ctgt	234

&lt;210&gt; 46

&lt;211&gt; 590

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(590)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 46

actttttatt	taaatgttta	taaggcagat	ctatgagaat	gatagaaaac	atggtgtgta	60
atttgatagc	aatatttttg	agattacaga	gttttagtaa	ttaccaatta	cacagttaaa	120
aagaagataa	tatattccaa	gcanatacaa	aatatcta	gaaagatcaa	ggcaggaaaa	180
tgantataac	taattgacaa	tggaatca	attttaatgt	gaattgcaca	ttatccttta	240
aaagctttca	aaanaanaa	ttattgcagt	ctanttaatt	caaacagtgt	ttaatgggtat	300
caggataaan	aactgaaggg	canaaagaat	taattttcac	ttcatgtaac	ncacccan	360
ttacaatggc	ttaaatgcan	ggaaaaagca	gtggaagtag	ggaagtantc	aaggtctttc	420
tggtctctaa	tctgccttac	tctttgggtg	tggttttgat	cctctggaga	cagctgccag	480
ggctcctgtt	atatccacaa	tcccagcagc	aagatgaagg	gatgaaaaag	gacacatgct	540
gccttccttt	gaggagactt	catctcactg	gccaacactc	agtcacatgt		590

&lt;210&gt; 47

&lt;211&gt; 774

<212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(774)  
 <223> n = A,T,C or G

<400> 47  
 acaagggggc ataatgaagg agtgggggana gatttttaaag aaggaaaaaa aacgaggccc 60  
 tgaacagaat tttcctgnac aacggggcctt caaaataatt ttcttgggga ggttcaagac 120  
 gcttactgc ttgaaactta atggatgtg ggacanaatt ttctgtaatg accctgaggg 180  
 cattacagac gggactctgg gaggaaggat aaacagaaag gggacaaagg ctaatcccaa 240  
 aacatcaaag aaaggaaggt ggcgtcatat ctcccagcct acacagttct ccagggtct 300  
 cctcatccct ggaggacgac agtggaggaa caactgacca tgtcccagg ctcctgtgtg 360  
 ctggctcctg gtcttcagcc cccagctctg gaagcccacc ctctgctgat cctgcgtggc 420  
 ccacactcct tgaacacaca tcccaggtt atattcctgg acatggctga acctcctatt 480  
 cctacttccg agatgccttg ctccctgcag cctgtcaaaa tcccactcac cctccaaacc 540  
 acggcatggg aagcctttct gacttgcttg attactccag catcttgga caatccctga 600  
 ttccccactc cttagaggca agataggggtg gttaagagta gggctggacc acttgagacc 660  
 aggtgctgg cttcaaattt tggctcattt acgagctatg ggaccttggg caagtnatct 720  
 tcacttctat gggcntcatt ttgttctacc tgcaaaatgg gggataataa tagt 774

<210> 48  
 <211> 124  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(124)  
 <223> n = A,T,C or G

<400> 48  
 canaaattga aattttataa aaaggcattt ttctottata tccataaaat gatataattt 60  
 ttgcaantat anaaatgtgt cataaattat aatgttcctt aattacagct caacgcaact 120  
 tggt 124

<210> 49  
 <211> 147  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(147)  
 <223> n = A,T,C or G

<400> 49  
 gccgatgcta ctattttatt gcaggagggtg ggggtgtttt tattattctc tcaacagctt 60  
 tgtggctaca ggtgggtgtc gactgcatna aaaanttttt tacgggtgat tgcaaaaatt 120  
 ttagggcacc catatcccaa gcantgt 147

<210> 50  
 <211> 107  
 <212> DNA  
 <213> Homo sapien

<400> 50  
acattaaatt aataaaagga ctgttggggt tctgctaaaa cacatggcctt gatataattgc 60  
atggtttgag gttaggagga gttaggcata tgttttggga gaggggt 107

<210> 51  
<211> 204  
<212> DNA  
<213> Homo sapien

<400> 51  
gtcctaggaa gtctagggga cacacgactc tggggtcacg gggccgacac acttgcacgg 60  
cgggaaggaa aggcagagaa gtgacaccgt cagggggaaa tgacagaaag gaaaatcaag 120  
gccttgcaag gtcagaaagg ggactcaggg cttccaccac agccctgccc cacttggcca 180  
cctccctttt gggaccagca atgt 204

<210> 52  
<211> 491  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(491)  
<223> n = A,T,C or G

<400> 52  
acaaagataa catttatctt ataacaaaaa tttgatagtt ttaaaggtta gtatttgtta 60  
gggtattttc caaaagacta aagagataac tcaggtaaaa agttagaaat gtataaaaca 120  
ccatcagaca ggttttttaa aaacaacata ttacaaaatt agacaatcat ctttaaaaaa 180  
aaaacttctt gtatcaattt cttttgttca aaatgactga cttaantatt tttaaatatt 240  
tcanaaacac ttcctcaaaa attttcaana tggtagcttt canatgtnc ctcagtccca 300  
atgttgctca gataaataaa tctcgtgaga acttaccacc caccacaagc tttctggggc 360  
atgcaacagt gtcttttctt tnccttttct tttttttttt ttacaggcac agaaactcat 420  
caatttttatt tggataacaa agggctctcca aattatattg aaaaataaat ccaagttaat 480  
atcactcttg t 491

<210> 53  
<211> 484  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(484)  
<223> n = A,T,C or G

<400> 53  
acataattta gcagggctaa ttaccataag atgctattta ttaanaggtn tatgatctga 60  
gtattaacag ttgctgaagt ttgggtatttt tatgcagcat tttctttttg ctttgataac 120  
actacagaac ccttaaggac actgaaaatt agtaagtaaa gttcagaaac attagctgct 180  
caatcaaato tctacataac actatagtaa ttaaaacggt aaaaaaaagt gttgaaatct 240  
gcactagtat anaccgctcc tgtcaggata anactgcttt ggaacagaaa gggaaaaanc 300  
agctttgant ttctttgtgc tgatangagg aaaggctgaa ttaccttggt gcctctccct 360  
aatgattggc aggtcnggta aatnccaaaa catattccaa ctcaacactt cttttccncg 420  
tancttgant ctgtgtatcc caggancagg cggatggaat gggccagccc ncggatgttc 480  
cant 484

<210> 54

<211> 151  
 <212> DNA  
 <213> Homo sapien

<400> 54  
 actaaacctc gtgcttgtga actccatata gaaaaagggtg ccatccctga aacgggtgg 60  
 ccactgggta tactgctgac aaccgcaaca acaaaaacac aaatccttgg cactggctag 120  
 tctatgtcct ctcaagtgcc tttttgtttg t 151

<210> 55  
 <211> 91  
 <212> DNA  
 <213> Homo sapien

<400> 55  
 acctggcttg tctccgggtg gttcccggcg cccccacagg tcccagaac ggacactttc 60  
 gccctccagt ggatactcga gccaaagtgg t 91

<210> 56  
 <211> 133  
 <212> DNA  
 <213> Homo sapien

<400> 56  
 ggcggatgtg cggttggttat atacaaatat gtcattttat gtaagggact tgagtatact 60  
 tggatttttg gtatctgtgg gttgggggga cgggccagga accaataccc catggatacc 120  
 aagggacaac tgt 133

<210> 57  
 <211> 147  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(147)  
 <223> n = A,T,C or G

<400> 57  
 actctggaga acctgagccg ctgctccgcc tctgggatga ggtgatgcan gcngtggcgc 60  
 gactgggagc tgagcccttc cctttgcgcc tgcctcagag gattgttgcc gacntgcana 120  
 tctcantggg ctggatncat gcagggt 147

<210> 58  
 <211> 198  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(198)  
 <223> n = A,T,C or G

<400> 58  
 acagggatat aggttttnaag ttattgtnat tgtaaaatac attgaatttt ctgtatactc 60  
 tgattacata catttatcct ttaaaaaaga tgtaaatctt aatttttatg ccacttatta 120  
 attaccaat gagttacctt gtaaatgaga agtcatgata gcactgaatt ttaactagtt 180  
 ttgacttcta agtttggt 198

<210> 59  
 <211> 330  
 <212> DNA  
 <213> Homo sapien

<400> 59  
 acaacaaatg ggttgtgagg aagtcttatac agcaaaactg gtgatggcta ctgaaaagat 60  
 ccattgaaaa ttatcattaa tgatttttaa tgacaagtta tcaaaaactc actcaatttt 120  
 cacctgtgct agcttgctaa aatgggagtt aactctagag caaatatagt atcttctgaa 180  
 tacagtcaat aaatgacaaa gccagggcct acaggtgggt tccagacttt ccagaccag 240  
 cagaaggaat ctattttatc acatggatct cgtctgtgc tcaaaatacc taatgatatt 300  
 tttcgtcttt attggacttc tttgaagagt 330

<210> 60  
 <211> 175  
 <212> DNA  
 <213> Homo sapien

<400> 60  
 accgtgggtg ccttctacat tcttgacggc tcttcacca acatctggtt ctacttcggc 60  
 gtcgtgggct ccttcctctt catcctcacc cagctgggtg tgctcatcga ctttgcgac 120  
 tcttggaacc agcgggtggct gggcaaggcc gaggagtgcg attcccgtag ctggt 175

<210> 61  
 <211> 154  
 <212> DNA  
 <213> Homo sapien

<400> 61  
 accccacttt tctcctctgtg agcagttctg acttctcact gctacatgat gaggggtgagt 60  
 ggttggttgc cttcaacagt atcctccctt ttccggatct gctgagccgg acagcagtag 120  
 tggactgcac agccccgggg ctccacattg ctgt 154

<210> 62  
 <211> 30  
 <212> DNA  
 <213> Homo sapien

<400> 62  
 cgctcgagcc ctatagtgag tcgtattaga 30

<210> 63  
 <211> 89  
 <212> DNA  
 <213> Homo sapien

<400> 63  
 acaagtcatt tcagcaccct ttgctcttca aaactgacca tcttttatat ttaatgcttc 60  
 ctgtatgaat aaaaatgggt atgtcaagt 89

<210> 64  
 <211> 97  
 <212> DNA  
 <213> Homo sapien

<400> 64  
 accggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa ggttctgcag 60

aatcagtgc tccaggattg gtccttggat ctgggggt

97

<210> 65  
 <211> 377  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(377)  
 <223> n = A,T,C or G

<400> 65  
 acaacaanaa ntcccttctt taggccaactg atggaaacct ggaaccccct tttgatggca 60  
 gcatggcgct ctaggccttg acacagcggc tggggtttgg gctntcccaa accgcacacc 120  
 ccaaccctgg tctaccaca nttctggcta tgggctgtct ctgccactga acatcagggt 180  
 tcggtcataa natgaaatcc caanggggac agaggtcagt agaggaagct caatgagaaa 240  
 ggtgctgttt gctcagccag aaaacagctg cctggcattc gccgctgaac tatgaacccg 300  
 tgggggtgaa ctacccccc gaggaatcat gcctgggcga tgcaanggtg ccaacaggag 360  
 gggcgggagg agcatgt 377

<210> 66  
 <211> 305  
 <212> DNA  
 <213> Homo sapien

<400> 66  
 acgcctttcc ctcagaattc agggaagaga ctgtcgcttg ccttctctcg ttgttgctg 60  
 agaaccctg tgccccttcc caccatatcc accctcgctc catctttgaa ctcaaacacg 120  
 aggaactaac tgcaccctgg tctctcccc agtccccagt tcaccctcca tccctcacct 180  
 tctccactc taagggatat caacactgcc cagcacaggg gccctgaatt tatgtggttt 240  
 ttatatattt tttaataaga tgcactttat gtcatttttt aataaagtct gaagaattac 300  
 tgttt 305

<210> 67  
 <211> 385  
 <212> DNA  
 <213> Homo sapien

<400> 67  
 actacacaca ctccacttgc ccttgtgaga cactttgtcc cagcacttta ggaatgctga 60  
 ggtcggacca gccacatctc atgtgcaaga ttgccagca gacatcagggt ctgagagttc 120  
 cccttttaaa aaaggggact tgcttaaaaa agaagtctag ccacgattgt gtagagcagc 180  
 tgtgctgtgc tggagattca cttttgagag agttctctc tgagacctga tcttttagagg 240  
 ctgggcagtc ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgcttg 300  
 cctctcccag ggccccagcc tggccacacc tgcttacagg gcactctcag atgccatac 360  
 catagtttct gtgctagtgg accgt 385

<210> 68  
 <211> 73  
 <212> DNA  
 <213> Homo sapien

<400> 68  
 acttaaccag atatattttt accccagatg gggatattct ttgtaaaaaa tgaaaataaa 60  
 gtttttttaa tgg 73

<210> 69

<211> 536  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(536)  
 <223> n = A,T,C or G

<400> 69  
 actagtccag tgtggtggaa ttccattgtg ttggggggctc tcaccctcct ctccctgcagc 60  
 tccagctttg tgctctgcct ctgaggagac catggcccag catctgagta ccctgctgct 120  
 cctgctggcc accctagctg tggccctggc ctggagcccc aaggaggagg ataggataat 180  
 ccgggtggc atctataacg cagacctcaa tgatgagtgg gtacagcgtg cccttcactt 240  
 cgccatcagc gagtataaca aggccaccaa agatgactac tacagacgtc cgctgcgggt 300  
 actaagagcc aggcaacaga ccgttggggg ggtgaattac ttcttcgacg tagagggtggg 360  
 ccgaaccata tgtaccaagt ccagcccaa cttggacacc tgtgccttcc atgaacagcc 420  
 agaactgcag aagaaacagt tgtgctcttt cgagatctac gaagttccct ggggagaaca 480  
 gaangtccct gggtgaaatc caggtgtcaa gaaatcctan ggatctgttg ccaggc 536

<210> 70  
 <211> 477  
 <212> DNA  
 <213> Homo sapien

<400> 70  
 atgacccta acagggggccc totcagccct cctaattgacc tccggcctag ccatgtgatt 60  
 tcacttccac tccataacgc tctcactact aggcctacta accaacacac taaccatata 120  
 ccaatgatgg cgcgatgtaa cacgagaaag cacataccaa ggccaccaca caccacctgt 180  
 ccaaaaaggc cttcgatacg ggataatcct atttattacc tcagaagttt ttttcttcgc 240  
 agggattttt ctgagccttt taccactcca gcctagcccc taccocccaa ctaggagggc 300  
 actggccccc aacaggcatc acccogctaa atcccctaga agtcccactc ctaaacacat 360  
 ccgtattact cgcacagga gtatcaatca cctgagctca ccatagtcta atagaaaaca 420  
 accgaaacca aattattcaa agcaactgctt attacaattt tactgggtct ctatttt 477

<210> 71  
 <211> 533  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(533)  
 <223> n = A,T,C or G

<400> 71  
 agagctatag gtacagtgtg atctcagctt tgcaaacaca ttttctacat agatagtact 60  
 aggtattaat agatatgtaa agaaagaaat cacaccatta ataatggtaa gattgggtta 120  
 tgtgatttta gtggtatttt tggcaccctt atatatgttt tocaaacttt cagcagtgat 180  
 attatttcca taacttaaaa agtgagtttg aaaaagaaaa tctccagcaa gcatctcatt 240  
 taaataaagg tttgtcatct ttaaaaatac agcaatatgt gactttttta aaaagctgtc 300  
 aaatagggtg gaccctacta ataattatta gaaatacatt taaaaacatc gagtacctca 360  
 agtcagtttg ccttgaaaaa tatcaaatat aactottaga gaaatgtaca taaaagaatg 420  
 cttcgtaatt ttggagtang aggttccctc ctcaattttg tattttttaa aagtacatgg 480  
 taaaaaaaaa aattcacaac agtatataag gctgtaaaat gaagaattct gcc 533

<210> 72  
 <211> 511

<212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(511)  
 <223> n = A,T,C or G

<400> 72  
 tattacggaa aaacacacca cataattcaa ctancaaaga anactgcttc agggcgtgta 60  
 aaatgaaagg cttccaggca gttatctgat taaagaacac taaaagaggg acaaggctaa 120  
 aagccgcagg atgtctacac tatancaggc gctatttggg ttggctggag gagctgtgga 180  
 aaacatggan agattggtgc tgganacgc cgtggctatt cctcattgtt attacanagt 240  
 gaggttctct gtgtgcccac tggtttgaaa accgttctnc aataatgata gaatagtaca 300  
 cacatgagaa ctgaaatggc ccaaaccag aaagaaagcc caactagatc ctcagaanac 360  
 gcttctaggg acaataaccg atgaagaaaa gatggcctcc ttgtgcccc gtctgttatg 420  
 atttctctcc attgcagcna naaaccggtt cttctaagca aacncagggtg atgatggcna 480  
 aaatacacc cctcttgaag naccnggagg a 511

<210> 73  
 <211> 499  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(499)  
 <223> n = A,T,C or G

<400> 73  
 cagtgccagc actggtgcc gtaccagtag caataacagt gccagtgcc gtgccagcac 60  
 cagtgggtggc ttcagtgtcg gtgccagcct gaccgccact ctcacatttg ggctcttcgc 120  
 tggccttggg ggagctggtg ccagcaccag tggcagctct ggtgcctgtg gtttctccta 180  
 caagtgagat tttagatatt gttaatcctg ccagtctttc tcttcaagcc aggggtgcac 240  
 ctcagaaacc tactcaacac agcactctag gcagccacta tcaatcaatt gaagttgaca 300  
 ctctgcatta aatctatttg ccatttctga aaaaaaaaaa aaaaaaaggg cggccgctcg 360  
 antctagagg gcccgtttaa acccgctgat cagcctcgac tgtgccttct anttgccagc 420  
 catctgttgt ttgccctcc cccgntgcct tccttgacct tggaaagtgc cactccact 480  
 gtcctttcct aantaaaat 499

<210> 74  
 <211> 537  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(537)  
 <223> n = A,T,C or G

<400> 74  
 tttcatagga gaacacactg aggagatact tgaagaattt ggattcagcc gcgaagagat 60  
 ttatcagctt aactcagata aaatcattga aagtaataag gtaaaagcta gtctctaact 120  
 tccaggccca cggctcaagt gaatttgaat actgcattta cagtgtagag taacacataa 180  
 cattgtatgc atggaaacat ggaggaacag tattacagtg tctaccact ctaatcaaga 240  
 aaagaattac agactctgat tctacagtga tgattgaatt ctaaaaatgg taatcattag 300  
 ggcttttgat ttataanact ttgggtactt atactaaatt atggtagtta tactgccttc 360  
 cagtttgctt gatataattg ttgatattaa gattccttgac ttatattttg aatgggttct 420



actgaaaaan gaatgatata ttcttgaaga catcgatata catttattta cactcttgat 480  
tctacaatgt agaaaatgaa ggaaatgcc caaattgtat ggtgataaaa gtcccg 537

<210> 75  
<211> 467  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(467)  
<223> n = A,T,C or G

<400> 75  
caaanacaat tgttcaaaag atgcaaatag tacactactg ctgcagctca caaacacctc 60  
tgcataattac acgtacctcc tctgtctcct caagtagtgt ggtctatatt gccatcatca 120  
cctgctgtct gcttagaaga acggctttct gctgcaangg agagaaatca taacagacgg 180  
tggcacaagg aggccatctt ttctcctcgt gttattgtcc ctagaagcgt cttctgagga 240  
tctagttggg ctttctttct gggtttgggc catttcantt ctcattgtgt tactattcta 300  
tcattattgt ataacgggtt tcaaaccngt gggcacncag agaacctcac tctgtaataa 360  
caatgaggaa tagccacggg gatctccagc accaaatctc tccatgttnt tccagagctc 420  
ctccagccaa cccaaatagc cgctgctatn gtgtagaaca tccctgn 467

<210> 76  
<211> 400  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(400)  
<223> n = A,T,C or G

<400> 76  
aagctgacag cattcggggc gagatgtctc gctccgtggc cttagctgtg ctgcgctac 60  
tctctctttc tggcctggag gctatccagc gtactccaaa gattcaggtt tactcacgtc 120  
atccagcaga gaatggaaa tcaaatttcc tgaattgcta tgtgtctggg ttcatccat 180  
ccgacattga agttgactta ctgaagaatg gagagagaat tgaaaaagt gagcattcag 240  
actgtctttt cagcaaggac tggctcttct atctcttgta ctacactgaa ttcccccca 300  
ctgaaaaaga tgagtatgcc tgccgtgtga accatgtgac tttgtcacag cccaagatng 360  
ttnagtggga tcganacatg taagcagcan catgggaggt 400

<210> 77  
<211> 248  
<212> DNA  
<213> Homo sapien

<400> 77  
ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcacctc tgaggcacct 60  
ccagctgccc cggcggggga tgcgaggctc ggagcaccct tgcccggctg tgattgtctc 120  
caggcactgt tcattctcagc ttttctgtcc ctttctccc ggcaagcgct tctgtgaaa 180  
gttcatactc ggagcctgat gtcttaacga ataaaggtcc catgctccac ccgaaaaaaa 240  
aaaaaaaa 248

<210> 78  
<211> 201  
<212> DNA  
<213> Homo sapien

<400> 78  
 actagtccag tgtggtggaa ttccattgtg ttgggcccaa cacaatggct acctttaaca 60  
 tcacccagac cccgccctgc ccgtgcccc aacgacagta tgatgcttac 120  
 tctgctactc ggaaactatt tttatgtaat taatgtatgc tttcttgttt ataaatgcct 180  
 gatttaaaaa aaaaaaaaaa a 201

<210> 79  
 <211> 552  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(552)  
 <223> n = A,T,C or G

<400> 79  
 tccttttggt aggtttttga gacaacccta gacctaaact gtgtcacaga cttctgaatg 60  
 tttaggcagt gctagtaatt tcctcgtaat gattctgtta ttactttcct attcctttatt 120  
 cctctttcct ctgaagatta atgaagttga aaattgaggt ggataaatac aaaaaggtag 180  
 tgtgatagta taagtatcta agtgcagatg aaagtgtgtt atatatatcc attcaaaatt 240  
 atgcaagtta gtaattactc aggtttaact aaattacttt aatatgctgt tgaacctact 300  
 ctgttccttg gctagaaaaa attataaaca ggactttggt agtttgggaa gccaaattga 360  
 taatattcta tgttctaaaa gttgggctat acataaanta tnaagaaata tggaatttta 420  
 ttcccaggaa tatgggggttc atttatgaat antacccggg anagaagttt tgantnaaac 480  
 cngttttggt taatacgtta atatgtcctn aatnaacaag gcntgactta tttccaaaaa 540  
 aaaaaaaaaa aa 552

<210> 80  
 <211> 476  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(476)  
 <223> n = A,T,C or G

<400> 80  
 acagggattt gagatgctaa ggccccagag atcgtttgat ccaaccctct tattttcaga 60  
 ggggaaaaatg gggcctagaa gttacagagc atctagctgg tgcgctggca cccctggcct 120  
 cacacagact cccgagtagc tgggactaca ggcacacagt cactgaagca ggccctgttt 180  
 gcaattcacg ttgccacctc caacttaaac attcttcata tgtgatgtcc ttagtcaacta 240  
 aggttaaact ttcccaccca gaaaaggcaa cttagataaa atcttagagt actttcatac 300  
 tcttetaagt cctcttccag cctcactttg agtcctcctt gggggttgat aggaantntc 360  
 tcttggtttt ctcaataaaa tctctatcca tctcatgttt aatttggtac gcntaaaaat 420  
 gctgaaaaaa ttaaaatggt ctggtttcnc tttaaaaaaa aaaaaaaaaa aaaaaa 476

<210> 81  
 <211> 232  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(232)  
 <223> n = A,T,C or G

<400> 81  
 tttttttttg tatgcntcn ctgtgnggtt attgttgctg ccaccctgga ggagcccagt 60  
 ttcttctgta tctttctttt ctgggggatc ttcttggtc tgcccctcca ttcccagcct 120  
 ctcaccccca tcttgcactt ttgctagggt tggaggcgct ttcttggtag cccctcagag 180  
 actcagtcag cggaataag tcctaggggt ggggggtgtg gcaagccggc ct 232

<210> 82  
 <211> 383  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(383)  
 <223> n = A,T,C or G

<400> 82  
 aggcggggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc 60  
 agtaccagta ccaataacat gccagtgcc gtgccagcac cagtgggtggc ttcagtgtctg 120  
 gtgccagcct gaccgccact ctcacatttg ggctcttcgc tggccttggg ggagctgggt 180  
 ccagcaaccag tggcagctct ggtgcctgtg gtttctccta caagtgagat tttagatatt 240  
 gttaatcctg ccagtctttc tcttcaagcc aggggtgcac ctcagaaacc tactcaacac 300  
 agcactctng gcagccacta tcaatcaatt gaagttgaca ctctgcatta aatctatttg 360  
 ccatttcaaa aaaaaaaaaa aaa 383

<210> 83  
 <211> 494  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(494)  
 <223> n = A,T,C or G

<400> 83  
 accgaattgg gaccgctggc ttataagcga tcatgtctc cagtattacc tcaacgagca 60  
 gggagatcga gtctatacgc tgaagaaatt tgaccgatg ggacaacaga cctgtctcagc 120  
 ccatcctgct cggttctccc cagatgacaa atactctcga caccgaatca ccatcaagaa 180  
 acgcttcaag gtgtcatga cccagcaacc ggcacctgtc ctctgagggt ccttaaactg 240  
 atgtcttttc tgccacctgt taccctcggg agactccgta accaaactct tcggactgtg 300  
 agccctgatg cctttttgcc agccatactc tttggctcc agtctctcgt ggcgattgat 360  
 tatgcttggt tgaggcaatc atggtggcat caccatnaa gggaacacat ttganttttt 420  
 tttncatat tttaaattac naccagaata nttcagaata aatgaattga aaaactctta 480  
 aaaaaaaaaa aaaa 494

<210> 84  
 <211> 380  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(380)  
 <223> n = A,T,C or G

<400> 84

```

gctggtagcc tatggcgtgg ccacggangg gctcctgagg cacgggacag tgacttccca      60
agtatcctgc gccgcgtctt ctaccgtccc tacctgcaga tcttcgggca gattccccag      120
gaggacatgg acgtggccct catggagcac agcaactgct cgtcggagcc cggcttctgg      180
gcacaccctc ctggggccca ggcgggcacc tgcgtctccc agtatgcca ctggctgggtg      240
gtgctgctcc tcgtcatctt cctgctcgtg gccaacatcc tgctggtcac ttgctcattg      300
ccatgttcag ttacacattc ggcaaagtac agggcaacag cnatctctac tgggaaggcc      360
agcgttnccg cctcatccgg                                     380

```

```

<210> 85
<211> 481
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(481)
<223> n = A,T,C or G

```

```

<400> 85
gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggcctctcgc ttcataccgc      60
tnccatcgtc atactgtagg ttggccacca cctcctgcat cttggggcgg ctaatatcca      120
ggaaactctc aatcaagtca ccgtcnatna aacctgtggc tggttctgtc ttccgctcgg      180
tgtgaaagga tctccagaag gagtgctcga tcttccccac acttttgatg actttattga      240
gtcgattctg catgtccagc aggaggttgt accagctctc tgacagtgag gtcaccagcc      300
ctatcatgcc nttgaacgtg ccgaagaaca ccgagccttg tgtggggggg gnagtctcac      360
ccagattctg cattaccaga nagccgtggc aaaaganatt gacaactcgc ccaggngaa      420
aaagaacacc tcctggaagt gctngccgct cctcgtccnt tgggtggngc gentnccttt      480
t                                     481

```

```

<210> 86
<211> 472
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(472)
<223> n = A,T,C or G

```

```

<400> 86
aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgctg agaattcatt      60
acttgaaaaa gcaacttnaa gcctggacac tggattataa attcacaata tgcaacactt      120
taaacagtgt gtcaatctgc tcccttactt tgtcatcacc agtctgggaa taagggtatg      180
ccctattcac acctgttaaa agggcgctaa gcatttttga ttcaacatct ttttttttga      240
cacaagtccg aaaaaagcaa aagtaaacag ttnttaattt gtagccaat tcactttctt      300
catgggacag agccatttga tttaaaaagc aaattgcata atattgagct ttgggagctg      360
atatntgagc ggaagantag cctttctact tcaccagaca caactccttt catattggga      420
tgttnacnaa agttatgtct cttacagatg ggatgctttt gtggcaattc tg                                     472

```

```

<210> 87
<211> 413
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(413)
<223> n = A,T,C or G

```

&lt;400&gt; 87

agaaccagct atctctnaaa acaacctctc ataccttggt gacctaat	60
ttgtgtgtgcg cgcataattat atagacaggc acatcttttt tacttttgta aaagcttatg	120
cctcttttgggt atctatatct gtgaaagttt taatgatctg ccataatgtc ttggggacct	180
ttgtcttctg tgtaaatggt actagagaaa acacctatnt tatgagtcaa tctagttngt	240
tttattcgac atgaaggaaa tttccagatn acaacactna caaactctcc cttgactagg	300
ggggacaaaag aaaagcnaaa ctgaacatna gaaacaattn cctgggtgaga aattncataa	360
acagaaattg ggtngtatat tgaaanannng catcattnaa acgttttttt ttt	413

&lt;210&gt; 88

&lt;211&gt; 448

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(448)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 88

cgcagcgggt cctctctatc tagctccagc ctctcgctg ccccaactccc cgcgtcccgc	60
gtcctagccn accatggccg ggcccctgcg cgccccgctg ctctgtctgg ccctcctggc	120
cgtggccctg gccgtgagcc ccgcggcccg ctccagtcgc ggcaagccgc cgcgcctggt	180
gggaggccca tggaccccg gtggaagaag aaggtgtgcg gcgtgcactg gactttgcgc	240
tcggenanta caacaaaccc gcaacnactt ttaccnagen cgcgtgcag gttgtgccgc	300
cccaancaaa ttgttactng gggtaantaa ttcttggaag ttgaacctgg gccaaacnng	360
tttaccagaa ccnagccaat tngaacaatt ncccctccat aacagcccct tttaaaaagg	420
gaancantcc tgntcttttc caaat	448

&lt;210&gt; 89

&lt;211&gt; 463

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(463)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 89

gaatthttgtg cactggccac tgtgatggaa ccattgggcc aggatgcttt gagtttatca	60
gtagtgattc tgccaaagtt ggtgttgtaa catgagtatg taaaatgtca aaaaattagc	120
agaggtctag gtctgcatat cagcagacag tttgtccgtg tattttgtag ccttgaagtt	180
ctcagtgaac agttntttct gatgcgaagt tctnatcca gtgttttagt cctttgcac	240
tttnatgtn agacttgct ctntnaaatt gctttgtnt tctgcaggta ctatctgtgg	300
tttaacaaaa tagaannact tctctgcttn gaanatttga atatcttaca tctnaaaatn	360
aattctctcc ccatannaaa acccangccc ttggganaat ttgaaaaang gntccttcnn	420
aattcnnana anttcagtn tcatacaaca naacngganc ccc	463

&lt;210&gt; 90

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(400)

<223> n = A,T,C or G

<400> 90

agggattgaa	gggtctntnt	actgtcggac	tgttcancca	ccaactctac	aagttgctgt	60
cttccactca	ctgtctgtaa	gcntnttaac	ccagactgta	tcttcataaa	tagaacaaat	120
tcttcaccag	tcacatcttc	taggaecttt	ttggattcag	ttagtataag	ctcttcact	180
tcctttgtta	agacttcctc	tggtaaagtc	ttaagttttg	tagaaaggaa	tttaattgct	240
cgttctctaa	caatgtcctc	tccttgaagt	atttggtgta	acaaccacc	tnaagtcct	300
ttgtgcatcc	attttaaata	tacttaatag	ggcattggtg	cactagggtta	aattctgcaa	360
gagtcctctg	tctgcaaaag	ttgcgttagt	atatctgcca			400

<210> 91

<211> 480

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(480)

<223> n = A,T,C or G

<400> 91

gagctoggat	ccaataatct	ttgtctgagg	gcagcacaca	tatncagtgc	catggnaact	60
gggtctacccc	acatgggagc	agcatgccgt	agntatataa	ggtcattccc	tgagtcagac	120
atgcctcttt	gactaccgtg	tgccagtgtc	gggtattctc	acacacctcc	nnccgctctt	180
tgtggaaaaa	ctggcacttg	nttggaacta	gcaagacatc	acttaciaat	tcaccacga	240
gacacttgaa	aggtgtaaca	aagcgactct	tgcattgctt	tttgtccctc	cggcaccagt	300
tgtcaataact	aaccgctgg	tttgcctcca	tcacatttgt	gatctgtagc	tctggatata	360
tctctgaca	gtactgaaga	acttcttctt	ttgtttcaaa	agcaactctt	ggtgcctgtt	420
ngatcagggt	cccatctccc	agtcggaatg	ttcacatggc	atatnttact	tcccacaaaa	480

<210> 92

<211> 477

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(477)

<223> n = A,T,C or G

<400> 92

atacagccca	natcccacca	cgaagatgcg	cttggtgact	gagaacctga	tgcggtcact	60
gggtcccgtg	tagccccagc	gactctccac	ctgctggaag	cggttgatgc	tgactcctt	120
cccacgcagg	cagcagcggg	gccggtcaat	gaactccact	cgtggcttgg	ggttgacggg	180
taantgcagg	aagaggctga	ccacctcgcg	gtccaccagg	atgcccgact	gtgcgggacc	240
tgcagcga	ctctcgatg	gtcatgagcg	ggaagcgaat	gangcccagg	gccttgccca	300
gaaccttccg	cctgttctct	ggcgctcaact	gcagctgctg	ccgctnacac	tcggcctcgg	360
accagcggac	aaacggcggt	gaacagccgc	acctcaaggga	tgcccantgt	gtcgcgctcc	420
aggaacggcn	ccagcgtgtc	caggtcaatg	tcggtgaanc	ctccgcgggt	aatggcg	477

<210> 93

<211> 377

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

&lt;222&gt; (1)...(377)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 93

gaacggctgg	accttgccctc	gcattgtgct	gctggcagga	ataccttggc	aagcagctcc	60
agtccgagca	gccccagacc	gctgccgccc	gaagctaagc	ctgcctctgg	ccttcccctc	120
cgctcaatg	cagaaccant	agtgggagca	ctgtgtttag	agttaagagt	gaacactgtn	180
tgattttact	tggaattttc	ctctgttata	tagcttttcc	caatgctaata	ttccaaacaa	240
caacaacaaa	ataacatggt	tgctgtttna	gttgataaaa	agtangtgat	tctgtatnta	300
aagaaaatat	tactgttaca	tatactgctt	gcaanttctg	tatttattgg	tnctctggaa	360
ataaatatat	tattaaa					377

&lt;210&gt; 94

&lt;211&gt; 495

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(495)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 94

ccctttgagg	ggttagggtc	cagttcccag	tggaagaaac	agggcaggag	aantgcgtgc	60
cgagctgang	cagatttccc	acagtgaccc	cagagccctg	ggctatagtc	tctgaccctt	120
ccaaggaaag	accaccttct	ggggacatgg	gctggagggc	aggacctaga	ggcaccaagg	180
gaaggcccca	ttccggggct	gttcccagag	gaggaaggga	aggggctctg	tgtgccccc	240
acgaggaana	ggccttgant	cctgggatca	nacacccctt	cacgtgtatc	cccacacaaa	300
tgcaagctca	ccaaggtccc	ctctcagtc	cttccctaca	ccctgaacgg	ncaactggcc	360
acaccacccc	agancancca	cccgccatgg	ggaatgtnt	caaggaatcg	cngggcaacg	420
tggactctng	tccnnaagg	gggcagaatc	tccaatagan	gganngaacc	cttgctnana	480
aaaaaaaaana	aaaaa					495

&lt;210&gt; 95

&lt;211&gt; 472

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(472)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 95

ggttacttgg	tttcattgcc	accacttagt	ggatgtcatt	tagaaccatt	ttgtctgctc	60
cctctggaag	ccttgccgag	agcggacttt	gtaattgttg	gagaataact	gctgaatttt	120
tagctgtttt	gagttgattc	gcaccactgc	accacaactc	aatatgaaaa	ctatttnact	180
tatttattat	cttgtgaaaa	gtatacaatg	aaaattttgt	tcatactgta	tttatcaagt	240
atgatgaaaa	gcaatagata	tatattcttt	tattatgttn	aattatgatt	gccattatta	300
atcggcaaaa	tgtggagtg	atgttctttt	cacagtaata	tatgcctttt	gtaacttcac	360
ttggttattt	tattgtaaat	gaattacaaa	attcttaatt	taagaaaatg	gtangttata	420
tttanttcan	taatttcttt	ccttgttttac	gttaattttg	aaaagaatgc	at	472

&lt;210&gt; 96

&lt;211&gt; 476

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(476)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 96

ctgaagcatt	tottcaaact	tntctacttt	tgtcattgat	acctgtagta	agttgacaat	60
gtggtgaaat	ttcaaaatta	tatgtaactt	ctactagttt	tactttctcc	cccaagtctt	120
ttttaactca	tgattttttac	acacacaatc	cagaacttat	tatatagcct	ctaagtcttt	180
attcttcaca	gtagatgatg	aaagagtctt	ccagtgtctt	gngcanaatg	ttctagntat	240
agctggatac	atacngtggg	agttctataa	actcatacct	cagtggggact	naaccaaaaat	300
tgtgttagtc	tcaattccta	ccacactgag	ggagcctccc	aaatcactat	attcttatct	360
gcaggctactc	ctccagaaaa	acngacaggg	caggcttgca	tgaaaaagtn	acatctgcgt	420
tacaaagtct	atcttctctca	nangtctgtn	aaggaacaat	ttaatcttct	agcttt	476

&lt;210&gt; 97

&lt;211&gt; 479

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(479)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 97

actctttcta	atgctgatat	gatcttgagt	ataagaatgc	atatgtcact	agaatggata	60
aaataatgct	gcaaaacttaa	tgttcttatg	caaaatggaa	cgctaataa	acacagctta	120
caatcgcaaa	tcaaaactca	caagtgtctca	tctgtttag	atttagtgta	ataagactta	180
gattgtgctc	cttcggatat	gattgtttct	canatcttgg	gcaatnttcc	ttagtcaa	240
caggctacta	gaattctgtt	attggatatn	tgagagcatg	aaatttttta	naatacactt	300
gtgattatna	aattaatcac	aaatttcact	tatacctgct	atcagcagct	agaaaaacat	360
ntnnttttta	natcaaagta	ttttgtgttt	ggaantgttn	aatgaaatc	tgaatgtggg	420
ttcnatctta	ttttttcccn	gacnactant	tnctttttta	gggnctattc	tgancctc	479

&lt;210&gt; 98

&lt;211&gt; 461

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 98

agtgaattgt	cctccaacaa	aacccttga	tcaagtttgt	ggcactgaca	atcagaccta	60
tgctagtctc	tgtcatctat	tcgctactaa	atgcagactg	gaggggacca	aaaaggggca	120
tcaactccag	ctggattatt	ttggagcctg	caaatctatt	cctacttgta	cggactttga	180
agtgattcag	tttcctctac	ggatgagaga	ctggctcaag	aatatcctca	tcagacttta	240
tgaagccact	ctgaacacgc	tggttatcta	gatgagaaca	gagaaataaa	gtcagaaaat	300
ttacctggag	aaaagaggct	ttggctgggg	accatcccat	tgaaccttct	cttaaggact	360
ttaagaaaaa	ctaccacatg	ttgtgtatcc	tggtgccggc	cgtttatgaa	ctgaccaccc	420
tttgaataaa	tcttgacgct	cctgaacttg	ctcctctgcg	a		461

&lt;210&gt; 99

&lt;211&gt; 171

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 99

gtggccgcgc	gcagggtgttt	cctcgtaaccg	cagggccccc	tccttcccc	aggcgccct	60
cggcgccctct	gcgggcccga	ggaggagcgg	ctggcgggtg	gggggagtg	gaccacccct	120



cggtgagaaa agccttctct agcgatctga gaggcgtgcc ttgggggtac c 171

<210> 100  
 <211> 269  
 <212> DNA  
 <213> Homo sapien

<400> 100  
 cgggcgcaag tgcaactcca gctggggccg tgcggacgaa gattctgcca gcagttggtc 60  
 cgactgcgac gacggcggcg gcgacagtcg caggtgcagc gcgggcgcct ggggtcttgc 120  
 aaggctgagc tgacgccgca gaggtcgtgt cacgtcccac gaccttgacg ccgtcgggga 180  
 cagccggaac agagcccggg gaagcgggag gcctcgggga gcccctcggg aagggcggcc 240  
 cgagagatac gcaggtgcag gtggccgcc 269

<210> 101  
 <211> 405  
 <212> DNA  
 <213> Homo sapien

<400> 101  
 tttttttttt ttttggatc tactgcgagc acagcaggtc agcaacaagt ttattttgca 60  
 gctagcaagg taacagggta gggcatggtt acatgttcag gtcaacttcc ttgtcgtgg 120  
 ttgattgggt tgtctttatg ggggcggggt ggggtagggg aaacgaagca aataacatgg 180  
 agtgggtgca ccctccctgt agaacctggt tacaagctt ggggcagttc acctggtctg 240  
 tgaccgtcat tttcttgaca tcaatgttat tagaagtcag gatattcttt agagagtcca 300  
 ctgttctgga gggagattag ggtttcttgc caaatccaac aaaatccact gaaaaagttg 360  
 gatgatcagt acgaataccg aggcattatc tcatatcggt ggcca 405

<210> 102  
 <211> 470  
 <212> DNA  
 <213> Homo sapien

<400> 102  
 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60  
 ggcacttaat ccatttttat ttcaaaatgt ctacaaattt aatccatta tacggtattt 120  
 tcaaaatcta aattattcaa attagccaaa tccttaccaa ataataccca aaaatcaaaa 180  
 atatacttct ttacgcaaac ttgttacata aattaaata atatatacgg ctggtgtttt 240  
 caaagtacaa ttatcttaac actgcaaaaca ttttaaggaa ctaaaataaa aaaaaact 300  
 ccgcaaaagt taaaggggaa aacaaattct ttacaacac cattataaaa atcatatctc 360  
 aaatcttagg ggaatatata cttcacacgg gatcttaact tttactcact ttgtttattt 420  
 ttttaaacca ttgtttgggc ccaacacaat ggaatcccc ctggactagt 470

<210> 103  
 <211> 581  
 <212> DNA  
 <213> Homo sapien

<400> 103  
 tttttttttt ttttttttga cccccctctt ataaaaaaca agttaccatt ttattttact 60  
 tacacatatt tattttataa ttggtattag atattcaaaa ggcagctttt aaaatcaaac 120  
 taaatggaaa ctgccttaga tacataattc ttaggaatta gcttaaaatc tgcctaaagt 180  
 gaaaatcttc tctagctctt ttgactgtaa atttttgact cttgtaaaac atccaaattc 240  
 atttttcttg tcttttaaaat tatctaattc ttccattttt tccctattcc aagtcatttt 300  
 gcttctctag cctcatttcc tagctcttat ctactattag taagtggctt ttttctaaa 360  
 agggaaaaca ggaagagaaa tggcacacaa aacaaacatt ttatattcat atttctacct 420  
 acgttaataa aatagcattt tgtgaagcca gctcaaaaaga aggcttagat ccttttatgt 480  
 ccatttttagt cactaaacga tatcaaagtg ccagaatgca aaagggtttg gaacatttat 540

tcaaaagcta atataagata tttcacatac tcatctttct g

581

<210> 104  
 <211> 578  
 <212> DNA  
 <213> Homo sapien

<400> 104  
 tttttttttt tttttttttt tttttctctt cttttttttt gaaatgagga tcgagttttt 60  
 cactctctag atagggcatg aagaaaactc atctttccag ctttaaaata acaatcaaat 120  
 ctcttatgct atatcatatt ttaagttaaa ctaatgagtc actggcttat cttctcctga 180  
 aggaaatctg ttcattcttc tcattcatat agttatatca agtactacct tgcattattga 240  
 gaggtttttc ttctctattt acacatatat ttccatgtga atttgtatca aacctttatt 300  
 ttcatgcaaa ctagaaaata atgtttcttt tgcataagag aagagaacaa tatagcatta 360  
 caaaactgct caaattgttt gtttaagttat ccattataat tagttggcag gagctaatac 420  
 aaatcacatt tacgacagca ataataaaac tgaagtacca gttaaatatc caaataatt 480  
 aaaggaacat ttttagcctg ggtataatta gctaattcac tttacaagca tttattagaa 540  
 tgaattcaca tgttattatt cctagcccaa cacaatgg 578

<210> 105  
 <211> 538  
 <212> DNA  
 <213> Homo sapien

<400> 105  
 tttttttttt tttttcagta ataatacagaa caatatattt ttttatattt aaaattcata 60  
 gaaaagtgcc ttacatttaa taaaagtttg tttctcaaaag tgatcagagg aattagatat 120  
 gtcttgaaca ccaatattaa tttgaggaaa atacacacaaa atacattaag taaattattt 180  
 aagatcatag agcttgtaag tgaaaagata aaatttgacc tcagaaaactc tgagcattaa 240  
 aaatccacta ttagcaata aattactatg gacttcttgc ttttaattttg tgatgaatat 300  
 ggggtgtcac tggtaaacca acacattctg aaggatacat tacttagtga tagattctta 360  
 tgtactttgc taatacgttg atatgagttg acaagtttct ctttcttcaa tcttttaagg 420  
 ggcgagaaat gaggaagaaa agaaaaggat tacgcatact gttctttcta tggaaggatt 480  
 agatatgttt cctttgccaa tattaataaaa ataataatgt ttactactag tgaaaccc 538

<210> 106  
 <211> 473  
 <212> DNA  
 <213> Homo sapien

<400> 106  
 tttttttttt ttttttagtc aagtttctat ttttattata attaaagtct tggtcatttc 60  
 atttatttagc tctgcaactt acatatttaa attaaagaaa cgttttagac aactgtacaa 120  
 tttataaatg taaggtgcca ttattgagta atatatctct ccaagagtgg atgtgtccct 180  
 tctccacca actaatgaac agcaacatta gtttaatttt attagtagat atacactgct 240  
 gcaaacgcta attctcttct ccattcccat gtgatattgt gtatatgtgt gagttggtag 300  
 aatgcatcac aatctacaat caacagcaag atgaagctag gctgggcttt cggtgaaaat 360  
 agactgtgtc tgtctgaatc aaatgatctg acctatctc ggtggcaaga actcttcgaa 420  
 ccgcttctc aaaggcgtg ccacatttgt ggctctttgc acttgtttca aaa 473

<210> 107  
 <211> 1621  
 <212> DNA  
 <213> Homo sapien

<400> 107  
 cgccatggca ctgcagggca tctcggtcat ggagctgtcc ggctgggcc cgggcccggt 60  
 ctgtgctatg gtcctggctg acttcggggc gcgtgtggta cgctgggacc ggcccggtc 120

```

ccgctacgac gtgagccgct tgggccgggg caagcgctcg ctagtgctgg acctgaagca 180
gccgcgggga gccgccgtgc tgcggcgctct gtgcaagcgg tcggatgtgc tgctggagcc 240
cttccgccgc ggtgtcatgg agaaactcca gctgggcccc gagattctgc agcgggaaaa 300
tccaaggcgtt atttatgcca ggctgagtgg atttgccag tcaggaagct tctgccggtt 360
agctggccac gatatacaact atttggtttt gtcaggtgtt ctctcaaaaa ttggcagaag 420
tggtgagaat ccgtatgccc cgctgaatct cctggctgac tttgctgggtg gtggccttat 480
gtgtgcactg ggcattataa tggctctttt tgaccgcaca cgcactgaca agggtcaggt 540
cattgatgca aatatggtgg aaggaacagc atatttaagt tcttttctgt ggaaaactca 600
gaaatcgagt ctgtgggaag cacctcgagg acagaacatg ttggatgggtg gagcaccttt 660
ctatacgact tacaggacag cagatgggga attcatggct gttggagcaa tagaacccca 720
gttctacgag ctgctgatca aaggacttgg actaaagtct gatgaacttc ccaatcagat 780
gagcatggat gattggccag aaatgaagaa gaagtttgca gatgtatttg caaagaagac 840
gaaggcagag tgggtgtcaaa tctttgacgg cacagatgcc tgtgtgactc cggttctgac 900
ttttgaggag gttgttcatac atgatcacia caaggaacgg ggctcgttta tcaccagtga 960
ggagcaggac gtgagccccc gccctgcacc tctgctgtta aacaccccag ccatcccttc 1020
tttcaaaagg gatcctttca taggagaaca cactgaggag atacttgaag aatttggatt 1080
cagccgcgaa gagatttatc agcttaactc agataaaatc attgaaagta ataaggtaaa 1140
agctagtctc taacttccag gccacggct caagtgaatt tgaatactgc atttacagt 1200
tagagtaaca cataacattg tatgcatgga aacatggagg aacagtatta cagtgtccta 1260
ccactctaata caagaaaaga attacagact ctgattctac agtgatgatt gaattctaaa 1320
aatggtttatc attagggctt ttgatttata aaactttggg tacttatact aaattatggt 1380
agttattctg ccttccagtt tgcttgatat atttgttgat attaagattc ttgacttata 1440
ttttgaatgg gttctagtga aaaaggaatg atatatctt gaagacatcg atatacattt 1500
atttacactc ttgattctac aatgtagaaa atgaggaaat gccacaaatt gtatgggtgat 1560
aaaagtcacg tgaacaacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1620
a

```

```

<210> 108
<211> 382
<212> PRT
<213> Homo sapien

```

```

<400> 108
Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
1 5 10 15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
20 25 30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35 40 45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50 55 60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65 70 75 80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85 90 95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100 105 110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115 120 125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130 135 140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
145 150 155 160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165 170 175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180 185 190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg

```

195	200	205
Gly Gln Asn Met Leu Asp	Gly Gly Ala Pro Phe	Tyr Thr Thr Tyr Arg
210	215	220
Thr Ala Asp Gly Glu Phe	Met Ala Val Gly Ala	Ile Glu Pro Gln Phe
225	230	235
Tyr Glu Leu Leu Ile Lys	Gly Leu Gly Leu Lys	Ser Asp Glu Leu Pro
245	250	255
Asn Gln Met Ser Met Asp	Asp Trp Pro Glu Met	Lys Lys Lys Phe Ala
260	265	270
Asp Val Phe Ala Lys Lys	Thr Lys Ala Glu Trp	Cys Gln Ile Phe Asp
275	280	285
Gly Thr Asp Ala Cys Val	Thr Pro Val Leu Thr	Phe Glu Glu Val Val
290	295	300
His His Asp His Asn Lys	Glu Arg Gly Ser Phe	Ile Thr Ser Glu Glu
305	310	315
Gln Asp Val Ser Pro Arg	Pro Ala Pro Leu Leu	Leu Asn Thr Pro Ala
325	330	335
Ile Pro Ser Phe Lys Arg	Asp Pro Phe Ile Gly	Glu His Thr Glu Glu
340	345	350
Ile Leu Glu Glu Phe Gly	Phe Ser Arg Glu Glu	Ile Tyr Gln Leu Asn
355	360	365
Ser Asp Lys Ile Ile Glu	Ser Asn Lys Val Lys	Ala Ser Leu
370	375	380

<210> 109  
 <211> 1524  
 <212> DNA  
 <213> Homo sapien

<400> 109

ggcagcaggc	tgcgccaggc	cctgagcgga	ggcgggggca	gcctcgccag	cgggggcccc	60
gggcctggcc	atgcctcact	gagccagcgc	ctgcgcctct	acctcgccga	cagctggaac	120
cagtgcgacc	tagtggtctt	cacctgcttc	ctcctgggcg	tgggctgccg	gctgaccccg	180
ggtttgtagc	acctggggcg	caactgtctc	tgcctcgact	tcattggttt	cacgggtgcg	240
ctgcttcaca	tcttcacggg	caacaaacag	ctggggccca	agatcgctcat	cgtgagcaag	300
atgatgaagg	acgtgttctt	cttctctctt	ttcctcgggc	tgtggctggg	agcctatggc	360
gtggccacgg	aggggctcct	gaggccacgg	gacagtgaat	tcccaagtat	cctgcgcgcg	420
gtcttctacc	gtccctacct	gcagatcttc	gggcagattc	cccaggagga	catggacgtg	480
gacctcatgg	agcacagcaa	ctgctcgctg	gagcccggtt	tctgggcaca	ccctcctggg	540
gccagggcgg	gcacctgcgt	ctcccagtat	gccaactggc	tgggtggtgt	gctcctcgtc	600
atcttctctg	tcgtggccaa	catectgctg	gtcaacttgc	tcattgccat	gttcagttac	660
acattcgcca	aagtacaggc	caacagcgat	ctctactgga	aggcgcagcg	ttaccgcctc	720
atccgggaat	tccactctcg	gcccgcgctg	gccccgccct	ttatcgctcat	ctcccacttg	780
cgcctcctgc	tcaggcaatt	gtgcaggcga	ccccggagcc	cccagccgtc	ctccccggcc	840
ctcgagcatt	tccgggttta	cctttctaag	gaagccgagc	ggaagctgct	aacgtgggaa	900
tgggtgcata	aggagaactt	tctgctggca	cgcgctaggg	acaagcggga	gagcgactcc	960
gagcgtctga	agcgacagtc	ccagaagggt	gacttggcac	tgaacagct	gggacacatc	1020
cgcgagtacg	aacagcgcc	gaaagtgtgt	gagcgggagg	tccagcagtg	tagccgcgtc	1080
ctgggggtgg	tggccgaggc	cctgagccgc	tctgccttgc	tgcccccagg	tgggcccgcc	1140
ccccctgacc	tgcctgggtc	caaagactga	gcccgtgtgg	cggacttcaa	ggagaagccc	1200
ccacagggga	ttttgtctct	agagtaaggc	tcattctggc	ctcgcccccc	gcacctggtg	1260
gccttgctct	tgaggtgagc	cccatgtcca	tctggggccac	tgtcaggacc	acctttggga	1320
gtgtcatctt	tacaaaccac	agcatgccc	gctcctccca	gaaccagtc	cagcctggga	1380
ggatcaaggc	ctggatcccc	ggccgttatc	catctggagg	ctgcagggtc	cttggggtaa	1440
cagggaccac	agacccctca	ccactcacag	attcctcaca	ctgggggaaat	aaagccattt	1500
cagaggaaaa	aaaaaaaaaa	aaaa				1524

<210> 110

<211> 3410  
 <212> DNA  
 <213> Homo sapien

<400> 110

gggaaccagc	ctgcacgcgc	tggctccggg	tgacagccgc	gcgcctcggc	caggatctga	60
gtgatgagac	gtgtccccac	tgaggtgccc	cacagcagca	ggtgttgagc	atgggctgag	120
aagctggacc	ggcaccaaag	ggctggcaga	aatgggcgcc	tggtgattc	ctaggcagtt	180
ggcggcagca	aggaggagag	gccgcagctt	ctggagcaga	gccgagacga	agcagttctg	240
gagtgcctga	acggccccct	gagccctacc	cgcttgcccc	actatggtcc	agaggctgtg	300
ggtgagccgc	ctgctgcggc	accggaaagc	ccagctcttg	ctggtcaacc	tgctaaccct	360
tggcctggag	gtgtgttttg	ccgcaggcat	cacctatgtg	ccgcctctgc	tgctggaagt	420
gggggtagag	gagaagttca	tgaccatggt	gctgggcatt	ggtccagtgc	tgggcctggt	480
ctgtgtcccc	ctcctaggct	cagccagtga	ccactggcgt	ggacgctatg	gccgccgcgc	540
gcccttcacg	tgggcaactg	ccttgggcag	cctgctgagc	ctctttctca	tcccaagggc	600
cggctggcta	gcagggctgc	tgtgcccggg	tcccaggccc	ctggagctgg	cactgctcat	660
cctgggcgtg	gggctgctgg	acttctgttg	ccaggtgtgc	ttcactccac	tggaggccct	720
gctctctgac	ctcttcgggg	acccggacca	ctgtcgccag	gcctactctg	tctatgcctt	780
catgatcagt	cttgggggct	gcctgggcta	cctcctgcct	gccattgact	gggacaccag	840
tgccctggcc	ccctacctgg	gcacccagga	ggagtgcctc	tttggcctgc	tcaccctcat	900
cttcctcacc	tgcgtagcag	ccacactgct	ggtggctgag	gaggcagcgc	tgggccccac	960
cgagccagca	gaagggtgtg	cggccccctc	cttgtcgccc	cactgctgtc	catgccgggc	1020
ccgcttggtc	ttccggaacc	tgggcgcctc	gcttccccgg	ctgcaccagc	tgtgctgccc	1080
catgccccgc	accctgcgcc	ggctcttcgt	ggctgagctg	tgacagctga	tggcactcat	1140
gaccttcacg	ctgtttttaca	cggatttcgt	gggcgagggg	ctgtaccagg	gcgtgccag	1200
agctgagccg	ggcaccgagg	cccggagaca	ctatgatgaa	ggcgttcgga	tgggcagcct	1260
ggggctgttc	ctgcagtgcg	ccatctccct	ggtcttctct	ctggctcatg	accggctggt	1320
gcagcgatcc	ggcactcgag	cagtctatct	ggccagtgtg	gcagctttcc	ctgtggctgc	1380
cgggtgccaca	tgcctgtccc	acagtgtggc	cgtgggtgaca	gcttcagccg	ccctcaccgg	1440
gttcacacctc	tcagccctgc	agatcctgcc	ctacacactg	gcctccctct	accaccggga	1500
gaagcagggtg	ttcctgcccc	aataccgagg	ggacactgga	ggtgctagca	gtgaggacag	1560
cctgatgacc	agcttcctgc	caggccctaa	gcctggagct	ccctcccta	atggacacgt	1620
gggtgctgga	ggcagtggcc	tgtctcccac	tccacccgcg	ctctgcgggg	cctctgcctg	1680
tgatgtctcc	gtacgtgtgg	tgggtgggtga	gccccaccag	gccagggtgg	ttccggggccg	1740
gggcatctgc	ctggacctcg	ccatcctgga	tagtgccctc	ctgctgtccc	aggtggcccc	1800
atccctgttt	atgggctcca	ttgtccagct	cagccagtct	gtcactgcct	atatggtgtc	1860
tgccgcaggc	ctgggtctgg	tcgccattta	ctttgttaca	caggtagtat	ttgacaagag	1920
cgacttggcc	aaatactcag	cgtagaaaac	ttccagcaca	ttgggggtgga	gggcctgcct	1980
cactgggtcc	cagctccccg	ctcctgttag	ccccatgggg	ctgccggggt	ggccgccagt	2040
ttctgttgct	gccaagtaaa	tgtggctctc	tgtgccacc	ctgtgctgct	gaggtgcgta	2100
gctgcacagc	tgggggctgg	ggcgtccctc	tctctctccc	ccagtctcta	gggctgcctg	2160
actggaggcc	ttccaagggg	gtttcagctc	ggacttatac	agggaggcca	gaagggtccc	2220
atgcactgga	atgcggggac	tctgcagggt	gattacccag	gctcagggtt	aacagctagc	2280
ctcctagtgt	agacacacct	agagaagggt	ttttgggagc	tgaataaact	cagtcacctg	2340
gtttcccatc	tctaagcccc	ttaacctgca	gcttcgttta	atgtagctct	tgcatgggag	2400
tttctaggat	gaaacactcc	tccatgggat	ttgaacatat	gacttatttg	taggggaaga	2460
gtcctgaggg	gcaacacaca	agaaccaggt	cccctcagcc	cacagcactg	tctttttgct	2520
gatccacccc	cctcttacct	tttatcagga	tgtggcctgt	tggtccttct	gttgccatca	2580
cagagacaca	ggcatttaaa	tatttaactt	atttatttaa	caaagtagaa	gggaatocat	2640
tgctagcttt	tctgtgttgg	tgtctaatat	ttgggtaggg	tgggggatcc	ccaacaatca	2700
ggtcccttga	gatagctggt	cattgggctg	atcattgccg	gaatcttctt	ctcctggggt	2760
ctggccccc	aaaatgccta	acccaggacc	ttggaaattc	tactcatccc	aaatgataat	2820
tccaaatgct	gttaccceaag	gttaggggtg	tgaagggaag	tagagggtgg	ggcttcagggt	2880
ctcaacggct	tccctaacca	cccctcttct	cttggcccag	cctgggtccc	cccacttcca	2940
ctccctctca	ctctctctag	gactgggctg	atgaaggcac	tgcccaaaat	ttcccttacc	3000
cccaactttc	ccctaccccc	aactttcccc	accagctcca	caaccctgtt	tggagctact	3060
gcaggaccag	aagcaciaag	tgcggtttcc	caagcctttg	tccatctcag	ccccagaggt	3120
atatctgtgc	ttggggaatc	tcacacagaa	actcaggagc	acccctgccc	tgagctaagg	3180

gaggtcttat	ctctcagggg	gggtttaagt	gccgtttgca	ataatgtcgt	cttattttatt	3240
tagcggggtg	aatattttat	actgtaagt	agcaatcaga	gtataatgtt	tatggtgaca	3300
aaattaaagg	ctttcttata	tgtttaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	3360
aaaaaaaaara	aaaaaaaaaa	aaaaaaaaaa	aaaaaaataa	aaaaaaaaaa		3410

<210> 111  
 <211> 1289  
 <212> DNA  
 <213> Homo sapien

<400> 111

agccaggcgt	ccctctgcct	gccactcag	tggcaacacc	cgggagctgt	tttgtccttt	60
gtggagcctc	agcagttccc	tctttcagaa	ctcactgcca	agagccctga	acaggagcca	120
ccatgcagtg	cttcagcttc	attaagacca	tgatgatcct	cttcaatttg	ctcatctttc	180
tgtgtggtgc	agccctggtg	gcagtgggca	tctgggtgtc	aatcgatggg	gcaccccttc	240
tgaagatcct	cgggccactg	tcgtccagtg	ccatgcagtt	tgtcaacgtg	ggctacttcc	300
tcatcgcagc	cggcgttgtg	gtctttgtct	ttggtttcct	gggctgctat	ggtgctaaga	360
ctgagagcaa	gtgtgccctc	gtgacgttct	tcttcaccc	cctcctcatc	ttcattgctg	420
aggttgacgc	tgctgtggtc	gccttggtgt	acaccacaat	ggctgagcac	ttcctgacgt	480
tgctggtagt	gcctgccatc	aagaaagatt	atggttccca	ggaagacttc	actcaagtgt	540
ggaacaccac	catgaaaggg	ctcaagtgt	gtggcttcac	caactatacg	gattttgagg	600
actcacccta	cttcaaagag	aacagtgcct	ttccccatt	ctgttgcaat	gacaacgtca	660
ccaacacagc	caatgaaacc	tgcaccaagc	aaaaggctca	cgaccaaaaa	gtagagggtt	720
gcttcaatca	gcttttgtat	gacatccgaa	ctaattgcagt	caccgtgggt	ggtgtggcag	780
ctggaattgg	gggcctcgag	ctggctgcca	tgattgtgtc	catgtatctg	tactgcaatc	840
tacaataagt	ccacttctgc	ctctgccact	actgctgcca	catgggaact	gtgaagaggc	900
accctggcaa	gcagcagtg	ttgggggagg	ggacaggatc	taacaatgtc	acttgggcca	960
gaatggacct	gccctttctg	ctccagactt	ggggctagat	agggaccact	ccttttagcg	1020
atgcctgact	ttccttccat	tggtgggtgg	atgggtgggg	ggcattccag	agcctctaag	1080
gtagccagtt	ctgttgccca	ttccccagt	ctattaaacc	cttgatatgc	cccctaggcc	1140
tagtggtgat	cccagtgctc	tactggggga	tgagagaaa	gcattttata	gcctgggcat	1200
aagtgaaatc	agcagagcct	ctgggtggat	gtgtagaagg	cacttcaaaa	tgcataaacc	1260
tgttacaatg	ttaaaaaaaa	aaaaaaaaaa				1289

<210> 112  
 <211> 315  
 <212> PRT  
 <213> Homo sapien

<400> 112

Met	Val	Phe	Thr	Val	Arg	Leu	Leu	His	Ile	Phe	Thr	Val	Asn	Lys	Gln
1				5					10					15	
Leu	Gly	Pro	Lys	Ile	Val	Ile	Val	Ser	Lys	Met	Met	Lys	Asp	Val	Phe
			20					25					30		
Phe	Phe	Leu	Phe	Phe	Leu	Gly	Val	Trp	Leu	Val	Ala	Tyr	Gly	Val	Ala
			35				40					45			
Thr	Glu	Gly	Leu	Leu	Arg	Pro	Arg	Asp	Ser	Asp	Phe	Pro	Ser	Ile	Leu
			50				55				60				
Arg	Arg	Val	Phe	Tyr	Arg	Pro	Tyr	Leu	Gln	Ile	Phe	Gly	Gln	Ile	Pro
							70			75				80	
Gln	Glu	Asp	Met	Asp	Val	Ala	Leu	Met	Glu	His	Ser	Asn	Cys	Ser	Ser
				85					90					95	
Glu	Pro	Gly	Phe	Trp	Ala	His	Pro	Pro	Gly	Ala	Gln	Ala	Gly	Thr	Cys
			100					105					110		
Val	Ser	Gln	Tyr	Ala	Asn	Trp	Leu	Val	Val	Leu	Leu	Leu	Val	Ile	Phe
			115				120					125			
Leu	Leu	Val	Ala	Asn	Ile	Leu	Leu	Val	Asn	Leu	Leu	Ile	Ala	Met	Phe
			130				135					140			

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys  
 145 150 155 160  
 Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu  
 165 170 175  
 Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln  
 180 185 190  
 Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu  
 195 200 205  
 His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr  
 210 215 220  
 Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp  
 225 230 235 240  
 Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val  
 245 250 255  
 Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg  
 260 265 270  
 Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly  
 275 280 285  
 Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly  
 290 295 300  
 Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp  
 305 310 315

<210> 113  
 <211> 553  
 <212> PRT  
 <213> Homo sapien

<400> 113  
 Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala  
 1 5 10 15  
 Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu  
 20 25 30  
 Ala Ala Gly Ile Thr Tyr Val Pro Leu Leu Leu Glu Val Gly Val  
 35 40 45  
 Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly  
 50 55 60  
 Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly  
 65 70 75 80  
 Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile  
 85 90 95  
 Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu  
 100 105 110  
 Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly  
 115 120 125  
 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu  
 130 135 140  
 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala  
 145 150 155 160  
 Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr  
 165 170 175  
 Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu  
 180 185 190  
 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu  
 195 200 205  
 Thr Cys Val Ala Ala Thr Leu Val Ala Glu Glu Ala Ala Leu Gly  
 210 215 220  
 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His

225                                      230                                      235                                      240  
 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu  
    245                                      250                                      255  
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg  
    260                                      265                                      270  
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe  
    275                                      280                                      285  
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val  
    290                                      295                                      300  
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
 305                                      310                                      315                                      320  
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu  
    325                                      330                                      335  
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg  
    340                                      345                                      350  
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Gly Ala  
    355                                      360                                      365  
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu  
    370                                      375                                      380  
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala  
 385                                      390                                      395                                      400  
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly  
    405                                      410                                      415  
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu  
    420                                      425                                      430  
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala  
    435                                      440                                      445  
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser  
    450                                      455                                      460  
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala  
 465                                      470                                      475                                      480  
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp  
    485                                      490                                      495  
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser  
    500                                      505                                      510  
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala  
    515                                      520                                      525  
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp  
    530                                      535                                      540  
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
 545                                      550

<210> 114  
 <211> 241  
 <212> PRT  
 <213> Homo sapien

<400> 114  
 Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu  
 1                                      5                                      10                                      15  
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val  
    20                                      25                                      30  
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser  
    35                                      40                                      45  
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly  
    50                                      55                                      60  
 Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr  
 65                                      70                                      75                                      80



Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile  
                   85                  90                  95  
 Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr  
                   100                  105                  110  
 Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys  
                   115                  120                  125  
 Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met  
                   130                  135                  140  
 Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp  
                   145                  150                  155                  160  
 Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn  
                   165                  170                  175  
 Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala  
                   180                  185                  190  
 His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile  
                   195                  200                  205  
 Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly  
                   210                  215                  220  
 Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu  
                   225                  230                  235                  240  
 Gln

<210> 115  
 <211> 366  
 <212> DNA  
 <213> Homo sapien

<400> 115  
 gctctttctc tcccctcctc tgaatttaat tctttcaact tgcaatttgc aaggattaca 60  
 catttcactg tgatgtatat tgtgttgcaa aaaaaaaaaa gtgtctttgt ttaaaattac 120  
 ttggtttggt aatccatctt gctttttccc cattggaaact agtcattaac ccatctctga 180  
 actggtagaa aaacatctga agagctagtc tatcagcatc tgacagggtga attggatggt 240  
 tctcagaacc atttcaccca gacagcctgt ttctatcctg tttaataaat tagtttgggt 300  
 tctctacatg cataacaaac cctgctccaa tctgtcacat aaaagtctgt gacttgaagt 360  
 ttagtc 366

<210> 116  
 <211> 282  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(282)  
 <223> n = A,T,C or G

<400> 116  
 acaaagatga accatttcct atattatagc aaaattaaaa tctaccogta ttctaattatt 60  
 gagaaatgag atnaaacaca atnttataaa gtctacttag agaagatcaa gtgacctcaa 120  
 agactttact attttcatat ttaagacac atgatttatt ctatttttagt aacctgggtc 180  
 atacgttaaa caaaggataa tgtgaacagc agagaggatt tgttggcaga aaatctatgt 240  
 tcaatctnga actatctana tcacagacat ttctattcct tt 282

<210> 117  
 <211> 305  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(305)  
 <223> n = A,T,C or G

<400> 117  
 acacatgtcg cttcactgcc ttcttagatg cttctgggtca acatanagga acagggacca 60  
 tattttatcct ccctcctgaa acaattgcaa aataanacaa aatatatgaa acaattgcaa 120  
 aataaggcaa aatatatgaa acaacaggtc tcgagatatt ggaaatcagt caatgaagga 180  
 tactgatccc tgatcactgt cctaattgcag gatgtgggaa acagatgagg tcacctctgt 240  
 gactgcccc gcttactgcc tgtagagagt ttctangctg cagttcagac agggagaaat 300  
 tgggt 305

<210> 118  
 <211> 71  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(71)  
 <223> n = A,T,C or G

<400> 118  
 accaaggtgt ntgaatctct gacgtgggga tctctgattc ccgcacaatc tgagtggaaa 60  
 aantcctggg t 71

<210> 119  
 <211> 212  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(212)  
 <223> n = A,T,C or G

<400> 119  
 actccggttg gtgtcagcag cacgtggcat tgaacatngc aatgtggagc ccaaaccaca 60  
 gaaaatgggg tgaaattggc caactttcta tnaacttatg ttggcaantt tgccaccaac 120  
 agtaagctgg cccttctaataaaaagaaaat tgaaagggtt ctcactaanc ggaattaant 180  
 aatggantca aganactccc aggcctcagc gt 212

<210> 120  
 <211> 90  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(90)  
 <223> n = A,T,C or G

<400> 120  
 actcgttgca natcaggggc cccccagagt caccgttgca ggagtccttc tgggtottgcc 60  
 ctccgccggc gcagaacatg ctggggtgggt 90

<210> 121  
 <211> 218  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(218)  
 <223> n = A,T,C or G

<400> 121  
 tgtanogtga anacgacaga nagggttgtc aaaaatggag aanccttgaa gtcattttga 60  
 gaataagatt tgctaaaaga tttggggcta aaacatgggt attgggagac atttctgaag 120  
 atatncangt aaattangga atgaattcat ggttcttttg ggaattcctt tacgatngcc 180  
 agcatanact tcatgtgggg atancageta cccttgta 218

<210> 122  
 <211> 171  
 <212> DNA  
 <213> Homo sapien

<400> 122  
 taggggtgta tgcaactgta aggacaaaaa ttgagactca actggcttaa ccaataaagg 60  
 catttgtag ctcatggaac aggaagtcgg atgggtggggc atcttcagtg ctgcatgagt 120  
 caccaccccg gcggggtcat ctgtgccaca ggtccctgtt gacagtgcgg t 171

<210> 123  
 <211> 76  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(76)  
 <223> n = A,T,C or G

<400> 123  
 tgtagcgtga agacnacaga atgggtgtgtg ctgtgctatc caggaacaca tttattatca 60  
 ttatcaanta ttgtgt 76

<210> 124  
 <211> 131  
 <212> DNA  
 <213> Homo sapien

<400> 124  
 acctttcccc aaggccaatg tcctgtgtgc taactggccg gctgcaggac agctgcaatt 60  
 caatgtgctg ggtcatatgg aggggaggag actctaaaat agccaatttt atttctcttg 120  
 ttaagatttg t 131

<210> 125  
 <211> 432  
 <212> DNA  
 <213> Homo sapien

<400> 125  
 actttatcta ctggctatga aatagatggg ggaaaattgc gttaccaact ataccactgg 60  
 cttgaaaaag aggtgatage tcttcagagg acttgtgact tttgctcaga tgctgaagaa 120

```

ctacagtctg catttggcag aaatgaagat gaatttggat taaatgagga tgetgaagat      180
ttgcctcacc aaacaaaagt gaaacaactg agagaaaatt ttcaggaaaa aagacagtgg      240
ctcttgaagt atcagtcact tttgagaatg tttcttagtt actgcatact tcatggatcc      300
catggtgggg gtcttgcacg tgtaagaatg gaattgattt tgcttttgca agaattctcag      360
caggaaacat cagaaccact attttctagc cctctgtcag agcaaaccctc agtgcctctc      420
ctctttgctt gt                                         432

```

```

<210> 126
<211> 112
<212> DNA
<213> Homo sapien

```

```

<400> 126
acacaacttg aatagtaaaa tagaaactga gctgaaattt ctaattcact ttctaaccat      60
agtaagaatg atatttcccc ccagggatca ccaaataattt ataaaaattt gt          112

```

```

<210> 127
<211> 54
<212> DNA
<213> Homo sapien

```

```

<400> 127
accacgaaac cacaacaag atggaagcat caatccactt gccaaagcaca gcag          54

```

```

<210> 128
<211> 323
<212> DNA
<213> Homo sapien

```

```

<400> 128
acctcattag taattgtttt gttgtttcat ttttttctaa tgtctcccct ctaccagctc      60
acctgagata acagaatgaa aatggaagga cagccagatt tctcctttgc tctctgctca      120
ttctctctga agtctagggt acccattttg gggaccatt ataggcaata aacacagttc      180
ccaaagcatt tggacagttt cttgttgtgt tttagaatgg ttttcctttt tcttagcctt      240
ttcctgcaaa aggctcactc agtcccttgc ttgctcagtg gactgggctc cccagggcct      300
aggctgcctt cttttccatg tcc                                         323

```

```

<210> 129
<211> 192
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(192)
<223> n = A,T,C or G

```

```

<400> 129
acatacatgt gtgtatatatt ttaaataatca cttttgtatc actctgactt tttagcatat      60
tgaaaacaca ctaacataat ttntgtgaac catgatcaga tacaacccaa atcattcatc      120
tagcacattc atctgtgata naaagatagg tgagtttcat ttctttcacg ttggccaatg      180
gataaacaaa gt                                         192

```

```

<210> 130
<211> 362
<212> DNA
<213> Homo sapien

```

<220>  
 <221> misc\_feature  
 <222> (1)...(362)  
 <223> n = A,T,C or G

<400> 130  
 ccctttttta tggaatgagt agactgtatg tttgaanatt tanccacaac ctcttttgaca 60  
 tataatgacg caacaaaaag gtgctgttta gtcctatggg tcagtttatg cccctgacaa 120  
 gtttccattg tgttttgccg atcttctggc taatcgtggg atcctccatg ttattagtaa 180  
 ttctgtattc cattttgtta acgcctggta gatgtaacct gctangaggc taactttata 240  
 cttattttaa agctcttatt ttgtgggcat taaaatggca atttatgtgc agcactttat 300  
 tgcagcagga agcacgtgtg ggttgggttg aaagctcttt gctaattcta aaaagtaatg 360  
 gg 362

<210> 131  
 <211> 332  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(332)  
 <223> n = A,T,C or G

<400> 131  
 ctttttgaaa gatcgtgtcc actcctgtgg acatcttgtt ttaatggagt ttcccatgca 60  
 gtangactgg tatggttgca gctgtccaga taaaaacatt tgaagagctc caaaatgaga 120  
 gttctcccag gttcgccctg ctgctccaag tctcagcagc agcctctttt aggaggcatc 180  
 ttctgaacta gattaaggca gcttgtaaat ctgatgtgat ttggtttatt atccaactaa 240  
 cttccatctg ttatcactgg agaaagccca gactcccan gacnggtacg gattgtgggc 300  
 atanaaggat tgggtgaagc tggcggttggt gt 332

<210> 132  
 <211> 322  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(322)  
 <223> n = A,T,C or G

<400> 132  
 acttttgcca ttttgtatat ataaacaatc ttgggacatt ctctgaaaa ctaggtgtcc 60  
 agtggctaag agaactcgat ttcaagcaat tctgaaagga aaaccagcat gacacagaat 120  
 ctcaaattcc caaacagggg ctctgtggga aaaatgaggg aggacctttg tatctcgggt 180  
 tttagcaagt taaaatgaan atgacaggaa aggcttattt atcaacaaag agaagagttg 240  
 ggatgcttct aaaaaaaact ttggtagaga aaataggaat gctnaatcct aggaagcct 300  
 gtaacaatct acaattgggtc ca 322

<210> 133  
 <211> 278  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(278)

<223> n = A,T,C or G

<400> 133

acaagccttc acaagtttaa ctaaattggg attaatcttt ctgtanttat ctgcataatt	60
cttggttttc tttccatctg gtcctgggt tgacaatttg tggaacaac tctattgcta	120
ctatttaaaa aaaatcacia atctttccct ttaagctatg ttnaattcaa actattcctg	180
ctattcctgt tttgtcaaag aaattatatt tttcaaaata tgtntatttg tttgatgggt	240
cccacgaac actaataaaa accacagaga ccagcctg	278

<210> 134

<211> 121

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(121)

<223> n = A,T,C or G

<400> 134

gtttanaaaa cttgttttagc tccatagagg aaagaatggt aaactttgta ttttaaaaca	60
tgattctctg aggttaaact tggttttcaa atgttatatt tacttgtatt ttgcttttgg	120
t	121

<210> 135

<211> 350

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(350)

<223> n = A,T,C or G

<400> 135

acttanaacc atgcctagca catcagaatc cctcaaagaa catcagtata atcctataacc	60
atancaagtg gtgactggtt aagcgtgcga caaaggctcag ctggcacatt acttgtgtgc	120
aaacttgata cttttgttct aagtaggaac tagtatacag tncctaggan tggtagtcca	180
gggtgcccc caactcctgc agccgtcct ctgtgccagn ccctgnaagg aactttcgtc	240
ccacctcaat caagccctgg gccatgctac ctgcaattgg ctgaacaaac gtttgctgag	300
ttcccaagga tgcaaagcct ggtgctcaac tcctggggcg tcaactcagt	350

<210> 136

<211> 399

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(399)

<223> n = A,T,C or G

<400> 136

tgtaccgtga agacgacaga agttgcatgg cagggacagg gcagggccga ggccagggtt	60
gctgtgattg tatccgaata ntctcgtga gaaaagataa tgagatgacg tgagcagcct	120
gcagacttgt gtctgccttc aanaagccag acaggaaggc cctgcctgcc ttggctctga	180
cctggggggc agccagccag ccacaggtgg gcttcttct tttgttgtga caacnccaag	240
aaaactgcag agggccaggg tcaggtgtna gtgggtangt gaccataaaa caccaggtgc	300

tcccaggaac cggggcaaag gccatcccca cctacagcca gcatgcccac tggcgtgatg 360  
 ggtgcagang gatgaagcag ccagntgttc tgctgtggt 399

<210> 137  
 <211> 165  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(165)  
 <223> n = A,T,C or G

<400> 137  
 actggtgtgg tngggggtga tgctggtggt anaagttgan gtgacttcan gatggtgtgt 60  
 ggaggaagtg tgtgaacgta gggatgtaga ngttttggcc gtgctaaatg agcttcggga 120  
 ttggctggtc ccactggtgg tcactgtcat tgggtggggt cctgt 165

<210> 138  
 <211> 338  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(338)  
 <223> n = A,T,C or G

<400> 138  
 actcactgga atgccacatt cacaacagaa tcagaggtct gtgaaaacat taatggctcc 60  
 ttaacttctc cagtaagaat cagggacttg aaatggaaac gttaacagcc acatgcccac 120  
 tgctgggcag tctcccatgc cttccacagt gaaagggctt gagaaaaatc acatccaatg 180  
 tcatgtgttt ccagccacac caaaaggtgc ttgggggtgga gggctggggg catananggt 240  
 cangcctcag gaagcctcaa gttccattca gctttgccac tgtacattcc ccatntttaa 300  
 aaaaactgat gcotTTTTTT ttttttttg taaaattc 338

<210> 139  
 <211> 382  
 <212> DNA  
 <213> Homo sapien

<400> 139  
 gggaatcttg gtttttggca tctggtttgc ctatagccga ggccactttg acagaacaaa 60  
 gaaagggact tcgagtaaga aggtgattta cagccagcct agtgcccgaa gtgaaggaga 120  
 attcaaacag acctcgatc tctggtgtg agcctggctg gctcaccgcc tatcatctgc 180  
 atttgcctta ctcaggtgct accgactct ggccctgat gtctgtagtt tcacaggatg 240  
 ccttatttgc cttctacacc ccacagggcc cctacttct tcggatgtgt ttttaataat 300  
 gtcagctatg tgcccatcc tccttcacgc cctccctccc tttcctacca ctgctgagtg 360  
 gcctggaact tgtttaaagt gt 382

<210> 140  
 <211> 200  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(200)

<223> n = A,T,C or G

<400> 140

accaaancctt	ctttctgttg	tgttngattt	tactataggg	gtttngcttn	ttctaaanat	60
acttttcatt	taacancctt	tgtaagtgt	caggctgcac	tttgcctcat	anaattattg	120
ttttcacatt	tcaacttgta	tgtgtttgtc	tcttanagca	ttggtgaaat	cacatatttt	180
atattcagca	taaaggagaa					200

<210> 141

<211> 335

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(335)

<223> n = A,T,C or G

<400> 141

actttatttt	caaaacactc	atatgttgca	aaaaacacat	agaaaaataa	agtttggtgg	60
gggtgctgac	taaacttcaa	gtcacagact	tttatgtgac	agattggagc	agggtttgtt	120
atgcatgtag	agaaccctaa	ctaatttatt	aaacaggata	gaaacaggct	gtctgggtga	180
aatggttctg	agaaccatcc	aattcacctg	tcagatgctg	atanactagc	tcttcagatg	240
tttttctacc	agttcagaga	tnggttaatg	actanttcca	atggggaaaa	agcaagatgg	300
attcacaaac	caagtaattt	taaacaaaga	cactt			335

<210> 142

<211> 459

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(459)

<223> n = A,T,C or G

<400> 142

accagggttaa	tattgccaca	tatatccttt	ccaattgctg	gctaaacaga	cgtgtattta	60
gggttggtta	aagacaaccc	agcttaatat	caagagaaat	tgtgaccttt	catggagtat	120
ctgatggaga	aaacactgag	ttttgacaaa	tcttatttta	ttcagatagc	agtctgatca	180
cacatggtcc	aacaacactc	aaataataaa	tcaaataatna	tcagatgtta	aagattggtc	240
ttcaaacatc	atagccaatg	atgccccgct	tgcctataat	ctctccgaca	taaaaccaca	300
tcaacacctc	agtggccacc	aaaccattca	gcacagcttc	cttaactgtg	agctgtttga	360
agctaccagt	ctgagcacta	ttgactatnt	ttttcangct	ctgaatagct	ctagggatct	420
cagcangggg	gggaggaacc	agctcaacct	tggcgtant			459

<210> 143

<211> 140

<212> DNA

<213> Homo sapien

<400> 143

acatttcctt	ccaccaagtc	aggactcctg	gcttctgtgg	gagttcttat	cacctgaggg	60
aaatccaaac	agtctctcct	agaaaggaat	agtgtcacca	acccaccca	tctccctgag	120
accatccgac	ttccctgtgt					140

<210> 144

<211> 164



<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(164)  
<223> n = A,T,C or G

<400> 144  
acttcagtaa caacatacaa taacaacatt aagtgtatat tgccatcttt gtcattttct 60  
atctatacca ctctcccttc tgaaaacaan aatcactanc caatcactta taaaaatttg 120  
aggcaattaa tccatatttg ttttcaataa ggaaaaaaag atgt 164

<210> 145  
<211> 303  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(303)  
<223> n = A,T,C or G

<400> 145  
acgtagacca tccaactttg tatttgtaat ggcaaacatc cagnagcaat tcctaaacaa 60  
actggagggt atttataccc aattatccca ttcattaaca tgccctcctc ctcaggctat 120  
gcaggacagc tatcataagt cggcccaggc atccagatac taccatttgt ataaacttca 180  
gtaggggagt ccatccaagt gacagggtcta atcaaaggag gaaatggaac ataagcccag 240  
tagtaaaatn ttgcttagct gaaacagcca caaaagactt accgccgtgg tgattaccat 300  
caa 303

<210> 146  
<211> 327  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(327)  
<223> n = A,T,C or G

<400> 146  
actgcagctc aattagaagt ggtctctgac tttcatcanc ttctccctgg gctccatgac 60  
actggcctgg agtgactcat tgctctgggt ggttgagaga gtccttttgc caacaggcct 120  
ccaagtcagg gctgggattt gtttcctttc cacattctag caacaatatg ctggccactt 180  
cctgaacagg gaggggtgga ggagccagca tggaacaagc tgccactttc taaagtagcc 240  
agacttgccc ctgggcctgt cacacctact gatgaccttc tgtgcctgca ggatggaatg 300  
taggggtgag ctgtgtgact ctatggt 327

<210> 147  
<211> 173  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(173)  
<223> n = A,T,C or G

<400> 147  
 acattgtttt tttagataa agcattgana gagctctcct taacgtgaca caatggaagg 60  
 actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120  
 atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gtt 173

<210> 148  
 <211> 477  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(477)  
 <223> n = A,T,C or G

<400> 148  
 acaaccactt tatctcatcg aattttttaac ccaaactcac tcaactgtgcc tttctatcct 60  
 atgggatata ttatttgatg ctccatttca tcacacatat atgaataata cactcatact 120  
 gccctactac ctgctgcaat aatcacattc ccttcctgtc ctgacctga agccattggg 180  
 gtggctcctag tggccatcag tccangcctg caccttgagc ccttgagetc cattgctcac 240  
 nccanccac ctcaccgacc ccctcctctt acacagctac ctccttgctc tctaaccoca 300  
 tagattatnt ccaaattcag tcaattaagt tactattaac actctaccg acatgtccag 360  
 caccactggt aagccttctc cagccaacac acacacacac acacncacac acacacatat 420  
 ccaggcacag gctacctcat cttcacaatc acccctttaa ttaccatgct atggtgg 477

<210> 149  
 <211> 207  
 <212> DNA  
 <213> Homo sapien

<400> 149  
 acagttgtat tataatatca agaaataaac ttgcaatgag agcatttaag agggaagaac 60  
 taacgtatatt tagagagcca aggaagggtt ctgtggggag tgggatgtaa ggtggggcct 120  
 gatgataaat aagagtcagc caggtaagtg ggtggtgtgg tatgggcaca gtgaagaaca 180  
 tttcaggcag agggaacagc agtgaaa 207

<210> 150  
 <211> 111  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(111)  
 <223> n = A,T,C or G

<400> 150  
 accttgattt cattgctgct ctgatggaaa cccaactatc taatttagct aaaacatggg 60  
 cacttaaattg tggtcagtgt ttggacttgt taactantgg catctttggg t 111

<210> 151  
 <211> 196  
 <212> DNA  
 <213> Homo sapien

<400> 151  
 agcgcggcag gtcatttga acattccaga tacctatcat tactcgatgc tgttgataac 60

agcaagatgg ctttgaactc agggtcacca ccagctattg gacottacta tgaaaaccat	120
ggataccaac cggaaaaccc ctatcccgcg cagcccaactg tggccccac tgtctacgag	180
gtgcatccgg ctcaagt	196

<210> 152  
 <211> 132  
 <212> DNA  
 <213> Homo sapien

<400> 152	
acagcacttt cacatgtaag aaggagagaa ttccataatg taggagaaag ataacagAAC	60
cttccccttt tcatctagt gtggaaacct gatgctttat gttgacagga atagaaccag	120
gagggagttt gt	132

<210> 153  
 <211> 285  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(285)  
 <223> n = A,T,C or G

<400> 153	
acaanaccca nganaggcca ctggccgtgg tgtcatggcc tccaaacatg aaagtgtcag	60
cttctgctct tatgtcctca tctgacaact ctttaccatt tttatcctcg ctcagcagga	120
gcacatcaat aaagtccaaa gtcttggaact tggccttggc ttggaggaag tcatcaacac	180
cctggctagt gaggggtgcgg cgccgctcct ggatgacggc atctgtgaag tctgtcacca	240
gtctgcaggc cctgtggaag cgccgtccac acggagtnag gaatt	285

<210> 154  
 <211> 333  
 <212> DNA  
 <213> Homo sapien

<400> 154	
accacagtcc tgttgggcca gggcttcagt accctttctg tgaaaagcca tattatcacc	60
accccaaatt tttccttaaa tatctttaac tgaaggggtc agcctcttga ctgcaaagac	120
cctaagccgg ttacacagct aactcccact ggccttgatt tgtgaaattg ctgtgcctg	180
attggcacag gagtccaagg ttttcagctc ccctcctccg tggaacgaga ctctgatttg	240
agtttcacaa attctcgggc cacctcgtca ttgtcctct gaaataaaat ccggagaatg	300
gtcaggcctg tctcatccat atggatcttc cgg	333

<210> 155  
 <211> 308  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(308)  
 <223> n = A,T,C or G

<400> 155	
actggaaata ataaaaccca catcacagt ttgtgtcaaa gatcatcagg gcatggatgg	60
gaaagtgcct tgggaactgt aaagtgccta acacatgatc gatgattttt gttataatat	120
ttgaatcacg gtgcatacaa actctcctgc ctgctcctcc tgggccccag cccagcccc	180

atcacagctc actgctctgt tcatccaggc ccagcatgta gtggctgatt cttcttggt	240
gcttttagcc tccanaagtt tctctgaagc caaccaaacc tctangtga aggcatgctg	300
gccctggg	308

<210> 156  
 <211> 295  
 <212> DNA  
 <213> Homo sapien

<400> 156	
accttgctcg gtgcttgga catattagga actcaaaata tgagatgata acagtgccta	60
ttattgatta ctgagagaac tgtagacat ttagttgaag attttctaca caggaaactga	120
gaataggaga ttatgtttgg cctcatatt ctctcctatc ctcttgccct cattctatgt	180
ctaatatatt ctcaatcaaa taaggtttagc ataatcagga aatcgaccaa ataccaatat	240
aaaaccagat gtctatcctt aagattttca aatagaaaac aaattaacag actat	295

<210> 157  
 <211> 126  
 <212> DNA  
 <213> Homo sapien

<400> 157	
acaagtttaa atagtgtgt cactgtgcat gtgctgaaat gtgaaatcca ccacatttct	60
gaagagcaaaa acaaattctg tcatgtaatc tctatcttgg gtcgtgggta tatctgtccc	120
cttagt	126

<210> 158  
 <211> 442  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(442)  
 <223> n = A,T,C or G

<400> 158	
accactggg cttggaaaca cccatcctta atacgatgat ttttctgtcg tgtgaaaatg	60
aanccagcag gctgccccta gtcagtccct ccttcagag aaaaagagat ttgagaaagt	120
gcctgggtaa ttaccatta atttcctccc ccaaactctc tgagtcttcc cttaatat	180
ctgggtggtc tgaccaaagc aggtcatggt ttgttgagca tttgggatcc cagtgaagta	240
natgtttgta gccttgcata cttagccctt cccacgcaca aacggagtgg cagagtggg	300
ccaacctgt tttcccagtc cacgtagaca gattcacagt gcggaattct ggaagctgga	360
nacagaoggg ctctttgcag agccgggact ctgagangga catgagggcc tctgcctctg	420
tgttcattct ctgatgtcct gt	442

<210> 159  
 <211> 498  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(498)  
 <223> n = A,T,C or G

<400> 159	
acttccagg aacgttggtg tttccgttga gcctgaactg atgggtgacg ttgtaggttc	60

```

tccaacaaga actgaggttg cagagcgggt aggggaagagt gctgttccag ttgcacctgg      120
gctgctgtgg actgttggtg attcctcact acggcccaag gttgtggaac tggcanaaag      180
gtgtgttggt gganttgagc tcgggcggct gtggtaggtt gtgggctctt caacaggggc      240
tgctgtggtg ccgggangtg aangtggtgt gtcacttgag cttggccagc tctggaaagt      300
antanattct tcctgaaggc cagcgcttgt ggagctggca ngggtcantg ttgtgtgtaa      360
cgaaccagtg ctgctgtggg tgggtgtana tcctccacaa agcctgaagt tatggtgten      420
tcaggtaana atgtggtttc agtgtccctg ggcngctgtg gaaggttgta nattgtcacc      480
aagggaataa gctgtggt                                     498

```

```

<210> 160
<211> 380
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(380)
<223> n = A,T,C or G

```

```

<400> 160
acctgcatcc agcttccctg ccaaactcac aaggagacat caacctctag acagggaaac      60
agcttcagga tacttccagg agacagagcc accagcagca aaacaaatat tcccatgcct      120
ggagcatggc atagaggaag ctganaaatg tggggtctga ggaagccatt tgagtctggc      180
cactagacat ctcatcagcc acttggtgta agagatgcc catgacccca gatgcctctc      240
ccacccttac ctccatctca cacacttgag ctttccactc tgtataattc taacatcctg      300
gagaaaaatg gcagtttgac cgaacctgtt cacaacggta gaggctgatt tctaacgaaa      360
cttgtagaat gaagcctgga                                     380

```

```

<210> 161
<211> 114
<212> DNA
<213> Homo sapien

```

```

<400> 161
actccacatc ccctctgagc aggcggttgt cgttcaaggt gtatttggcc ttgcctgtca      60
cactgtccac tggcccctta tccacttggt gcttaatccc tcgaaagagc atgt      114

```

```

<210> 162
<211> 177
<212> DNA
<213> Homo sapien

```

```

<400> 162
actttctgaa tcgaatcaaa tgatacttag tgtagtttta atatcctcat atatatcaaa      60
gttttactac tctgataatt ttgtaaacca ggtaaccaga acatccagtc atacagcttt      120
tggtgatata taacttggca ataaccagc ctggtgatac ataaaactac tcactgt      177

```

```

<210> 163
<211> 137
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(137)
<223> n = A,T,C or G

```

```

<400> 163

```

```

catttataca gacaggcgtg aagacattca cgacaaaaac gcgaaattct atcccgtgac      60
canagaaggc agctacggct actcctacat cctggcgtgg gtggccttcg cctgcacctt      120
catcagcggc atgatgt                                     137

```

```

<210> 164
<211> 469
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(469)
<223> n = A,T,C or G

```

```

<400> 164
cttatcacaa tgaatgttct cctgggcagc gttgtgatct ttgccacctt cgtgacttta      60
tgcaatgcat catgctatct catacctaata gagggagttc caggagattc aaccaggaaa      120
tgcatggatc tcaaaggaaa caaacaccca ataaactcgg agtggcagac tgacaactgt      180
gagacatgca cttgctacga aacagaaatt tcatgttgca cccttgtttc tacacctgtg      240
ggttatgaca aagacaactg ccaaagaatc ttcaagaagg aggactgcaa gtatatcgtg      300
gtggagaaga aggacccaaa aaagacctgt tctgtcagtg aatggataat ctaatgtgct      360
tctagtaggc acagggtcc caggccaggc ctcattctcc tctggcctct aatagtcaat      420
gattgtgtag ccatgcctat cagtaaaaag atntttgagc aaacacttt                469

```

```

<210> 165
<211> 195
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(195)
<223> n = A,T,C or G

```

```

<400> 165
acagtttttt atanatatcg acattgccgg cacttgtgtt cagtttcata aagctgggtg      60
atccgctgtc atccactatt ccttggttag agtaaaaatt attcttatag cccatgtccc      120
tgcaggccgc ccgcccgtag ttctcgttcc agtcgtcttg gcacacaggg tgccaggact      180
tcctctgaga tgagt                                     195

```

```

<210> 166
<211> 383
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

```

```

<400> 166
acatcttagt agtgtggcac atcagggggc catcagggtc acagtcactc atagcctcgc      60
cgaggtcgga gtccacacca ccggtgtagg tgtgtcfaat cttgggcttg gcgcccacct      120
ttggagaagg gatatgctgc acacacatgt ccacaaagcc tgtgaactcg ccaaagaatt      180
tttgagacc agcctgagca aggggaggat gttcagcttc agtcctcctc tcgtcagggtg      240
gatgccaaac tcgtctangg tccgtgggaa gctggtgtcc acntcaccta caacctgggc      300
gangatctta taaagaggct ccnagataaa ctccacgaaa cttctctggg agctgctagt      360
nggggccttt ttggtgaact ttc                                     383

```

<210> 167  
 <211> 247  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(247)  
 <223> n = A,T,C or G

<400> 167  
 acagagccag accttggcca taaatgaanc agagattaag actaaacccc aagtcganat 60  
 tggagcagaa actggagcaa gaagtgggcc tggggctgaa gtagagacca aggccactgc 120  
 tatanccata cacagagcca actctcaggc caaggcnatg gttggggcag anccagagac 180  
 tcaatctgan tccaaagtgg tggttggaac actggtcatg acanaggcag tgactctgac 240  
 tgangtc 247

<210> 168  
 <211> 273  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(273)  
 <223> n = A,T,C or G

<400> 168  
 acttctaagt tttctagaag tggaaggatt gtantcatcc tgaaaatggg tttacttcaa 60  
 aatccctcan ccttgttctt cacnactgtc tatactgana gtgtcatgtt tccacaaagg 120  
 gctgacacct gagcctgnat tttcactcat ccctgagaag ccctttccag taggggtggc 180  
 aattcccaac ttccttgcca caagcttccc aggetttctc cccttgaaaa ctccagcttg 240  
 agtcccagat acactcatgg gctgccctgg gca 273

<210> 169  
 <211> 431  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(431)  
 <223> n = A,T,C or G

<400> 169  
 acagccttgg cttccccaaa ctccacagtc tcagtgcaga aagatcatct tccagcagtc 60  
 agctcagacc aggggtcaaag gatgtgacat caacagtttc tgggttcaga acaggttcta 120  
 ctactgtcaa atgacccccc atacttcctc aaaggctgtg gtaagttttg cacaggtgag 180  
 ggcagcagaa aggggggtant tactgatgga caccatcttc tctgtatact ccacactgac 240  
 cttgccatgg gcaaaggccc ctaccacaaa aacaatagga tcaactgctgg gcaccagctc 300  
 acgcacatca ctgacaaccg ggatggaaaa agaantgccca actttcatac atccaactgg 360  
 aaagtgatct gatactggat tcttaattac cttcaaaagc ttctgggggc catcagctgc 420  
 tcgaacactg a 431

<210> 170  
 <211> 266  
 <212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(266)

<223> n = A,T,C or G

<400> 170

acctgtgggc	tgggctgtta	tgectgtgcc	ggctgctgaa	agggagttca	gagggtggagc	60
tcaaggagct	ctgcaggcat	tttgccaanc	ctctccanag	canagggagc	aacctacact	120
ccccgctaga	aagacaccag	attggagtc	tgggaggggg	agttgggggtg	ggcatttgat	180
gtatacttgt	cacctgaatg	aangagccag	agaggaanga	gacgaanatg	anattggcct	240
tcaaagctag	gggtctggca	ggtgga				266

<210> 171

<211> 1248

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(1248)

<223> n = A,T,C or G

<400> 171

ggcagccaaa	tcataaacgg	cgaggactgc	agcccgcact	cgagccctg	gcaggcggca	60
ctgggtcatg	aaaacgaatt	gttctgctcg	ggcgtcctgg	tgcacccgca	gtgggtgctg	120
tcagccgcac	actgtttcca	gaagtgaagt	cagagctcct	acaccatcgg	gctgggcctg	180
cacagtcttg	aggccgacca	agagccagg	agccagatgg	tggaggccag	cctctccgta	240
cggcaccag	agtacaacag	acccttgctc	gctaaccgacc	tcatgctcat	caagttggac	300
gaatccgtgt	ccgagtctga	caccatccgg	agcatcagca	ttgcttcgca	gtgccctacc	360
gcggggaact	cttgccctcg	ttctggctgg	ggtctgctgg	cgaacggcag	aatgcctacc	420
gtgctgcagt	gcgtgaacgt	gtcggtggtg	tctgaggagg	tctgcagtaa	gctctatgac	480
ccgctgtacc	acccagcat	gttctgcgcc	ggcggagggg	aagaccagaa	ggactcctgc	540
aacggtgact	ctggggggcc	cctgatctgc	aacgggtact	tgcagggcct	tgtgtctttc	600
ggaaaagccc	cgtgtggcca	agttggcgtg	ccagggtgtc	acaccaacct	ctgcaaattc	660
actgagtgg	tagagaaaac	cgtccaggcc	agttaactct	ggggactggg	aacctatgaa	720
attgaccccc	aaatacatcc	tgcggaagga	attcaggaat	atctgttccc	agccctcct	780
ccctcaggcc	caggagtcca	ggccccccag	ccctcctccc	tcaaaccaag	ggtacagatc	840
cccagcccct	cctccctcag	acccaggagt	ccagaccccc	cagcccctcc	tccctcagac	900
ccaggagtcc	agccccctcc	ccctcagacc	caggagtcca	gacccccag	cccctcctcc	960
ctcagaccca	ggggtccagg	cccccaaccc	ctcctccctc	agactcagag	gtccaagccc	1020
ccaaccntc	attccccaga	cccagaggtc	cagggtcccag	cccctcntcc	ctcagaccca	1080
gcggtccaat	gccacctaga	ctntccctgt	acacagtgcc	cccttggtgg	acgttgaccc	1140
aaccttacca	gttggttttt	catttttngt	ccctttcccc	tagatccaga	aataaagttt	1200
aagagaagng	caaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaa		1248

<210> 172

<211> 159

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> (1)...(159)

<223> Xaa = Any Amino Acid

<400> 172



Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro  
 1 5 10 15  
 Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser  
 20 25 30  
 Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr  
 35 40 45  
 Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly  
 50 55 60  
 Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu  
 65 70 75 80  
 Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe  
 85 90 95  
 Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser  
 100 105 110  
 Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe  
 115 120 125  
 Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn  
 130 135 140  
 Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser  
 145 150 155

<210> 173  
 <211> 1265  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(1265)  
 <223> n = A,T,C or G

<400> 173  
 ggcagcccgc actcgcagcc ctggcaggcg gcaactgggtca tggaaaacga attgtttctgc 60  
 tcgggcgctcc tgggtgcatcc gcagtgggtg ctgtcagccg cacactgttt ccagaactcc 120  
 tacaccatcg ggctgggctt gcacagtctt gagggccagg aagagccagg gagccagatg 180  
 gtggaggcca gcctctccgt acggcaccca gactacaaca gacccttgct cgctaaccgac 240  
 ctcatgtctca tcaagttgga cgaatccgtg tccgagtctg acaccatccg gagcatcagc 300  
 attgcttcgc agtgccttac cgcggggaac tcttgccctg tttctggctg ggtctgtctg 360  
 gcgaacggtg agctcacggg tgtgtgtctg ccctcttcaa ggaggtcctc tgcccagtcg 420  
 cgggggctga ccagagctc tgcgtcccag gcagaatgcc taccgtgctg cagtgcgtga 480  
 acgtgtcgtt ggtgtctgag gaggtctgca gtaagctcta tgaccgcgtg taccaccca 540  
 gcatgttctg cgccggcgga gggcaagacc agaaggactc ctgcaacggt gactctgggg 600  
 ggcccctgat ctgcaacggg tacttgagg gccttggtg tttcggaaaa gcccctgtg 660  
 gccaaagtgg cgtgccagg gtctacacca acctctgcaa attcactgag tggatagaga 720  
 aaaccgtcca ggccagttaa ctctggggac tgggaaccca tgaaattgac ccccaaatac 780  
 atcctgcgga aggaattcag gaatatctgt tcccagcccc tcctccctca ggcccaggag 840  
 tccaggcccc cagcccctcc tccctcaaac caagggtaca gatcccagc ccctcctccc 900  
 tcagaccag gagtccagac ccccagccc ctctccctc agaccagga gtccagcccc 960  
 tcctccntca gaccagagg tccagacccc ccagcccctc ctccctcaga cccaggggtt 1020  
 gagggcccca accctcctc cttcagagtc agaggccaa gcccacaacc cctcgttccc 1080  
 cagaccaga ggttnnaggtc ccagcccctc ttcctcaga cccagnngtc caatgccacc 1140  
 tagattttcc ctgnacacag tgccccctt tggngangttg acccaacctt accagttggt 1200  
 ttttcatttt tngtcccttt ccctagatc cagaaataaa gtttaagaga ngngcaaaaa 1260  
 aaaa 1265

<210> 174  
 <211> 1459  
 <212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(1459)

<223> n = A,T,C or G

<400> 174

ggtcagccgc	acactgtttc	cagaagtgcg	tgcagagctc	ctacaccatc	gggctgggcc	60
tgcacagtct	tgaggccgac	caagagccag	ggagccagat	ggaggaggcc	agcctctccg	120
tacggcacc	agagtacaac	agacccttgc	tcgctaacga	cctcatgtct	atcaagttgg	180
acgaatccgt	gtccgagtct	gacaccatcc	ggagcatcag	cattgcttcg	cagtgcctta	240
ccgcggggaa	ctcttgccct	gtttctggct	ggggtctgct	ggcgaacggt	gagctcacgg	300
gtgtgtgtct	gccctcttca	aggaggtcct	ctgcccagtc	gcgggggctg	acccagagct	360
ctgcgtccca	ggcagaatgc	ctaccgtgct	gcagtgcgtg	aacgtgtcgg	tggtgtctga	420
ngaggtctgc	antaagctct	atgacccgct	gtaccacccc	ancatgttct	gcgccggcgg	480
agggcaagac	cagaaggact	cctgcaacgt	gagagagggg	aaaggggagg	gcaggcgact	540
cagggaagg	tggagaagg	ggagacagag	acacacagg	ccgcatggcg	agatgcagag	600
atggagagac	acacagggag	acagtgacaa	ctagagagag	aaactgagag	aaacagagaa	660
ataaacacag	gaataaagag	aagcaaagga	agagagaaac	agaaacagac	atggggaggc	720
agaaacacac	acacatagaa	atgcagttga	ccttccaaca	gcatggggcc	tgaggcggt	780
gacctccacc	caatagaaaa	tcctcttata	acttttgact	ccccaaaaac	ctgactagaa	840
atagcctact	gttgacgggg	agccttacca	ataacataaa	tagtcgattt	atgcatacgt	900
tttatgcatt	catgatatac	ctttgttgga	attttttgat	atttctaagc	tacacagttc	960
gtctgtgaat	tttttttaaa	tgttgcaact	ctcctaaaat	ttttctgatg	tgtttattga	1020
aaaaatccaa	gtataagtgg	acttgtgcat	tcaaaccagg	gttggtcaag	gggtcaactgt	1080
gtacccagag	ggaaacagtg	acacagattc	atagaggtga	aacacgaaga	gaaacaggaa	1140
aaatcaagac	tctacaaaga	ggctgggcag	gggtggtcat	gcctgtaatc	ccagcacttt	1200
gggaggcgag	gcaggcagat	cacttgaggt	aaggagttca	agaccagcct	ggccaaaatg	1260
gtgaaatcct	gtctgtacta	aaaatacaaa	agttagctgg	atatgggtgg	aggcgccctgt	1320
aatcccagct	acttgggagg	ctgaggcagg	agaattgctt	gaatatggga	ggcagaggtt	1380
gaagtgaagt	gagatcacac	cactatactc	cagctggggc	aacagagtaa	gactctgtct	1440
caaaaaaaaa	aaaaaaaaaa					1459

<210> 175

<211> 1167

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(1167)

<223> n = A,T,C or G

<400> 175

gcgcagccct	ggcaggcgcc	actgggtcatg	gaaaacgaat	tggtctgtct	gggcgtcctg	60
gtgcatccgc	agtgggtgct	gtcagccgca	cactgtttcc	agaactccta	caccatcggt	120
ctgggcctgc	acagtcttga	ggccgaccaa	gagccaggga	gccagatggt	ggaggccagc	180
ctctccgtac	ggcaccacga	gtacaacaga	ctcttgctcg	ctaaccacct	catgtctatc	240
aagttggacg	aatccgtgtc	cgagtctgac	accatccgga	gcatacagat	tgcttcgcag	300
tgccctaccg	cggggaactc	ttgcctcgtn	tctggctggg	gtctgctggc	gaacggcaga	360
atgcctaccg	tgctgcaact	cgtgaacgtg	tcgggtggtg	ctgaggangt	ctgcagtaag	420
ctctatgacc	cgctgtacca	ccccagcatg	ttctgcgccg	gcggagggca	agaccagaag	480
gactcctgca	acggtgactc	tgggggggcc	ctgatctgca	acgggtactt	gcagggcctt	540
gtgtctttcg	gaaaagcccc	gtgtggccaa	cttggcgtgc	caggtgtcta	caccaacctc	600
tgcaaattca	ctgagtggat	agagaaaacc	gtccagncca	gttaactctg	gggactggga	660
acccatgaaa	ttgaccccca	aatacatcct	gcggaangaa	ttcaggaata	tctgttccca	720
gccccctctc	cctcaggccc	aggagtccag	gccccagcc	cctcctccct	caaaccaagg	780

```

gtacagatcc ccagcccctc ctccctcaga cccaggagtc cagaccccc agccccctent 840
ccntcagacc caggagtcca gcccctcctc cntcagacgc aggagtccag accccccagc 900
ccntcntccg tcagaccagc ggggtgcaggc ccccaacccc tcntcntca gagtcagagg 960
tccaagcccc caacccctcg ttccccagac ccagaggtnc aggtcccagc cctcctccc 1020
tcagaccagc cgggtccaatg ccacctagan tntccctgta cacagtgcgc ccttggtggca 1080
ngttgaccca acctaccag ttgggttttc attttttgtc cctttcccct agatccagaa 1140
ataaagtnta agagaagcgc aaaaaaa 1167

```

<210> 176  
 <211> 205  
 <212> PRT  
 <213> Homo sapien

<220>  
 <221> VARIANT  
 <222> (1)...(205)  
 <223> Xaa = Any Amino Acid

<400> 176

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
1           5           10           15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
          20          25          30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
          35          40          45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
          50          55          60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
65          70          75          80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
          85          90          95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
          100         105         110
Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
          115         120         125
Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
          130         135         140
Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
145         150         155         160
Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
          165         170         175
Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
          180         185         190
Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
          195         200         205

```

<210> 177  
 <211> 1119  
 <212> DNA  
 <213> Homo sapien

<400> 177

```

gcgcactcgc agccctggca ggcggcactg gtcattgaaa acgaattgtt ctgctcgggc 60
gtcctgggtgc atccgcagtg ggtgctgtca gccgcacact gtttcagaa ctcctacacc 120
atcgggctgg ccctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag 180
gccagcctct ccgtacggca cccagagtac aacagaccct tgctcgctaa cgacctcatg 240
ctcatcaagt tggacgaatc cgtgtccgag totgacacca tccggagcat cagcattgct 300
tcgcagtgcc ctaccgcggg gaactcttgc ctgctttctg gctggggtct gctggcgaac 360

```

```

gatgctgtga ttgccatcca gtcccagact gtgggaggct gggagtgtga gaagctttcc 420
caaccctggc aggggtgtac catttcggca acttccagtg caaggacgtc ctgctgcatc 480
ctcactgggt gctcactact gctcactgca tcacccggaa cactgtgata aactagccag 540
caccatagtt ctccgaagtc agactatcat gattactgtg ttgactgtgc tgtctattgt 600
actaaccatg ccgatgttta ggtgaaatta gcgtcacttg gcctcaacca tcttggtatc 660
cagttatcct cactgaattg agatttcctg cttcagtgtc agccattccc acataatttc 720
tgacctacag aggtgaggga tcatatagct cttcaaggat gctgggtactc ccctcacaaa 780
ttcatttctc ctgtttagt gaaagggtgcg ccctctggag cctcccaggg tgggtgtgca 840
ggtcacaatg atgaatgtat gatcgtgttc ccattaccca aagcctttaa atccctcatg 900
ctcagtacac cagggcaggt ctacgatttc ttcathtagt gtatgctgtc cattcatgca 960
accacctcag gactcctgga ttctctgcct agttgagctc ctgcatgctg cctccttggg 1020
gaggtgaggg agagggccca tggttcaatg ggatctgtgc agttgtaaca cattaggtgc 1080
ttaataaaca gaagctgtga tgtaaaaaa aaaaaaaaa 1119

```

<210> 178  
 <211> 164  
 <212> PRT  
 <213> Homo sapien

<220>  
 <221> VARIANT  
 <222> (1)...(164)  
 <223> Xaa = Any Amino Acid

<400> 178  
 Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp  
 1 5 10 15  
 Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu  
 20 25 30  
 Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val  
 35 40 45  
 Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu  
 50 55 60  
 Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser  
 65 70 75 80  
 Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly  
 85 90 95  
 Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val  
 100 105 110  
 Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu  
 115 120 125  
 Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg  
 130 135 140  
 Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser  
 145 150 155 160  
 Pro Gly Thr Leu

<210> 179  
 <211> 250  
 <212> DNA  
 <213> Homo sapien

```

ctggagtgcc ttggtgtttc aagcccctgc aggaagcaga atgcaccttc tgaggcacct 60
ccagctgccc ccggccgggg gatgcgagge tgggagcacc cttgcccggc tgtgattgct 120
gccaggcact gttcatctca gcttttctgt ccctttgctc ccggcaagcg cttctgctga 180
aagttcatat ctggagcctg atgtcttaac gaataaaggt cccatgctcc acccgaaaaa 240

```

aaaaaaaaaa

250

<210> 180  
 <211> 202  
 <212> DNA  
 <213> Homo sapien

<400> 180  
 actagtccag tgtggtggaa ttccattgtg ttgggcccac cacaatggct acctttaaca 60  
 tcacccagac cccgcccctg cccgtgcccc acgtgtgtgc taacgacagt atgatgctta 120  
 ctctgtact cggaactat ttttatgtaa ttaatgtatg ctttcttgtt tataaatgcc 180  
 tgatttaaaa aaaaaaaaaa aa 202

<210> 181  
 <211> 558  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(558)  
 <223> n = A,T,C or G

<400> 181  
 tccytttght naggtttkkg agacamccck agacctwaan ctgtgtcaca gacttcyngg 60  
 aatgttttagg cagtgttagt aatttcytcg taatgattct gttattactt tcctnattct 120  
 ttattcctct ttcttctgaa gattaatgaa gttgaaaatt gaggtggata aatacaaaaa 180  
 ggtagtgtga tagtataagt atctaagtgc agatgaaagt gtgttatata tatccattca 240  
 aaattatgca agttagtaat tactcagggg taactaaatt actttaatat gctgttgaac 300  
 ctactctgtt ccttggctag aaaaaattat aaacaggact ttgttagttt gggaagccaa 360  
 attgataata ttctatgttc taaaagttgg gctatacata aattattaag aaatatggaw 420  
 ttttattccc aggaatatgg kgttcatttt atgaatatta cscrggatag awgtwtgagt 480  
 aaaaycagtt ttggtwaata ygtwaatatg tcmtaataaa acaakgcttt gacttatttc 540  
 caaaaaaaaa aaaaaaaa 558

<210> 182  
 <211> 479  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(479)  
 <223> n = A,T,C or G

<400> 182  
 acagggwttk grggatgcta agsccccrga rwtygtttga tocaaccctg gcttwttttc 60  
 agaggggaaa atggggccta gaagttacag mscatytagy tgggtgcgmtg gcacccctgg 120  
 cstcacacag astcccgagt agctgggact acaggcacac agtcaactgaa gcaggccctg 180  
 ttwgcaattc acgttgccac ctccaactta aacattcttc atatgtgatg tccttagtca 240  
 ctaaggttaa actttcccac ccagaaaagg caacttagat aaaatcttag agtactttca 300  
 tactmttcta agtcctcttc cagcctcact kkgagtcctm cytgggggtt gataggaant 360  
 ntctcttggc tttctcaata aartctctat ycatctcatg ttttaatttg tatcgcatara 420  
 awtgstgata aaattaaaaat gttctggtty mactttaaaa aaaaaaaaaa aaaaaaaa 479

<210> 183  
 <211> 384  
 <212> DNA

<213> Homo sapien

<400> 183

```

aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactggtgcc      60
agtaccagta ccaataacag tgccagtgcc agtgccagca ccagtgggtg cttcagtgtc      120
ggtgccagcc tgaccgccac tctcacattt gggtctctcg ctggccttgg tggagctggt      180
gccagcacca gtggcagctc tggcgctgtt gggttctcct acaagtgaga ttttagatat      240
tgtaaatcct gccagtcttt ctcttcaagc caggggtgcat cctcagaaac ctactcaaca      300
cagcactcta ggcagccact atcaatcaat tgaagttgac actctgcatt aratctattt      360
gccatttcaa aaaaaaaaaa aaaa                                     384

```

<210> 184

<211> 496

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(496)

<223> n = A,T,C or G

<400> 184

```

accgaattgg gaccgctggc ttataagcga tcatgttynt ccrgtatkac ctcaacgagc      60
aggagatcgc agtctatacg ctgaagaaat ttgaccgatg gggacaacag acctgctcag      120
cccattctgc tcggttctcc ccagatgaca aatactctsg acaccgaatc accatcaaga      180
aacgcttcaa ggtgctcatg acccagcaac cgcgcctgtt cctctgaggg tcccttaaac      240
tgatgtcttt tctgccacct gttacccctc ggagactccg taaccaaact cttcggactg      300
tgagccctga tgcctttttg ccagccatac tctttggcat ccagtctctc gtggcgattg      360
attatgcttg tgtgaggcaa tcatggtggc atcaccataa aagggaacac atttgacttt      420
tttttctcat attttaaatt actacmagaw tattwmagaw waaatgawtt gaaaaactst      480
taaaaaaaaa aaaaaa                                         496

```

<210> 185

<211> 384

<212> DNA

<213> Homo sapien

<400> 185

```

gctggtagcc tatggcgkkg ccacaggagg ggctcctgag gccacggrac agtgacttcc      60
caagtatcyt ggcsgcgtc ttctaccgtc cctacctgca gatcttcggg cagattcccc      120
aggaggacat ggacgtggcc ctcatggagc acagcaactg ytcgtcggag ccggtcttct      180
gggcacaccc tcctggggcc caggcgggca cctgcgtctc ccagtatgcc aactggcttg      240
tggtgctgct cctcgtcctc ttctgctcgc tggccaacat cctgctgggt aacttgctca      300
ttgccatggt cagttacaca ttcggaagaa tacagggcaa cagcgatctc tactgggaag      360
gcgcagcggt accgcctcat ccgg                                     384

```

<210> 186

<211> 577

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(577)

<223> n = A,T,C or G

<400> 186

```

gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggcctctcgc ttcataccgc      60

```

tnccatcgtc	atactgtagg	tttgccacca	cytcctggca	tcttggggcg	gentaatatt	120
ccaggaaact	ctcaatcaag	tcaccgtcga	tgaaacctgt	gggctgggtc	tgtcttccgc	180
tcgggtgtgaa	aggatctccc	agaaggagtg	ctcgatcttc	cccacacttt	tgatgacttt	240
attgagtcga	ttctgcatgt	ccagcaggag	gttgtaccag	ctctctgaca	gtgaggtcac	300
cagccctatc	atgccgttga	mogtgccgaa	garcaccgag	ccttgtgtgg	gggkkgaagt	360
ctcaccacaga	ttctgcatta	ccagagagcc	gtggcaaaag	acattgacaa	actcgcccag	420
gtggaaaaag	amcamctcct	ggargtgctn	gcgcctcttc	gtcmgttggt	ggcagcgctw	480
tccttttgac	acacaaacaa	gttaaaggca	ttttcagccc	ccagaaantt	gtcatcatcc	540
aagatntcgc	acagcactna	tccagttggg	attaaat			577

<210> 187  
 <211> 534  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(534)  
 <223> n = A,T,C or G

<400> 187						
aacatcttcc	tgtataatgc	tgtgtaatat	cgatccgatn	ttgtctgstg	agaatycatw	60
actkggaaaa	gmaacattaa	agcctggaca	ctggatttaa	aattcacaat	atgcaacact	120
ttaaacagtg	tgtcaatctg	ctcccyynac	tttgtcatca	ccagtctggg	aakaagggta	180
tgccctattc	acacctgtta	aaagggcgct	aagcattttt	gattcaacat	cttttttttt	240
gacacaagtc	cgaaaaaagc	aaaagtaaac	agttatyaat	ttgttagcca	attcactttc	300
ttcatgggac	agagccatyt	gatttaaaaa	gcaaattgca	taatattgag	cttygggagc	360
tgatatttga	gcggaagagt	agcctttcta	cttcaccaga	cacaactccc	tttcatattg	420
ggatgttnac	naaagtwatg	tctctwacag	atgggatgct	tttgtggcaa	ttctgttctg	480
aggatctccc	agtttattta	ccacttgcac	aagaaggcgt	tttcttcttc	agge	534

<210> 188  
 <211> 761  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(761)  
 <223> n = A,T,C or G

<400> 188						
agaaaccagt	atctctnaaa	acaacctctc	ataccttggtg	gacctaatth	tgtgtgcgtg	60
tgtgtgtgcg	cgcataattat	atagacaggc	acatcttttt	tacttttgta	aaagcttatg	120
cctcttttgg	atctatatct	gtgaaagttt	taatgatctg	ccataatgtc	ttggggacct	180
ttgtcttctg	tgtaaatggg	actagagaaa	acacctatnt	tatgagtcaa	tctagttngt	240
tttattcgcg	atgaaggaaa	tttccagatn	acaacactna	caaactctcc	ctkgackarg	300
ggggacaaaag	aaaagcaaaa	ctgamcataa	raaacaatwa	cctgggtgaga	arttgcataa	360
acagaaatwr	ggtagtatat	tgaarnacag	catcattaaa	rmgttwtktt	wttctccctt	420
gcaaaaaaca	tgtacngact	tcccgttgag	taatgccaa	ttgttttttt	tatnataaaa	480
cttgcccttc	attacatggt	tnaaagtggg	gtgggtggcc	aaaatattga	aatgatggaa	540
ctgactgata	aagctgtaca	aataagcagt	gtgcctaaca	agcaacacag	taatgttgac	600
atgcttaatt	cacaaatgct	aatttcatta	taaatgtttg	ctaaaataca	ctttgaacta	660
tttttctgtg	ttcccagagc	tgagatntta	gattttatgt	agtatnaagt	gaaaaantac	720
gaaaataata	acattgaaga	aaaananaaa	aaanaaaaaa	a		761

<210> 189  
 <211> 482

<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(482)  
<223> n = A,T,C or G

<400> 189  
 tttttttttt tttgccgatn ctactatttt attgcaggan gtgggggtgt atgcaccgca 60  
 caccggggct atnagaagca agaaggaagg agggagggca cagccccttg ctgagcaaca 120  
 aagccgcctg ctgccttctc tgtctgtctc ctggtgcagg cacatgggga gaccttcccc 180  
 aaggcagggg ccaccagtcc aggggtggga atacaggggg tgggangtgt gcataagaag 240  
 tgataggcac aggccacccg gtacagaccc ctcggtcctt gacaggtnga tttcgaccag 300  
 gtcattgtgc cctgcccagg cacagcgtan atctggaaaa gacagaatgc tttccttttc 360  
 aaatttggtc ngtcatngaa ngggcanttt tccaanttng gctnggtctt ggtaacnctg 420  
 gttcggecca gctcncgctc caaaaantat tcaccnnet ccnaattgct tgcnggnccc 480  
 cc 482

<210> 190  
<211> 471  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(471)  
<223> n = A,T,C or G

<400> 190  
 tttttttttt ttttaaaaca gtttttcaca aaaaaattta ttagaagaat agtggttttg 60  
 aaaactctcg catccagtga gaactacat acaccacatt acagctngga atgtntctca 120  
 aatgtctggt caaatgatac aatggaacca ttcaatctta cacatgcacg aaagaacaag 180  
 cgcttttgac atacaatgca caaaaaaaaa aggggggggg gaccacatgg attaaaattt 240  
 taagtactca tcacatacat taagacacag ttctagtcca gtcnaaaatc agaactgcnt 300  
 tgaaaaattt catgtatgca atccaaccaa agaacttnat tgggtgatcat gantnctota 360  
 ctacatcnac cttgatcatt gccaggaacn aaaagtnaa ancacncngt acaaaaaanaa 420  
 tctgtaattn anttcaacct ccgtacngaa aaatnttntt tatacactcc c 471

<210> 191  
<211> 402  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(402)  
<223> n = A,T,C or G

<400> 191  
 gagggattga aggtctgttc tastgtcggm ctgttcagcc accaactcta acaagttgct 60  
 gtcttccact cactgtctgt aagcttttta acccagacwg tatcttcata aatagaacaa 120  
 attcttcacc agtcacatct totaggacct ttttggattc agttagtata agctcttcca 180  
 ctctctttgt taagacttca tctggttaaag tcttaagttt tgtagaaagg aattyaattg 240  
 ctggttctct aacaatgtcc tctccttgaa gtatttggct gaacaacca cctaaagtcc 300  
 ctttgtgcat ccatttttaa tatacttaat agggcattgk tncactaggt taaattctgc 360  
 aagagtcac tgtctgcaaa agttgcgtta gtatatctgc ca 402



<210> 192  
 <211> 601  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(601)  
 <223> n = A,T,C or G

<400> 192  
 gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact 60  
 ggtctacccc acatgggagc agcatgccgt agntatataa ggtcattccc tgagtcagac 120  
 atgcytyttt gaytaccgtg tgccaagtgc tgggtgattct yaacacacyt ccatcccggt 180  
 cttttgtgga aaaactggca cttktctgga actagcarga catcacttac aaattcaccc 240  
 acgagacact tgaaaggtgt aacaaagcga ytcttgcat gctttttgtc cctccggcac 300  
 cagttgtcaa tactaaccgg ctggtttgcc tccatcacat ttgtgatctg tagctctgga 360  
 tacatctcct gacagtactg aagaacttct tcttttgttt caaaagcarg tcttggtgcc 420  
 tgttggtatca gggtcccat tcccagtcyg aatgttcaca tggcatattt wacttccac 480  
 aaaacattgc gatttgaggc tcagcaacag caaatcctgt tccggcattg gctgcaagag 540  
 cctcgatgta gccggccagc gccaaaggcag gcgcctgtgag ccccaccagc agcagaagca 600  
 g 601

<210> 193  
 <211> 608  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(608)  
 <223> n = A,T,C or G

<400> 193  
 atacagccca natcccacca cgaagatgcg cttgttgact gagaacctga tgcggtcact 60  
 ggtcccgctg tagccccagc gactctccac ctgctggaag cggttgatgc tgcactcytt 120  
 cccaacgcag gcagmagcgg gscgggtcaa tgaactccay tcgtggcttg gggtkgacgg 180  
 tkaagtgcag gaagaggctg accacctcgc ggtccaccag gatgcccagc tgtgcgggac 240  
 ctgcagcgaa actcctcgat ggtcatgagc gggaagcgaa tgaggcccag ggccttgccc 300  
 agaaccttcc cctgtttctc tggcgtcacc tgcagctgct gccgctgaca ctccggcctc 360  
 gaccagcgga caaacggcrt tgaacagccg cacctcacgg atgcccagtg tgtcgcgctc 420  
 caggammgsc accagcgtgt ccaggtcaat gtcggtgaag ccctccgcgg gtrattggcgt 480  
 ctgcagtgtt tttgtcgatg ttctccaggc acaggctggc cagctgcggt tcatcgaaga 540  
 gtcgcgcctg cgtgagcagc atgaaggcgt tgtcggctcg cagttcttct tcaggaactc 600  
 cacgcaat 608

<210> 194  
 <211> 392  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(392)  
 <223> n = A,T,C or G

<400> 194  
 gaacggctgg accttgcctc gcattgtgct tgctggcagg gaataccttg gcaagcagyt 60

ccagtcgag	cagccccaga	ccgctgccgc	ccgaagctaa	gcctgcctct	ggccttcccc	120
tccgcctcaa	tgcagaacca	gtagtgggag	cactgtgttt	agagttaaga	gtgaacactg	180
tttgatttta	cttgggaatt	tcctctgtta	tatagctttt	cccaatgcta	atttccaaac	240
aacaacaaca	aaataacatg	tttgctgttt	aagttgtata	aaagtaggtg	attctgtatt	300
taaagaaaat	attactgtta	catatactgc	ttgcaatttc	tgtattttatt	gktnctstgg	360
aaataaatat	agttattaaa	ggttgtcant	cc			392

&lt;210&gt; 195

&lt;211&gt; 502

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(502)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 195

ccsttkgagg	ggtkaggkyc	cagttyccga	gtggaagaaa	caggccagga	gaagtgcgtg	60
ccgagctgag	gcagatgttc	ccacagtgc	ccccagagcc	stgggstata	gtytctgacc	120
cctcncaagg	aaagaccacs	ttctggggac	atgggctgga	gggcaggacc	tagaggcacc	180
aagggaaggc	cccattccgg	ggstgttccc	cgaggaggaa	gggaaggggc	tctgtgtgcc	240
ccccasgagg	aagaggccct	gagtcctggg	atcagacacc	ccttcacgtg	tatccccaca	300
caaatgcaag	ctcaccaagg	tcccctctca	gtccccttcc	stacaccctg	amcggccact	360
gscscacacc	caccagagc	acgccacccg	ccatggggar	tgtgctcaag	gartcgcnng	420
gcarcgtgga	catctngtcc	cagaaggggg	cagaatctcc	aatagangga	ctgarcmstt	480
gctnanaaaa	aaaaanaaaa	aa				502

&lt;210&gt; 196

&lt;211&gt; 665

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(665)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 196

ggttacttgg	tttcattgcc	accacttagt	ggatgtcatt	tagaaccatt	ttgtctgctc	60
cctctggaag	ccttgccgag	agcggacttt	gtaattgttg	gagaataact	gctgaatttt	120
wagctgtttk	gagttgatts	gcaccactgc	accacaact	tcaatatgaa	aacyawttga	180
actwatttat	tatcttgtga	aaagtataac	aatgaaaatt	ttgttcatac	tgtattkatc	240
aagtatgatg	aaaagcaawa	gatatatatt	cttttattat	gttaaattat	gattgccatt	300
attaatcggc	aaaatgtgga	gtgtatgttc	ttttcacagt	aatatatgcc	ttttgtaact	360
tcacttggtt	attttattgt	aaatgartta	caaaattctt	aatttaagar	aatggatgtg	420
watatttatt	tcattaattt	ctttcctkgt	ttacgtwaat	tttgaaaaga	wtgcatgatt	480
tcttgacaga	aatcgatctt	gatgctgtgg	aagtagtttg	accacatcc	ctatgagttt	540
ttcttagaat	gtataaagg	tgtagcccat	onaacttcaa	agaaaaaat	gaccacatac	600
tttgcaatca	ggctgaaatg	tggcatgctn	ttctaattcc	aaactttataa	actagcaaan	660
aagtg						665

&lt;210&gt; 197

&lt;211&gt; 492

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

<221> misc\_feature  
 <222> (1)...(492)  
 <223> n = A,T,C or G

<400> 197  
 tttntttttt ttttttttgc aggaaggatt ccattttattg tggatgcatt ttcacaatat 60  
 atgtttattg gagcgatcca ttatcagtga aaagtatcaa gtgtttataa nttttttagg 120  
 aaggcagatt cacagaacat gctngtcngc ttgcagtttt acctcgtana gatnacagag 180  
 aattatagtc naaccagtaa acnaggaatt tactttttcaa aagattaaat ccaaactgaa 240  
 caaaattcta ccctgaaact tactccatcc aaatattgga ataanagtca gcagtgtatc 300  
 attctcttct gaactttaga ttttctagaa aaatattgta tagtgatcag gaagagctct 360  
 tgttcaaaag tacaacnaag caatgttccc ttacatagg ccttaattca aactttgatc 420  
 catttcactc ccatcacggg agtcaatgct acctgggaca cttgtatttt gttcatnctg 480  
 ancntggctt aa 492

<210> 198  
 <211> 478  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(478)  
 <223> n = A,T,C or G

<400> 198  
 tttnttttgn atttcantct gtannaanta ttttcattat gtttattana aaaatatnaa 60  
 tgtntccacn acaaactcatn ttacntnagt aagaggccan ctacattgta caacatacac 120  
 tgagtatatt ttgaaaagga caagtittaaa gtanacncat attgccganc atancacatt 180  
 tatacatggc ttgattgata tttagcacag canaaactga gtgagttacc agaaanaaat 240  
 nataatgtc aatcngattt aagatacaaa acagatccta tggtagatan catcntgtag 300  
 gagttgtggc tttatgttta ctgaaagtca atgcagttcc tgtacaaaga gatggccgta 360  
 agcattctag tacctctact ccatgggttaa gaatcgtaca cttatgttta catatgtnc 420  
 gggtaagaat tgtgttaaagt naanttatgg agaggtccan gagaaaaatt tgatncaa 478

<210> 199  
 <211> 482  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(482)  
 <223> n = A,T,C or G

<400> 199  
 agtgacttgt cctccaacaa aacccttga tcaagtttgt ggcactgaca atcagaccta 60  
 tgctagttcc tgtcatctat tgcgtactaa atgcagactg gaggggacca aaaaggggca 120  
 tcaactccag ctggattatt ttggagcctg caaatctatt cctacttgta cggactttga 180  
 agtgattcag tttcctctac ggatgagaga ctggctcaag aatatcctca tgcagcttta 240  
 tgaagccnac tctgaacacg ctggttatct nagatgagaa ncagagaaat aaagtcnaga 300  
 aaatttacct ggangaaaag aggctttngg ctggggacca tccattgaa ccttctctta 360  
 anggacttta agaanaaact accacatgtn tgtngtatcc tgggtgccngg ccgtttantg 420  
 aacntngacn ncacccttnt ggaatanant cttgacngcn tctgaactt gctcctctgc 480  
 ga 482

<210> 200  
 <211> 270

<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(270)  
<223> n = A,T,C or G

<400> 200  
cggccgcaag tgcaactcca gctggggccg tgcggacgaa gattctgcc a gcagttggtc 60  
cgactgcgac gacggcgccg gcgacagtcg caggtgcagc gcgggcgcct ggggtcttgc 120  
aaggctgagc tgacgccgca gaggtcgtgt cacgtcccac gaccttgacg ccgtcgggga 180  
cagccggaac agagcccggt gaangcggga ggcctcgggg agccctcgg gaagggcgcg 240  
ccgagagata cgcaggtgca ggtggccgcc 270

<210> 201  
<211> 419  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(419)  
<223> n = A,T,C or G

<400> 201  
tttttttttt ttttggaaat tactgcgagc acagcaggtc agcaacaagt ttattttgca 60  
gctagcaagg taacagggtg gggcatgggt acatgttcag gtcaacttcc tttgtcgtgg 120  
ttgattggtt tgtctttatg ggggcggggg ggggtagggg aaancgaagc anaantaaca 180  
tggagtgggt gcacctccc tgtagaacct gggtacnaaa gcttggggca gttcacctgg 240  
tctgtgaccg tcattttctt gacatcaatg ttattagaag tcaggatata ttttagagag 300  
tccactgtnt ctggaggag attagggttt cttgccanaa tccaancaa atccacntga 360  
aaaagttgga tgatncangt acngaatacc ganggcatan ttctcatant cgggtggcca 419

<210> 202  
<211> 509  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(509)  
<223> n = A,T,C or G

<400> 202  
tttntttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60  
tggcacttaa tccattttta tttcaaaatg tctacaaant ttnaatncnc cattatacng 120  
gtnattttnc aaaatctaaa nnttattcaa atntnagcca aantccttac ncaaattnaa 180  
tacnncnaaa aatcaaaaat atacntntct ttcagcaaac ttngttacat aaattaaana 240  
aataatatac gctgggtgtt tcaaagtaca attatcttaa cactgcaaac atnttttnaa 300  
ggaactaaaa taataaaaaa cactnccgca aaggttaaag ggaacaacaa attcntttta 360  
caacancnnc nattataaaa atcatatctc aaatcttagg ggaatatata cttcacacng 420  
ggatcttaac ttttactnca ctttgtttat ttttttanaa ccattgtntt gggcccaaca 480  
caatggnaat nccnccnncn tgactagt 509

<210> 203  
<211> 583  
<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(583)

<223> n = A,T,C or G

<400> 203

tttttttttt	ttttttttga	ccccctctt	ataaaaaaca	agttaccatt	ttattttact	60
tacacatatt	tattttataa	ttggtattag	atattcaaaa	ggcagctttt	aaaatcaaac	120
taaattggaaa	ctgccttaga	tacataattc	ttaggaatta	gcttaaaatc	tgccataaagt	180
gaaaatcttc	tctagctctt	ttgactgtaa	atttttgact	cttgtaaaac	atccaaattc	240
atttttcttg	tctttaaaat	tatctaattc	ttccattttt	tccctattcc	aagtcaattt	300
gcttctctag	cctcatttcc	tagctcttat	ctactattag	taagtggcct	ttttcctaaa	360
agggaaaaaca	ggaagagana	atggcacaca	aaacaaacat	tttatattca	tattttctacc	420
tacgttaata	aaatagcatt	ttgtgaagcc	agctcaaaag	aaggcttaga	tccttttatg	480
tccatttttag	tcactaaacg	atatcnaaag	tgccagaatg	caaaagggtt	gtgaacattt	540
attcaaaagc	taatataaga	tatttcacat	actcatcttt	ctg		583

<210> 204

<211> 589

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(589)

<223> n = A,T,C or G

<400> 204

ttttttttnt	tttttttttt	ttttttntct	tttttttttt	ttganaatga	ggatcgagtt	60
tttcaactct	tagatagggc	atgaagaaaa	ctcatctttc	cagctttaaa	ataacaatca	120
aatctottat	gctatatcat	attttaagtt	aaactaatga	gtcactggct	tatctttctc	180
tgaaggaaat	ctgttcattc	ttctcattca	tatagttata	tcaagtacta	ccttgcatat	240
tgagagggtt	ttcttctcta	tttacacata	tatttccatg	tgaatttgta	tcaaaccctt	300
attttcaatg	aaactagaaa	ataatgtntt	cttttgcata	agagaagaga	acaatatnag	360
cattacaaaa	ctgctcaaat	tgtttggtta	gnttatccat	tataattagt	tnggcaggag	420
ctaatacaaa	tcacattttac	ngacnagcaa	taataaaact	gaagtaccag	ttaaatatcc	480
aaaataatta	aaggaacatt	tttagcctgg	gtataattag	ctaattcact	ttacaagcat	540
ttattnagaa	tgaattcaca	tgttattatt	ccntagccca	acacaatgg		589

<210> 205

<211> 545

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(545)

<223> n = A,T,C or G

<400> 205

ttttnttttt	ttttttcagt	aataatcaga	acaatatatta	tttttatatt	taaaattcat	60
agaaaagtgc	cttacattta	ataaaagttt	gtttctcaaa	gtgatcagag	gaattagata	120
tngtcttgaa	caccaatatt	aatttgagga	aaatacacca	aaatacatta	agtaaattat	180
ttaagatcat	agagcttgta	agtgaagaaga	taaaatttga	cctcagaaac	tctgagcatt	240
aaaaatccac	tattagcaaa	taaattacta	tggacttctt	gctttaattt	tgtgatgaat	300
atgggggtgtc	actggtaaac	caacacattc	tgaaggatac	attacttagt	gatagattct	360

tatgtacttt	gctanatnac	gtggatatga	gttgacaagt	ttctctttct	tcaatctttt	420
aaggggcn	ga	ngaaatgagg	aagaaaagaa	aaggattacg	catactgttc	480
aaggattaga	tatgttttct	ttgccaatat	taaaaaata	ataatgttta	ctactagtga	540
aacc						545

<210> 206  
 <211> 487  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(487)  
 <223> n = A,T,C or G

<400> 206						
tttttttttt	tttttttagtc	aagtttctna	tttttattat	aattaaagtc	ttgggtcattt	60
catttattag	ctctgcaact	tacatattta	aattaaagaa	acgttnttag	acaactgtna	120
caatttataa	atgtaagggtg	ccattattga	gtanatata	tcctccaaga	gtggatgtgt	180
cccttctccc	accaactaat	gaancagcaa	cattagttaa	atatttattag	tagatnatac	240
actgctgcaa	acgctaattc	tcttctccat	ccccatgtng	atattgtgta	tatgtgtgag	300
ttggttagaa	tgcatacanca	atctnacaat	caacagcaag	atgaagctag	gcntgggctt	360
tcggtgaaaa	tagactgtgt	ctgtctgaat	caaatgatct	gacctatcct	cggtggcaag	420
aactcttcga	accgcttcct	caaaggcngc	tgccacattt	gtggcntctn	ttgcacttgt	480
ttcaaaa						487

<210> 207  
 <211> 332  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(332)  
 <223> n = A,T,C or G

<400> 207						
tgaattggct	aaaagactgc	atttttanaa	ctagcaactc	ttattttcttt	ccttttaaaaa	60
tacatagcat	taaatcccaa	atcctattta	aagacctgac	agcttgagaa	ggtcactact	120
gcattttatag	gaccttctgg	tggttctgct	gttacntttg	aantctgaca	atccttgana	180
atctttgcat	gcagaggagg	taaaagggtat	tggattttca	cagaggaana	acacagcgca	240
gaaatgaagg	ggccaggctt	actgagcttg	tccactggag	ggctcatggg	tgggacatgg	300
aaaagaaggc	agcctaggcc	ctggggagcc	ca			332

<210> 208  
 <211> 524  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(524)  
 <223> n = A,T,C or G

<400> 208						
agggcgtggt	gcggaggggcg	ttactgtttt	gtctcagtaa	caataaatac	aaaaagactg	60
gttgtgttcc	ggccccatcc	aaccacgaag	ttgatttctc	ttgtgtgcag	agtgactgat	120
tttaaaggac	atggagcttg	tcacaatgtc	acaatgtcac	agtggtgaagg	gcacactcac	180

tcccgcgtga	ttcacattta	gcaaccaaca	atagctcatg	agtccatact	tgtaaatact	240
tttggcagaa	tacttnttga	aacttgcaga	tgataactaa	gatccaagat	atttcccaaa	300
gtaaatagaa	gtgggtcata	atattaatta	cctgttcaca	tcagcttcca	tttacaagtc	360
atgagcccag	acactgacat	caaactaagc	ccacttagac	tcctcaccac	cagtctgtcc	420
tgtcatcaga	caggaggctg	tcaccttgac	caaattctca	ccagtcaatc	atctatccaa	480
aaaccattac	ctgatccact	tccggtaatg	caccaccttg	gtga		524

<210> 209  
 <211> 159  
 <212> DNA  
 <213> Homo sapien

<400> 209						
gggtgaggaa	atccagagtt	gcatggaga	aaattccagt	gtcagcattc	ttgctccttg	60
tggccctctc	ctacactctg	gccagagata	ccacagtcaa	acctggagcc	aaaaaggaca	120
caaaggactc	tcgacccaaa	ctgccccaga	ccctctcca			159

<210> 210  
 <211> 256  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(256)  
 <223> n = A,T,C or G

<400> 210						
actccctggc	agacaaaggc	agaggagaga	gctctgttag	ttctgtgttg	ttgaactgcc	60
actgaatttc	tttccacttg	gactattaca	tgccanttga	gggactaatg	gaaaaacgta	120
tggggagatt	ttanccaatt	tangtntgta	aatggggaga	ctggggcagg	cgggagagat	180
ttgcaggggtg	naaatgggan	ggctggtttg	ttanatgaac	agggacatag	gaggtaggca	240
ccaggatgct	aatca					256

<210> 211  
 <211> 264  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(264)  
 <223> n = A,T,C or G

<400> 211						
acattgtttt	tttgagataa	agcattgaga	gagctctcct	taacgtgaca	caatggaagg	60
actggaacac	atacccat	ctttgttctg	agggataatt	ttctgataaa	gtcttgctgt	120
atattcaagc	acatatgtta	tatattattc	agttccatgt	ttatagccta	gttaaggaga	180
ggggagatac	attcngaaag	aggactgaaa	gaaatactca	agtnngaaaa	cagaaaaaga	240
aaaaaaggag	caaatgagaa	gcct				264

<210> 212  
 <211> 328  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature

&lt;222&gt; (1)...(328)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 212

acccaaaaat ccaatgctga atatttggct tcattattcc canattcttt gattgtcaaa	60
ggatttaatg ttgtctcagc ttgggcactt cagttaggac ctaaggatgc cagccggcag	120
gtttatatat gcagcaacaa tattcaagcg cgacaacagg ttattgaact tgcccggcag	180
ttnaatttca ttcccattga cttgggatcc ttatcatcag ccagagagat tgaaaattta	240
cccctacnac tctttactct ctgganaggg ccagtggtgg tagctataag cttggccaca	300
tttttttttc ctttattcct ttgtcaga	328

&lt;210&gt; 213

&lt;211&gt; 250

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(250)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 213

acttatgagc agagcgacat atccnagtgt agactgaata aaactgaatt ctctccagtt	60
taaagcattg ctacatgaag ggatagaagt gactgccagg agggaaaagta agccaaggct	120
cattatgcc aagganatat acatttcaat tctccaaact tcttcctcat tccaagagtt	180
ttcaatattt gcatgaacct gctgataanc catgttaana aacaaatata tctctnacct	240
tctcatcggt	250

&lt;210&gt; 214

&lt;211&gt; 444

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(444)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 214

accagaatc caatgctgaa tatttggctt cattattccc agattctttg attgtcaaag	60
gatttaaatg tgtctcagct tgggcacttc agttaggacc taaggatgcc agccggcagg	120
tttatatatg cagcaacaat attcaagcgc gacaacagggt tattgaactt gcccgccagt	180
tgaatttcat tcccattgac ttgggatcct tatcatcagc canagagatt gaaaatttac	240
ccctacgact ctttactctc tggagagggc cagtggtggg agctataagc ttggccacat	300
ttttttttcc tttattcctt tgtcagagat gcgattcatc catatgctan aaaccaacag	360
agtactttt acaaaaattcc tataganatt gtgaataaaa ccttacctat agttgccatt	420
actttgctct ccctaataata cctc	444

&lt;210&gt; 215

&lt;211&gt; 366

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(366)

&lt;223&gt; n = A,T,C or G



<400> 215  
 acttatgagc agagcgacat atccaagtgt anactgaata aaactgaatt ctctccagtt 60  
 taaagcattg ctccactgaag ggatagaagt gactgccagg agggaaagta agccaaggct 120  
 cattatgcc aagganatat acatttcaat tctccaaact tcttcctcat tccaagagtt 180  
 ttcaatatatt gcatgaacct gctgataagc catgttgaga aacaaatata tctctgacct 240  
 tctcatcggg aagcagaggc tgtaggcaac atggaccata gcgaanaaaa aacttagtaa 300  
 tccaagctgt tttctacact gtaaccagggt ttccaaccaa ggtggaaata tctataactt 360  
 ggtgcc 366

<210> 216  
 <211> 260  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(260)  
 <223> n = A,T,C or G

<400> 216  
 ctgtataaac agaactccac tgcangaggg agggccgggc caggagaatc tccgcttgtc 60  
 caagacaggg gcctaaggag ggtctccaca ctgctnntaa gggctnttnc atttttttat 120  
 taataaaaag tnnaaaaggc ctcttctcaa cttttttccc ttnggctgga aaatttaaaa 180  
 atcaaaaatt tcctnaagtt ntcaagctat catatatact ntatcctgaa aaagcaacat 240  
 aattcttcct tccctccttt 260

<210> 217  
 <211> 262  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(262)  
 <223> n = A,T,C or G

<400> 217  
 acctacgtgg gtaagtttan aaatgttata atttcaggaa naggaacgca tataattgta 60  
 tcttgccat aattttctat ttttaataagg aaatagcaaa ttgggggtgg gggaatgtag 120  
 ggcattctac agtttgagca aaatgcaatt aaatgtggaa ggacagcact gaaaaatttt 180  
 atgaataatc tgtatgatta tatgtctcta gagtagattt ataattagcc acttacccta 240  
 atatccttca tgcttgtaaa gt 262

<210> 218  
 <211> 205  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(205)  
 <223> n = A,T,C or G

<400> 218  
 accaaggtgg tgcattaccg gaantggatc aangacacca tcgtggccaa cccctgagca 60  
 cccctatcaa ctcccttttg tagtaaaactt ggaaccttgg aaatgaccag gccaaagactc 120  
 aggctcccc agttctactg acctttgtcc ttangntna ngtccagggt tgctaggaaa 180  
 anaaatcagc agacacagggt gtaaa 205

<210> 219  
 <211> 114  
 <212> DNA  
 <213> Homo sapien

<400> 219  
 tactgttttg tctcagtaac aataaatata aaaagactgg ttgtgttccg gccccatcca 60  
 accacgaagt tgattttctct tgtgtgcaga gtgactgatt ttaaaggaca tgga 114

<210> 220  
 <211> 93  
 <212> DNA  
 <213> Homo sapien

<400> 220  
 actagccagc acaaaaggca gggtagcctg aattgctttc tgctctttac atttctttta 60  
 aaataagcat ttagtgctca gtccctactg agt 93

<210> 221  
 <211> 167  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(167)  
 <223> n = A,T,C or G

<400> 221  
 actangtgca ggtgcgcaca aatatttgtc gatattccct tcattcttga ttccatgagg 60  
 tcttttgccc agcctgtggc tctactgtag taagtctctg ctgatgagga gccagnatgc 120  
 cccccactac cttccctgac gctccccana aatcacccaa cctctgt 167

<210> 222  
 <211> 351  
 <212> DNA  
 <213> Homo sapien

<400> 222  
 agggcgtggt gcgaggggcg gtactgacct cattagtagg aggatgcatt ctggcacccc 60  
 gttcttcacc tgtcccccaa tccttaaaag gccatactgc ataaagtcaa caacagataa 120  
 atgtttgctg aattaaagga tggatgaaaa aaattaataa tgaatttttg cataatccaa 180  
 ttttctcttt tatatttcta gaagaagttt ctttgagcct attagatccc gggaatcttt 240  
 taggtgagca tgattagaga gcttgtaggt tgcttttaca tatatctggc atatttgagt 300  
 ctcgtatcaa aacaatagat tggtaaagggt ggtattattg tattgataag t 351

<210> 223  
 <211> 383  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(383)  
 <223> n = A,T,C or G

<400> 223

aaaacaaaca	aacaaaaaaa	acaattcttc	attcagaaaa	attatcttag	ggactgatat	60
tggttaattat	ggtcaattta	atwrrtrttkt	ggggcatttc	cttacattgt	cttgacaaga	120
ttaaaatgtc	tgtgccaaaa	tttgtatttt	tatttggaga	cttcttatca	aaagtaatgc	180
tgccaaagga	agtctaagga	attagtagtg	ttcccmtcac	ttgtttggag	tgtgctattc	240
taaaagattt	tgatttcctg	gaatgacaat	tatattttaa	ctttggtggg	ggaaanagtt	300
ataggaccac	agtcttcact	tctgatactt	gtaaattaat	cttttattgc	acttgttttg	360
accattaagc	tatatgttta	aaa				383

&lt;210&gt; 224

&lt;211&gt; 320

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 224

cccctgaagg	cttcttggtta	gaaaatagta	cagttacaac	caataggaac	aacaaaaaga	60
aaaagtttgt	gacattgtag	tagggagtg	gtacccctta	ctcccatca	aaaaaaaaat	120
ggatacatgg	ttaaaggata	raagggaat	attttatcat	atgttctaaa	agagaaggaa	180
gagaaaatac	tactttctcr	aatggaagc	ccttaaaggt	gctttgatac	tgaaggacac	240
aatgtggcc	gtccatcctc	ctttaragtt	gcattgacttg	gacacggtaa	ctgttgagc	300
tttaractcm	gcattgtgac					320

&lt;210&gt; 225

&lt;211&gt; 1214

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 225

gaggactgca	gcccgcactc	gcagccctgg	caggcgccac	tggtcatgga	aaacgaattg	60
ttctgctcgg	gcgtcctgg	gcattccgag	tggtgctgt	cagccgcaca	ctgtttccag	120
aactcctaca	ccatcgggt	gggcctgcac	agtcttgagg	ccgaccaaga	gccagggagc	180
cagatggtgg	aggccagcct	ctccgtacgg	caccagaggt	acaacagacc	cttgctcgct	240
aacgacctca	tgctcatcaa	gttgagcga	tccgtgtccg	agtctgacac	catccggagc	300
atcagcattg	cttcgcagtg	ccctaccgcg	gggaactctt	gcctcgtttc	tggctggggg	360
ctgctggcga	acggcagaat	gcctaccgtg	ctgcagtgcg	tgaacgtgtc	ggtgggtgtc	420
gaggaggtct	gcagtaagct	ctatgaccgg	ctgtaccacc	ccagcatgtt	ctgcgccggc	480
ggaggggcaag	accagaagga	ctcctgcaac	ggtgactctg	gggggcccct	gatctgcaac	540
gggtacttgc	agggccttgt	gtctttcgga	aaagccccgt	gtggccaagt	tggcgtgcca	600
ggtgtctaca	ccaacctctg	caaattcact	gagtggatag	agaaaaccgt	ccaggccagt	660
taactctggg	gactgggaac	ccatgaaatt	gacccccaaa	tacatcctgc	ggaagggaatt	720
caggaatatc	tgttcccagc	ccctcctccc	tcaggcccag	gagtcagacc	cccagcccc	780
tcctccctca	aaccaagggt	acagatcccc	agccccctct	ccctcagacc	caggagtcca	840
gacccccag	cccctcctcc	ctcagaccca	ggagtccagc	ccctcctccc	tcagaccccag	900
gagtcagac	ccccagccc	ctcctccctc	agaccaggg	gtccaggccc	ccaacccctc	960
ctccctcaga	ctcagaggtc	caagccccca	acccctcctt	ccccagaccc	agaggtccag	1020
gtcccagccc	ctcctccctc	agaccagcg	gtccaatgcc	acctagactc	tccctgtaca	1080
cagtgcctcc	ttgtggcacg	ttgacccaac	cttaccagtt	ggtttttcat	tttttgtccc	1140
tttcccttag	atccagaaat	aaagtctaag	agaagcgcaa	aaaaaaaaaa	aaaaaaaaaa	1200
aaaaaaaaaa	aaaa					1214

&lt;210&gt; 226

&lt;211&gt; 119

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 226

accagtatg	tgcagggaga	cggaaaccca	tgtgacagcc	cactccacca	gggttcccaa	60
agaacctggc	ccagtcataa	tcattcatcc	tgacagtggc	aataatcacg	ataaccagt	119

<210> 227  
 <211> 818  
 <212> DNA  
 <213> Homo sapien

<400> 227  
 acaattcata gggacgacca atgaggacag ggaatgaacc cggctctccc ccagccctga 60  
 tttttgctac atatgggggtc ccttttcatt ctttgcaaaa acactgggtt ttctgagaac 120  
 acggacgggtt cttagcaciaa tttgtgaaat ctgtgtaraa ccgggctttg caggggagat 180  
 aattttcctc ctctggagga aaggtggtga ttgacaggca gggagacagt gacaaggcta 240  
 gagaaagcca cgctcggcct tctctgaaac aggatggaac ggcagacccc tgaaaacgaa 300  
 gcttgtcccc ttccaatcag ccacttctga gaacccccat ctaacttcct actggaaaag 360  
 agggcctcct caggagcagt ccaagagttt tcaaagataa cgtgacaact accatctaga 420  
 ggaaaggggtg caccctcagc agagaagccg agagcttaac tctggctggt tccagagaca 480  
 acctgctggc tgtcttgga tgcgcccagc ctttgagagg ccactacccc atgaacttct 540  
 gccatccact ggacatgaag ctgaggacac tgggcttcaa cactgagttg tcatgagagg 600  
 gacaggctct gccctcaagc cggtgaggg cagcaaccac tctcctcccc tttctcacgc 660  
 aaagccattc ccacaaatcc agaccatacc atgaagcaac gagacccaaa cagtttggct 720  
 caagaggata tgaggactgt ctgagcctgg ctttgggctg acaccatgca cacacacaag 780  
 gtccacttct aggttttcag cctagatggg agtcgtgt 818

<210> 228  
 <211> 744  
 <212> DNA  
 <213> Homo sapien

<400> 228  
 actggagaca ctggtgaact tgatcaagac ccagaccacc ccaggtctcc ttcgtgggat 60  
 gtcattgacgt ttgacatacc tttggaacga gcctcctcct tggaagatgg aagaccgtgt 120  
 tcgtggccga cctggcctct cctggcctgt ttcttaagat gcggagtcac atttcaatgg 180  
 taggaaaagt ggcttcgtaa aatagaagag cagtcactgt ggaactacca aatggcgaga 240  
 tgctcgggtgc acattgggggt gctttgggat aaaagattta tgagccaact attctctggc 300  
 accagattct aggccagttt gttccactga agcttttccc acagcagtcc acctctgag 360  
 gctggcagct gaattggctt cggtggctc tgtggcaaga tcacactgag atcgatgggt 420  
 gagaaggcta ggatgcttgt ctagtgttct tagctgtcac gttggctcct tccaggttgg 480  
 ccagacgggtg ttggccactc ccttctaaaa cacaggcgcc ctccctggtga cagtgacctg 540  
 ccgtgggtatg cctttggcca ttccagcagt cccagttatg catttcaagt ttggggtttg 600  
 ttcttttctgt taatgttct ctgtgttgtc agctgtcttc atttctctgg ctaagcagca 660  
 ttgggagatg tggaccagag atccactcct taagaaccag tggcgaaaga cactttcttt 720  
 cttcactctg aagtagctgg tgggt 744

<210> 229  
 <211> 300  
 <212> DNA  
 <213> Homo sapien

<400> 229  
 cgagtctggg ttttgtctat aaagtttgat ccctcctttt ctcatccaaa tcatgtgaac 60  
 cattacacat cgaaataaaa gaaaggtggc agacttgccc aacgccaggc tgacatgtgc 120  
 tgcagggttg ttgtttttta attattattg ttgaaaacgt caccacagc ccctgttaat 180  
 ttgtatgtga cagccaactc tgagaaggct ctatttttcc acctgcagag gatccagtct 240  
 cactaggctc ctccttgccc tcacactgga gtctccgcca gtgtgggtgc ccactgacat 300

<210> 230  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 230  
 cagcagaaca aatacaaata tgaagagtgc aaagatctca taaaatctat gctgaggaat 60  
 gagcgacagt tcaaggagga gaagcttgca gagcagctca agcaagctga ggagctcagg 120  
 caatataaag tcttggttca cactcaggaa cgagagctga cccagttaag ggagaagttg 180  
 cgggaaggga gagatgcctc cctctcattg aatgagcatc tccaggecct cctcactccg 240  
 gatgaaccgg acaagtccca ggggcaggac ctccaagaaa cagacctcgg ccgcgaccac 300  
 g 301

<210> 231  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 231  
 gcaagcacgc tggcaaactc ctgtcaggtc agctccagag aagccattag tcatttttagc 60  
 caggaactcc aagtccacat ccttggaac tggggacttg cgcaggttag ccttgaggat 120  
 ggcaacacgg gacttctcat caggaagtgg gatgtagatg agctgatcaa gacggccagg 180  
 tctgaggatg gcaggatcaa tgatgtcagg ccggttggtta ccgccaatga tgaacacatt 240  
 tttttttgtg gacatgccat ccatttctgt caggatctgg ttgatgactc ggtcagcagc 300  
 c 301

<210> 232  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 232  
 agtaggtatt tctgtagaag ttcaacacca aaactggaac atagtctctc ttcaagtgtt 60  
 ggcgacacgc gggcttcctg attctggaat ataactttgt gtaaattaac agccacctat 120  
 agaagagtcc atctgctgtg aaggagagac agagaactct gggttccgtc gtcctgtcca 180  
 cgtgctgtac caagtgtggtg tgccagcctg ttacctgttc tactgaaaa tctggctaata 240  
 gctcttgtgt atcacttctg attctgacaa tcaatcaatc aatggcctag agcactgact 300  
 g 301

<210> 233  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 233  
 atgactgact tcccagtaag gctctctaag gggtaagtag gaggatccac aggattttgag 60  
 atgctaaggc cccagagatc gtttgatcca accctcttat ttccagaggg gaaaatgggg 120  
 cctagaagtt acagagcatc tagctggtgc gctggcacc cttggcctcac acagactccc 180  
 gagtagctgg gactacaggc acacagtcac tgaagcaggc cctgttagca attctatgcg 240  
 tacaaattaa catgagatga gtagagactt tattgagaaa gcaagagaaa atcctatcaa 300  
 c 301

<210> 234  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 234  
 aggtcctaca catcgagact catccatgat tgatatgaat ttaaaaatta caagcaaaga 60  
 cattttattc atcatgatgc tttcttttgt ttcttctttt cgttttcttc tttttctttt 120  
 tcaatttcag caacatactt ctcaatttct tcaggattta aaatcttgag ggattgatct 180  
 cgctcatga cagcaagttc aatgtttttg ccacctgact gaaccacttc caggagtgcc 240  
 ttgatcacca gcttaatggt cagatcatct gcttcaatgg cttcgtcagt atagttcttc 300

t

301

<210> 235  
 <211> 283  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 235

tggggctgtg catcaggcgg gtttgagaaa tattcaattc tcagcagaag ccagaatttg	60
aattccctca tcttttaggg aatcatttac caggtttgga gaggattcag acagctcagg	120
tgctttcact aatgtctctg aacttctgtc cctctttgtt catggatagt ccaataaata	180
atgttatctt tgaactgatg ctcataggag agaataaag aactctgagt gatatacaaca	240
ttagggattc aaagaaatat tagatttaag ctacactgg tca	283

<210> 236  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 236

aggctctcca ccaactgcct gaagcacggt taaaattggg aagaagtata gtgcagcata	60
aatactttta aatcgatcag atttccctaa cccacatgca atcttcttca ccagaagagg	120
tcggagcagc atcattaata ccaagcagaa tgcgtaatag ataaatacaa tggatatatag	180
tgggtagacg gcttcatgag tacagtgtac tgtggtatcg taatctggac ttgggttgta	240
aagcatcgtg taccagtcag aaagcatcaa tactcgacat gaacgaatat aaagaacacc	300
a	301

<210> 237  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 237

cagtggtagt ggtggtggac gtggcggttg tcgtggtgcc ttttttggtg cccgtcacaa	60
actcaatttt tggtcgctcc ttttggcct tttccaattt gtccatctca attttctggg	120
ccttggtctaa tgcctcatag taggagtcct cagaccagcc atggggatca aacatatcct	180
ttgggtagtt ggtgccaagc tcgtcaatgg cacagaatgg atcagcttct cgtaaatcta	240
gggttccgaa attctttctt cctttggata atgtagttca tatccattcc ctccctttatc	300
t	301

<210> 238  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 238

gggcaggttt tttttttttt ttttttgatg gtgcagaccc ttgctttatt tgtctgactt	60
gttcacagtt cagccccctg ctcaaaaaac caacgggcca gctaaggaga ggaggaggca	120
ccttgagact tccggagtcg aggcctctcca gggttcccca gcccatcaat cattttctgc	180
acccccctgc tgggaagcag ctccctgggg ggtgggaatg ggtgactaga agggatttca	240
gtgtgggacc cagggtctgt tcttcacagt aggaggtgga agggatgact aatttcttta	300
t	301

<210> 239  
 <211> 239  
 <212> DNA  
 <213> Homo sapien

<400> 239  
 ataagcagct aggggaattct ttatttagta atgtcctaac ataaaaagttc acataactgc 60  
 ttctgtcaaa ccatgatact gagctttgtg acaaccaga aataactaag agaaggcaaa 120  
 cataatacct tagagatcaa gaaacattta cacagttcaa ctgtttaaaa atagctcaac 180  
 attcagccag tgagtagagt gtgaatgccg gcatacacag tatacaggtc cttcagggg 239

<210> 240  
 <211> 300  
 <212> DNA  
 <213> Homo sapien

<400> 240  
 gggtcctaagt aagcagcagc ttccacattt taacgcaggt ttacgggtgat actgtccttt 60  
 gggatctgcc ctccagtggg accttttaag gaagaagtgg gcccaagcta agttccacat 120  
 gctgggtgag ccagatgact tctgttccct gggtcactttc ttcaatgggg cgaatggggg 180  
 ctgccaggtt tttaaaatca tgcttcatct tgaagcacac gggtcacttca cctcctcac 240  
 gctgtgggtg tactttgatg aaaataccca ctttggttggc ctttctgaag ctataatgtc 300

<210> 241  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 241  
 gaggtctggt gctgaggtct ctgggctagg aagaggaggt ctgtggagct ggaagccaga 60  
 cctctttgga ggaaactcca gcagctatgt tgggtgtctct gagggaatgc aacaaggctg 120  
 ctctccatg tattggaaaa ctgcaactg gactcaactg gaaggaagtg ctgctgccag 180  
 tgtgaagaac cagcctgagg tgacagaaac ggaagcaaac aggaacagcc agtcttttct 240  
 tctctctct gtcatacggg ctctctcaag catcctttgt tgtcaggggc ctaaaaggga 300  
 g 301

<210> 242  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 242  
 ccgaggtcct gggatgcaac caatcactct gtttcacgtg acttttatca ccatacaatt 60  
 tgtggcattt cctcattttc tacattgtag aatcaagagt gtaaataaat gtatatcgat 120  
 gtcttcaaga atatatcatt cctttttcac tagaaccat tcaaatata agtcaagaat 180  
 cttaatatca acaaatatat caagcaaact ggaaggcaga ataactacca taatttagta 240  
 taagtaccca aagttttata aatcaaaagc cctaatagata accattttta gaattcaatc 300  
 a 301

<210> 243  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 243  
 aggtaagtcc cagtttgaag ctcaaaagat ctggtatgag catagggtca tcgacgacat 60  
 ggtggcccaa gctatgaaat cagagggagg cttcatctgg gcctgtaaaa actatgatgg 120  
 tgacgtgcag tcggactctg tggcccaagg gtatggctct ctcggcattg tgaccagcgt 180  
 gctggtttgt ccagatggca agacagtaga agcagagggt gccacaggga ctgtaaccgg 240  
 tcaactaccg atgttcaga aaggacagga gacgtccacc aatccattg cttccatttt 300  
 t 301

<210> 244

<211> 300  
 <212> DNA  
 <213> Homo sapien

<400> 244  
 gctggtttgc aagaatgaaa tgaatgattc tacagctagg acttaacctt gaaatggaaa 60  
 gtcattgcaat cccatttgca ggatctgtct gtgcacatgc ctctgtagag agcagcattc 120  
 ccagggacct tggaaacagt tgacactgta aggtgcttgc tcccccaagac acatcctaaa 180  
 aggtgttgta atggtgaaaa cgtcttcctt ctttattgcc ccttcttatt tatgtgaaca 240  
 actgtttgtc ttttgtgtat cttttttaaa ctgtaaagtt caattgtgaa aatgaatatc 300

<210> 245  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 245  
 gtctgagtat ttaaaatggt attgaaatta tccccaacca atggttagaaa agaaagaggt 60  
 tatatactta gataaaaaat gaggtgaatt actatccatt gaaatcatgc tcttagaatt 120  
 aaggccagga gatattgtca ttaatgtara cttcaggaca ctagagtata gcagccctat 180  
 gttttcaaag agcagagatg caattaaata ttgttttagca tcaaaaaggc cactcaatac 240  
 agctaataaa atgaaagacc taatttctaa agcaattctt tataattttac aaagttttaa 300  
 g 301

<210> 246  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 246  
 ggtctgtcct acaatgcctg cttcttgaaa gaagtcggca ctttctagaa tagctaaata 60  
 acctgggctt attttaaga actatttgta gctcagattg gttttcctat ggctaaaata 120  
 agtgcttctt gtgaaaatta aataaaacag ttaattcaaa gccttgatat atgttaccac 180  
 taacaatcat actaaatata ttttgaagta caaagtttga catgctctaa agtgacaacc 240  
 caaatgtgtc ttacaaaaca cgttcctaac aaggatatgtc ttacactacc aatgcagaaa 300  
 c 301

<210> 247  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 247  
 aggtcctttg gcagggtca tggatcagag ctcaaactgg agggaaaggc atttcgggta 60  
 gcctaagagg ggcactggcg gcagcacaac caaggaaggc aaggttggtt cccccacgct 120  
 gtgtcctgtg ttcagggtgcg acacacaatc ctcatgggaa caggatcacc catgcgctgc 180  
 ccttgatgat caaggttggg gcttaagtgg attaagggag gcaagttctg ggttccttgc 240  
 cttttcaaac catgaagtca ggctctgtat cctcctttt cctaactgat attctaacta 300  
 a 301

<210> 248  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 248  
 aggtccttgg agatgccatt tcagccgaag gactcttctw ttcggaagta caccctcact 60  
 attaggaaga ttcttagggg taatttttct gaggaaggag aactagccaa cttaagaatt 120



acaggaagaa agtgggtttgg aagacagcca aagaaataaa agcagattaa attgtatcag 180  
 gtacattcca gcctgtttggc aactccataa aaacatttca gattttaatc ccgaatttag 240  
 ctaatgagac tggatTTTTTg ttttttatgt tgtgtgtcgc agagctaaaa actcagttcc 300  
 c 301

<210> 249  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 249  
 gtccagagga agcacctggt gctgaactag gcttgccctg ctgtgaactt gcacttggag 60  
 ccctgacgct gctgttctcc ccgaaaaacc cgaccgacct ccgcatctc cgtcccggcc 120  
 ccagggagac acagcagtga ctcagagctg gtcgcacact gtgcctccct cctcaccgcc 180  
 catcgtaatg aattattttg aaaattaatt ccaecatcct ttcagattct ggatggaaag 240  
 actgaatcct tgactcagaa ttgtttgctg aaaagaatga tgtgacttcc ttagtcattt 300  
 a 301

<210> 250  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 250  
 ggtctgtgac aaggacttgc aggctgtggg aggcaagtga cccttaacac tacacttctc 60  
 cttatcttta ttggcttgat aaacataatt atttctaaca ctagcttatt tccagttgcc 120  
 cataagcaca tcagtacttt tctctggctg gaatagtaaa ctaaagtatg gtacatctac 180  
 ctaaaagact actatgtgga ataatacata ctaatgaagt attacatgat ttaaagacta 240  
 caataaaacc aaacatgctt ataacattaa gaaaaacaat aaagatacat gattgaaacc 300  
 a 301

<210> 251  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 251  
 gccgaggtcc tacatttggc ccagtttccc cctgcacccct ctccagggcc cctgcctcat 60  
 agacaacctc atagagcata ggagaactgg ttgccctggg ggcaggggga ctgtctggat 120  
 ggcagggggtc ctcaaaaatg ccactgtcac tgccaggaaa tgcttctgag cagtacacct 180  
 cattggggtc aatgaaaagc ttcaagaaat cttcaggctc actctcttga aggcccggaa 240  
 cctctggagg ggggcagtggt aatcccagct ccaggacgga tcctgtcgaa aagatatcct 300  
 c 301

<210> 252  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 252  
 gcaaccaatc actctgtttc acgtgacttt tatcaccata caatttgtgg catttcctca 60  
 ttttctacat tgtagaatca agagtgtaaa taaatgtata tcgatgtctt caagaatata 120  
 tcatttccttt ttcactagga acccattcaa aatataagtc aagaatctta atatcaacaa 180  
 atatatcaag caaactggaa ggcagaataa ctaccataat ttagtataag tacccaaagt 240  
 tttataaatc aaaagcccta atgataacca tttttagaat tcaatcatca ctgtagaatc 300  
 a 301

<210> 253

<211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 253  
 ttccctaaga agatgttatt ttgttgggtt ttgttccccc tccatctcga ttctcgtacc 60  
 caactaaaaa aaaaaataa agaaaaaatg tgctgcgttc tgaaaaataa ctcccttagct 120  
 tgggtctgatt gttttcagac cttaaaaatat aaacttgttt cacaagcttt aatccatgtg 180  
 gatttttttt cttagagaac cacaaaaacat aaaaggagca agtcggactg aatacctgtt 240  
 tccatagtgc ccacagggtta ttcttcacat tttctccata ggaaaatgct ttttcccaag 300  
 g 301

<210> 254  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 254  
 cgctgcgcct ttccottggg ggaggggcaa ggccagaggg ggtccaagtg cagcacgagg 60  
 aacttgacca attcccttga agcgggtggg ttaaaccctg taaatgggaa caaaatcccc 120  
 ccaaactctt tcatcttacc ctggtggact cctgactgta gaattttttg gttgaaacaa 180  
 gaaaaaataa agcctttgga cttttcaagg ttgcttaaca ggtactgaaa gactggcctc 240  
 acttaaaactg agccaggaaa agctgcagat ttattaatgg gtgtgttagt gtgcagtgcc 300  
 t 301

<210> 255  
 <211> 302  
 <212> DNA  
 <213> Homo sapien

<400> 255  
 agcttttttt tttttttttt tttttttttt ttcattaaaa aatagtgtct tttattataa 60  
 attactgaaa tgtttctttt ctgaatataa atataaatat gtgcaaagtt tgacttgat 120  
 tgggattttt ttgagttctt caagcatctc ctaataccct caagggcctg agtagggggg 180  
 aggaaaaagg actggaggtg gaatctttat aaaaaacaag agtgattgag gcagattgta 240  
 aacattatta aaaaacaaga aacaaacaaa aaaatagaga aaaaaaccac cccaacacac 300  
 aa 302

<210> 256  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 256  
 gttccagaaa acattgaagg tggcttccca aagtctaact agggataccc cctctagcct 60  
 aggaccctcc tccccacacc tcaatccacc aaaccatcca taatgcaccc agataggccc 120  
 acccccacaaa gcctggacac cttgagcaca cagttatgac caggacagac tcatctctat 180  
 aggcaaatag ctgctggcaa actggcatta cctggtttgt ggggatgggg gggcaagtgt 240  
 gtggcctctc ggcctgggta gcaagaacat tcagggttagg cctaagttan tcgtgttagt 300  
 t 301

<210> 257  
 <211> 301

<212> DNA  
<213> Homo sapien

<400> 257  
gttggtggagg aactctggct tgctcattaa gtcctactga ttttcactat cccctgaatt 60  
tccccactta tttttgtctt tcactatcgc aggccttaga agaggtctac ctgcctccag 120  
tcttacctag tccagtctac cccctggagt tagaatggcc atcctgaagt gaaaagtaat 180  
gtcacattac tcccttcagt gatttcttgt agaagtgcc atccctgaat gccaccaaga 240  
tcttaatctt cacatcttta atcttatctc tttgactcct ctttacaccg gagaaggctc 300  
c 301

<210> 258  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(301)  
<223> n = A,T,C or G

<400> 258  
cagcagtagt agatgccgta tgccagcacg cccagcactc ccaggatcag caccagcacc 60  
agggggccag ccaccaggcg cagaagcaag ataaacagta ggctcaagac cagagccacc 120  
cccagggcaa caagaatcca ataccaggac tgggcaaaat cttcaaagat cttaacactg 180  
atgtctcggg cattgaggct gtcaataana cgctgatccc ctgctgtatg gtggtgtcat 240  
tggtgatccc tgggagcgcc ggtggagtaa cgttgggtcca tggaaagcag cgcccacaac 300  
t 301

<210> 259  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(301)  
<223> n = A,T,C or G

<400> 259  
tcatatatgc aaacaaatgc agactangcc tcaggcagag actaaaggac atctcttggg 60  
gtgtcctgaa gtgatttggg cccctgaggg cagacaccta agtaggaatc ccagtgggaa 120  
gcaaagccat aaggaagccc aggattcctt gtgatcagga agtggggccag gaaggtctgt 180  
tccagctcac atctcatctg catgcagcac ggaccggatg cgccactgg gtcttggctt 240  
ccctcccatc ttctcaagca gtgtccttgt tgagccattt gcatccttgg ctccagggtg 300  
c 301

<210> 260  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 260  
tttttttttct ccctaaggaa aaagaaggaa caagtctcat aaaaccaaatt aagcaatggt 60  
aaggtgtctt aacttgaaaa agattaggag tcactggttt acaagttata attgaatgaa 120  
agaactgtaa cagccacagt tggccatttc atgccaatgg cagcaaaca caggattaac 180  
tagggcaaaa taaataagtg tgtggaagcc ctgataagtg cttaataaac agactgattc 240  
actgagacat cagtacctgc ccgggcggcc gctcgagccg aattctgcag atatccatca 300

c

301

<210> 261  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 261  
 aaatattcga gcaaactctg taactaatgt gtctccataa aaggctttga actcagtgaa 60  
 tctgcttcca tccacgattc tagcaatgac ctctcggaca tcaaagctcc tottaagggtt 120  
 agcaccaact attccataca attcatcagc aggaaataaa ggctcttcag aagggttcaat 180  
 ggtgacatcc aatttcttct gataatttag attcctcaca accttcctag ttaagtgaag 240  
 ggcattgatga tcatccaaag cccagtggtc acttactcca gactttctgc aatgaagatc 300  
 a 301

<210> 262  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 262  
 gaggagagcc tgttacagca tttgtaagca cagaatactc caggagtatt tgtaattgtc 60  
 tgtgagcttc ttgccgcaag tctctcagaa atttaaaaag atgcaaatcc ctgagtcacc 120  
 cctagacttc ctaaaccaga tcctctgggg ctggaacctg gcactctgca tttgtaatga 180  
 gggctttctg gtgcacacct aattttgtgc atctttgccc taaatcctgg attagtgcc 240  
 catcattacc cccacattat aatgggatag attcagagca gatactctcc agcaaagaat 300  
 c 301

<210> 263  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 263  
 tttagcttgt ggtaaatgac tcacaaaact gattttaaaa tcaagttaat gtgaattttg 60  
 aaaattacta cttaatccta attcacaata acaatggcat taaggtttga cttgagttgg 120  
 ttcttagtat tatttatggg aaataggctc ttaccacttg caaataactg gccacatcat 180  
 taatgactga cttcccagta aggtctctta aggggtaagt angaggatcc acaggatttg 240  
 agatgctaag gccccagaga tcgtttgatc caaccctctt attttcagag gggaaaatgg 300  
 g 301

<210> 264  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 264  
 aaagacgtta aaccactcta ctaccacttg tggaactctc aaagggtaaa tgacaaascc 60  
 aatgaatgac tctaaaaaca atattttatc ttaatggttt gtagacaata aaaaaacaag 120  
 gtggatagat ctagaattgt aacattttta gaaaaccata scatttgaca gatgagaaag 180  
 ctcaattata gatgcaaagt tataactaaa ctactatagt agtaaagaaa tacatttcac 240  
 acccttcata taaattcact atcttggctt gaggcactcc ataaaatgta tcacgtgcat 300  
 a 301

<210> 265  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 265  
 tgcccaagtt atgtgtaagt gtatccgcac ccagaggtaa aactacactg tcattctttgt 60  
 cttcttgtga cgcagtattt cttctctggg gagaagccgg gaagtcttct cctggctota 120  
 catattcttg gaagtctcta atcaactttt gttccatttg ttctatttct tcaggaggga 180  
 ttttcagttt gtcaacatgt tctctaacia cacttgcca tttctgtaa gaatccaaag 240  
 cagtccaagg ctttgacatg tcaacaacca gcataactag agtatccttc agagatacgg 300  
 c 301

<210> 266  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 266  
 taccgtctgc ccttctctcc atccaggcca tctgcgaatc tacatgggtc ctctattctg 60  
 acaccagatc actctttcct ctaccacacg gcttgctatg agcaagagac acaacctcct 120  
 ctcttctgtg ttccagcttc ttttctgttt cttccacccc cttaagttct attcctgggg 180  
 atagagacac caatacccat aacctctctc ctaagcctcc ttataaccca ggggtgcacag 240  
 cacagactcc tgacaactgg taaggccaat gaactgggag ctcacagctg gctgtgcctg 300  
 a 301

<210> 267  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 267  
 aaagagcaca ggccagctca gcttgccctg gccatctaga ctacgcctgg ctccatgggg 60  
 gttctcagtg ctgagtcctat ccaggaaaag ctacacctaga ctttctgagg ctgaatcttc 120  
 atcctcacag gcagcttctg agagcctgat attcctagcc ttgatgggtc ggagtaaagc 180  
 ctcatctga ttctctctct tcttttcttt caagttggct ttctcacat cctctgttc 240  
 aattcgcttc agcttgtctg ctttagccct catttcacga agcttcttct ctttggcatc 300  
 t 301

<210> 268  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 268  
 aatgtctcac tcaactactt ccagcctac cgtggcctaa ttctgggagt tttcttctta 60  
 gatcttggga gagctgggtc ttctaaggag aaggaggaag gacagatgta actttggatc 120  
 tcgaagagga agtctaattg aagtaattag tcaacgggtc ttgttttagac tcttggaaata 180  
 tgctgggtgg ctacgtgagc ctttttggag aaagcaagta ttattcttaa ggagtaacca 240  
 cttcccatg ttctactttc taccatcctc aattgtatat tatgtattct ttggagaact 300  
 a 301

<210> 269  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 269  
 taacaatata cactagctat ctttttaact gtccatcatt agcaccaatg aagattcaat 60  
 aaaattacct ttattcacac atctcaaaac aattctgcaa attcttagtg aagtttaact 120  
 atagtcacag accttaaata ttcacattgt tttctatgtc tactgaaaat aagttcacta 180  
 cttttctgga tattctttac aaaatcttat taaaattcct ggtattatca cccccaatta 240  
 tacagtagca caaccacctt atgtagtttt tacatgatag ctctgtagaa gtttcacatc 300  
 t 301

<210> 270  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 270  
 cattgaagag cttttgcgaa acatcagaac acaagtgcctt ataaaattaa ttaagcctta 60  
 cacaagaata catattcctt ttatttctaa ggagttaaac atagatgtag ctgatgtgga 120  
 gagcttgctg gtgcagtgca tattggataa cactattcat ggccgaattg atcaagtcaa 180  
 ccaactcctt gaactggatc atcagaagaa ggtggtgca cgatatactg cactagataa 240  
 tggaccaacc aactaaattc tctcaccagg ctgtatcagt aaactggctt aacagaaaac 300  
 a 301

<210> 271  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 271  
 aaaaggttct cataagatta acaatttaaa taaatatttg atagaacatt cttttctcatt 60  
 tttatagctc atcttttaggg ttgatattca gttcatgcctt cccttgctgt tcttgatcca 120  
 gaattgcaat cacttcatca gcctgtattc gctccaattc tctataaagt ggggtccaagg 180  
 tgaaccacag agccacagca cacctctttc ccttggtgac tgcccttcacc ccatganggt 240  
 tctctcctcc agatganaac tgatcatgcg cccacatttt ggggtttata gaagcagtca 300  
 c 301

<210> 272  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 272  
 taaattgcta agccacagat aacaccaatc aaatggaaca aatcactgtc ttcaaagtgc 60  
 ttatcagaaa accaaatgag cctggaatct tcataatacc taaacatgcc gtatttagga 120  
 tccaataatt ccctcatgat gagcaagaaa aattctttgc gcacccctcc tgcattccaca 180  
 gcatcttctc caacaaatat aaccttgagt ggcttcttgt aatctatgtt ctttgttttc 240  
 ctaaggactt ccattgcac tctacaata ttttctctac gcaccactag aattaagcag 300  
 g 301

<210> 273  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>

<221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 273  
 acatgtgtgt atgtgtatct ttgggaaaaa aanaagacat cttgtttayt atttttttgg 60  
 agagangctg ggacatggat aatcacwtaa tttgctayta tyactttaat ctgactygaa 120  
 gaaccgtcta aaaataaaat ttaccatgtc dtatatccct tatagtatgc ttatttcacc 180  
 ttytttctgt ccagagagag tatcagtgac ananatttma ggggtgaamac atgmattggt 240  
 gggacttnty tttacngagm accctgcccg sgcgccctcg makcngantt ccgcsananc 300  
 t 301

<210> 274  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 274  
 cttatatact ctttctcaga ggcaaaagag gagatgggta atgtagacaa ttctttgagg 60  
 aacagtaaat gattattaga gagaangaat ggaccaagga gacagaaatt aacttgtaaa 120  
 tgattctctt tggaatctga atgagatcaa gaggccagct ttagcttggt gaaaagtcca 180  
 tctaggtatg gttgcattct cgtcttcttt tctgcagtag ataatgaggt aaccgaaggc 240  
 aattgtgctt cttttgataa gaagctttct tggatcatatc aggaaattcc aganaaagtc 300  
 c 301

<210> 275  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 275  
 tcggtgtcag cagcacgtgg cattgaacat tgcaatgtgg agcccaaacc acagaaaatg 60  
 gggtgaaatt ggccaacttt ctattaactt atgttggcaa ttttgccacc aacagtaagc 120  
 tggcccttct aataaaagaa aattgaaagg tttctcacta aacggaatta agtagtggag 180  
 tcaagagact ccagggcctc agcgtacctg cccgggcggc cgctcgaagc cgaattctgc 240  
 agatatccat cacactggcg gncgctcgan catgcatcta gaaggnccaa ttcgcacctat 300  
 a 301

<210> 276  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 276  
 tgtacacata ctcaataaat aaatgactgc attgtggtat tattactata ctgattatat 60  
 ttatcatgtg acttctaatt agaaaatgta tccaaaagca aaacagcaga tatacaaaat 120  
 taaagagaca gaagatagac attaacagat aaggcaactt atacattgag aatccaaatc 180  
 caatacattt aaacatttgg gaaatgaggg ggacaaatgg aagccagatc aaatttgtgt 240

aaaactattc agtatgtttc ccttgcttca tgtctgagaa ggctctcctt caatggggat 300  
g 301

<210> 277  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1) ... (301)  
<223> n = A,T,C or G

<400> 277  
tttgttgatg tcagtatttt attacttgcg ttatgagtgc tcacctgga aattctaaag 60  
atacagagga cttggaggaa gcagagcaac tgaatttaat ttaaaagaag gaaaacattg 120  
gaatcatggc actcctgata ctttcccaaa tcaacactct caatgcccc cctcgtcct 180  
caccatagtg gggagactaa agtggccacg gatttgccct angtgtcag tgcgttctga 240  
gttcnctgtc gattacatct gaccagtctc ctttttccga agtcnctccg ttcaatcttg 300  
c 301

<210> 278  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1) ... (301)  
<223> n = A,T,C or G

<400> 278  
taccactaca ctccagcctg ggcaacagag caagacctgt ctcaaagcat aaaatggaat 60  
aacatatcaa atgaaacagg gaaaatgaag ctgacaattt atggaagcca gggcttgtca 120  
cagtctctac tgttattatg cattacctgg gaatttatat aagcccttaa taataatgcc 180  
aatgaacatc tcatgtgtgc tcacaatgtt ctggcactat tataagtgtc tcacaggttt 240  
tatgtgttct tcgtaacttt atggantagg tactcggccg cgaacacgct aagccgaatt 300  
c 301

<210> 279  
<211> 301  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1) ... (301)  
<223> n = A,T,C or G

<400> 279  
aaagcaggaa tgacaaagct tgctttttctg gtatgttcta ggtgtattgt gacttttact 60  
gttatattaa ttgccaatat aagtaaatat agattatata tgtatagtgt ttcacaaagc 120  
ttagaccttt accttcacgc caccacacag tgcttgatat ttcagagtca gtcattgggt 180  
atacatgtgt agttccaaag cacataagct agaanaanaa atatttctag ggagcactac 240  
catctgtttt cacatgaaat gccacacaca tagaactcca acatcaattt cattgcacag 300  
a 301

<210> 280



<211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 280  
 ggtactggag ttttcctccc ctgtgaaaac gtaactactg ttgggagtga attgaggatg 60  
 tagaaagggtg gtggaaccaa attgtgggtca atggaaatag gagaatatgg ttctcactct 120  
 tgagaaaaaa acctaagatt agcccaggta gttgcctgta acttcagttt ttctgcctgg 180  
 gtttgatata gtttaggggtt ggggttagat taagatctaa attacatcag gacaaagaga 240  
 cagactatta actccacagt taattaagga ggtatgttcc atgtttattt gttaaagcag 300  
 t 301

<210> 281  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 281  
 aggtacaaga aggggaatgg gaaagagctg ctgctgtggc attgttcaac ttggatattc 60  
 gccgagcaat ccaaactcctg aatgaagggg catcttctga aaaaggagat ctgaatctca 120  
 atgtggtagc aatggcttta tcgggttata cggatgagaa gaactccctt tggagagaaa 180  
 tgtgtagcac actgcgatta cagctaaata acccgatatt gtgtgtcatg tttgcatttc 240  
 tgacaagtga aacaggatct tacgatggag ttttgtatga aaacaaagtt gcagtacctc 300  
 g 301

<210> 282  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 282  
 cagggtactac agaattaaaa tactgacaag caagtagttt cttggcgtgc acgaattgca 60  
 tccagaaccc aaaaattaag aaattcaaaa agacattttg tgggcacctg ctacacaga 120  
 agcgcagaag caaagcccag gcagaacctat gctaacctta cagctcagcc tgcacagaag 180  
 cgcagaagca aagcccaggc agaacctatg taaccttaca gctcagcctg cacagaagcg 240  
 cagaagcaaa gcccaggcag aacatgctaa ccttacagct cagcctgcac agaagcacag 300  
 a 301

<210> 283  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 283  
 atctgtatac ggcagacaaa ctttatarag tgtagagagg tgagcgaaag gatgcaaaag 60  
 cactttgagg gctttataat aatatgctgc ttgaaaaaaa aaatgtgtag ttgatactca 120  
 gtgcatctcc agacatagta aggggttgct ctgaccaatc aggtgatcat tttttctatc 180  
 acttcccagg ttttatgcaa aaattttgtt aaattctata atgggtgatat gcattcttta 240  
 ggaaacatat acatttttaa aaatctattt tatgtaagaa ctgacagacg aatttgcttt 300  
 g 301

<210> 284  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 284  
 caggtaaaa acgctattaa gtggcttaga atttgaacat ttgtgggtctt tatttacttt 60

```

gcttcgtgtg tgggcaaagc aacatcttcc ctaaatatat attaccaaga aaagcaagaa 120
gcagattagg tttttgacaa aacaaacagg ccaaaagggg gctgacctgg agcagagcat 180
ggtgagaggg aaggcatgag agggcaagtt tgttgtggac agatctgtgc ctactttatt 240
actggagtaa aagaaaacaa agttcattga tgtcgaagga tatatacagt gttagaaatt 300
a 301

```

```

<210> 285
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 285
acatcaccat gatcggatcc cccacccatt atacgttgta tgtttacata aatactcttc 60
aatgatcatt agtgttttaa aaaaaatact gaaaactcct tctgcatccc aatctcctaac 120
caggaaagca aatgctattt acagacctgc aagccctccc tcaaacnaaa ctatttctgg 180
attaaatatg tctgacttct tttgaggtca cagcactagg caaatgctat ttacgatctg 240
caaaagctgt ttgaagagtc aaagccccc a tgtgaacacg atttctggac cctgtaacag 300
t 301

```

```

<210> 286
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 286
taccactgca ttccagcctg ggtgacagag tgagactccg tctccaaaaa aaactttgct 60
tgtatattat ttttgcctta cagtggatca ttctagtagg aaaggacagt aagatttttt 120
atcaaaatgt gtcattgccag taagagatgt tatattcttt tctcatttct tccccaccca 180
aaaataagct accatatagc ttataagtct caaatttttg ccttttacta aaatgtgatt 240
gtttctgttc attgtgtatg cttcatcacc tatatttaggc aaattccatt ttttccttg 300
t 301

```

```

<210> 287
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 287
tacagatctg ggaactaaat attaaaaatg agtgtggctg gatatatgga gaatgttggg 60
cccagaagga acgtagagat cagatattac aacagctttg ttttgagggg tagaaatatg 120
aaatgatttg gttatgaacg cacagtttag gcagcagggc cagaatcctg accctctgcc 180
ccgtggttat ctctcccca gcttggctgc ctcatgttat cacagtattc cattttgttt 240
gttgcattgc ttgtgaagcc atcaagattt tctcgtctgt tttcctctca ttggaatgc 300
t 301

```

```

<210> 288
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 288
gtacacctaa ctgcaaggac agctgaggaa tgtaatgggc agccgctttt aaagaagtag 60
agtcaatagg aagacaaatt ccagttccag ctcagtctgg gtatctgcaa agctgcaaaa 120

```

```

gatcttttaa gacaatttca agagaatatt tccttaaagt tggcaatttg gagatcatat 180
aaaagcatct gcttttgtga ttttaatttag ctcatctggc cactggaaga atccaaacag 240
tctgccttaa ttttgatga atgcatgatg gaaattcaat aatttagaaa gttaaaaaaa 300
a 301

```

```

<210> 289
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 289
ggtacactgt ttccatgtta tgtttctaca cattgctacc tcagtgtcc tggaaactta 60
gcttttgatg tctccaagta gtccaccttc atttaactct ttgaaactgt atcatctttg 120
ccaagtaaga gtggtggcct atttcagctg ctttgacaaa atgactggct cctgacttaa 180
cgttctataa atgaatgtgc tgaagcaaag tgcccatggg ggcggcgaan aagagaaaaga 240
tggttttgt tttggactct ctgtggtccc ttccaatgct gtgggtttcc aaccagnnga 300
a 301

```

```

<210> 290
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 290
acactgagct cttcttgata aatatacaga atgcttggca tatacaagat tctatactac 60
tgactgatct gttcatttct ctcacagctc ttaccccca aagcttttcc accctaagtg 120
ttctgacctc cttttctaata cacagtaggg atagaggcag anccacctac aatgaacatg 180
gagttctatc aagaggcaga aacagcacag aatcccagtt ttaccattcg ctagcagtgc 240
tgccttgaac aaaaacattt ctccatgtct cattttcttc atgcctcaag taacagtgcg 300
a 301

```

```

<210> 291
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 291
caggtaccaa tttcttctat cctagaaaca tttcatttta tgttgttgaa acataacaac 60
tatacagct agattttttt tctatgcttt acctgctatg gaaaatttga cacattctgc 120
tttactcttt tgtttatagg tgaatcacia aatgtatttt tatgtattct gtagtccaat 180
agccatggct gtttacttca ttttaatttat ttagcataaa gacattatga aaaggcctaa 240
acatgagctt cacttcccca ctaactaatt agcatctgtt atttcttaac cgtaatgcct 300
a 301

```

```

<210> 292
<211> 301
<212> DNA
<213> Homo sapien

```

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 292  
 accttttagt agtaatgtct aataataaat aagaaatcaa ttttataagg tccatatagc 60  
 tgtattaaat aatttttaag tttaaaagat aaaataccat catttttaaat gttggtattc 120  
 aaaaccaaag natataaccg aaaggaaaaa cagatgagac ataaaatgat ttgcnagatg 180  
 ggaaatatag tasttyatga atgttnatta aattccagtt ataatagtgg ctacacactc 240  
 tcactacaca cacagacccc acagtcttat atgccacaaa cacatttcca taacttgaaa 300  
 a 301

<210> 293  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 293  
 ggtaccaagt gctgggtgcc gctgtttacc tgtttctcact gaaaagtctg gctaattgctc 60  
 ttgtgtagtc acttctgatt ctgacaatca atcaatcaat ggcttagagc actgactgtt 120  
 aacacaaaacg tcactagcaa agtagcaaca gctttaagtc taaatacaaa gctgtttctgt 180  
 gtgagaattt tttaaaaggc tacttgtata ataacccttg tcattttttaa tgtacctcgg 240  
 ccgcgaccac gctaagccga attctgcaga tatccatcac actggcgggc gctcgagcat 300  
 g 301

<210> 294  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 294  
 tgaccataa caatatacac tagctatctt tttaaactgtc catcattagc accaatgaag 60  
 attcaataaa attaccttta ttcacacatc tcaaaaacaat tctgcaaatt cttagtgaag 120  
 tttaaactata gtcacaganc ttaaattatc acattgtttt ctatgtctac tgaaaataag 180  
 ttcactactt ttctgggata ttctttacaa aatcttatta aaattcctgg tattatcacc 240  
 cccaattata cagtagcaca accaccttat gtagttttta catgatagct ctgtagaggt 300  
 t 301

<210> 295  
 <211> 305  
 <212> DNA  
 <213> Homo sapien

<400> 295  
 gtactctttc tctcccctcc tctgaattta attctttcaa cttgcaattt gcaaggatta 60  
 cacatttcac tgtgatgtat attgtgttgc aaaaaaaaaa gtgtctttgt ttaaaattac 120  
 ttggtttgtg aatccatctt gctttttccc cattggaact agtcattaac ccatctctga 180  
 actggtagaa aaacrtctga agagctagtc tatcagcatc tgacagggtga attggatgg 240  
 tctcagaacc atttcaccca gacagcctgt ttctatcctg ttttaataaat tagtttgggt 300  
 tctct 305

<210> 296  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 296  
 aggtactatg ggaagctgct aaaataatat ttgatagtaa aagtatgtaa tgtgctatct 60  
 cacctagtag taaactaaaa ataaactgaa actttatgga atctgaagtt attttccttg 120  
 attaaataga attaataaac caatatgagg aaacatgaaa ccatgcaatc tactatcaac 180  
 tttgaaaaag tgattgaacg aaccacttag ctttcagatg atgaacactg ataagtcatt 240  
 tgtcattact ataaatttta aaatctgtta ataagatggc ctatagggag gaaaaagggg 300  
 c 301

<210> 297  
 <211> 300  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(300)  
 <223> n = A,T,C or G

<400> 297  
 actgagtttt aactggacgc caagcaggca aggctggaag gttttgctct ctttgtgcta 60  
 aaggttttga aaaccttgaa ggagaatcat tttgacaaga agtacttaag agtctagaga 120  
 acaaagangt gaaccagctg aaagctctcg ggggaanott acatgtgttg ttaggcctgt 180  
 tccatcattg ggagtgcact ggccatccct caaaatttgt ctgggctggc ctgagtggtc 240  
 accgcacctc ggccgcgacc acgctaagcc gaattctgca gatatccatc acactggcgg 300

<210> 298  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(301)  
 <223> n = A,T,C or G

<400> 298  
 tatggggttt gtcacccaaa agctgatgct gagaaaggcc tccctggggc ccctcccgcg 60  
 ggcattctgag agacctggtg ttccagtgtt tctggaaatg ggtcccagtg ccgcgggtg 120  
 tgaagctctc agatcaatca cggaaggcgt ctggcggtgg tggccacctg gaaccaccct 180  
 gtccctgtctg tttacatttc actaycaggt tttctctggg cattacnatt tgttccccta 240  
 caacagtgac ctgtgcattc tgctgtggcc tgctgtgtct gcaggtggct ctcagcgagg 300  
 t 301

<210> 299  
 <211> 301  
 <212> DNA  
 <213> Homo sapien

<400> 299  
 gttttgagac ggagttttcac tcttgttgcc cagactggac tgcaatggca gggctctctgc 60  
 tcaactgcacc ctctgcctcc caggttcgag caattctcct gcctcagcct ccaggttagc 120  
 tgggattgca ggctcacgcc accataccca gctaattttt ttgtatTTTT agtagagacg 180  
 gagtttcgcc atgttgGCCa gctgggtctca aactcctgac ctcaagcgac ctgcctgcct 240

cggcctccca aagtgctgga attataggca tgagtcaaca cgcccagcct aaagatatatt 300  
t 301

<210> 300  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 300  
attcagtttt atttgctgcc ccagtatctg taaccaggag tgccacaaaa ttttgccaga 60  
tatgtccac acccactggg aaaggctccc acctggctac ttctctatc agctgggtca 120  
gtgcattcc acaaggttct cagcctaatt agtttcaacta cctgccagtc tcaaaactta 180  
gtaaagcaag accatgacat tccccacgg aaatcagagt ttgccccacc gtcttggtac 240  
tataaagcct gcctctaaca gtccttgctt cttcacacca atcccgagcg catcccccat 300  
g 301

<210> 301  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 301  
ttaaattttt gagaggataa aaaggacaaa taatctagaa atgtgtcttc ttcagtctgc 60  
agaggacccc aggtctccaa gcaaccacat ggtcaagggc atgaataatt aaaagttggt 120  
gggaactcac aaagaccctc agagctgaga caccacacaac agtgggagct cacaagacc 180  
ctcagagctg agacaccac aacagtggga gtcacaaaag accctcagag ctgagacacc 240  
cacaacagca cctcgttcag ctgccacatg tgtgaataag gatgcaatgt ccagaagtgt 300  
t 301

<210> 302  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 302  
aggtacacat ttagcttgtg gtaaatgact cacaaaaactg attttaaaat caagttaatg 60  
tgaattttga aaattactac ttaatcctaa ttcacaataa caatggcatt aaggtttgac 120  
ttgagttggt tcttagtatt atttatggta aataggctct taccacttgc aaataactgg 180  
ccacatcatt aatgactgac ttcccagtaa ggctctctaa ggggtaagta ggaggatcca 240  
caggatttga gatgctaagg cccagagat cgtttgatcc aaccctctta ttttcagagg 300  
g 301

<210> 303  
<211> 301  
<212> DNA  
<213> Homo sapien

<400> 303  
aggtaccaac tgtggaaata ggtagaggat cattttttct ttccatatca actaagttgt 60  
atattgtttt ttgacagttt aacacatctt cttctgtcag agattctttc acaatagcac 120  
tggctaattg aactaccgct tgcatgttaa aaatgggtgg ttgtgaaatg atcataggcc 180  
agtaacgggt atgtttttct aactgatctt ttgctcgttc caaagggacc tcaagacttc 240  
catcgatttt atatctgggg tctagaaaag gagttaatct gttttccctc ataaattcac 300  
c 301

<210> 304  
<211> 301  
<212> DNA

<213> Homo sapien

<400> 304

acatggatgt	tattttgcag	actgtcaacc	tgaatttgta	tttgcttgac	attgcctaata	60
tattagtttc	agtttcagct	taccacattt	ttgtctgcaa	catgcaraas	agacagtgcc	120
cttttttagtg	tatcatatca	ggaatcatct	cacattgggt	tgtgccatta	ctgggtgcagt	180
gactttcagc	cacttgggta	aggtggagtt	ggccatatgt	ctccactgca	aaattactga	240
ttttcctttt	gtaattaata	agtgtgtgtg	tgaagattct	ttgagatgag	gtatataatct	300
c						301

<210> 305

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 305

gangtacagc	gtgggtcaagg	taacaagaag	aaaaaaatgt	gagtggcatc	ctgggatgag	60
caggggggaca	gacctggaca	gacacgttgt	catttgctgc	tgtgggtagg	aaaatgggag	120
taaaggagga	gaaacagata	caaaatctcc	aactcagtat	taaggatttc	tcatgcctag	180
aattattgga	gaaacaagaa	tacattcata	tggcaaataa	ctaaccatgg	tggaaacaaa	240
ttctgggatt	taagttggat	accaangaaa	ttgtattaaa	agagctgttc	atggaataag	300
a						301

<210> 306

<211> 8

<212> PRT

<213> Homo sapien

<400> 306

Val Leu Gly Trp Val Ala Glu Leu

1

5

<210> 307

<211> 637

<212> DNA

<213> Homo sapien

<400> 307

acagggratg	aagggaagg	gagaggatga	ggaagcccc	ctggggattt	ggtttggtcc	60
ttgtgatcag	gtgggtctatg	gggttatcc	ctacaaagaa	gaatccagaa	ataggggcac	120
attgaggaat	gatacttgag	cccaaagagc	attcaatcat	tgttttat	gccttmtttt	180
cacaccattg	gtgaggagg	gattaccacc	ctgggggtat	gaagatgggt	gaacacccca	240
cacatagcac	cggagatatg	agatcaacag	tttcttagcc	atagagattc	acagcccaga	300
gcaggaggac	gcttgacac	catgcaggat	gacatggggg	atgcgctcgg	gattgggtgtg	360
aagaagcaag	gactgttaga	ggcaggcttt	atagtaacaa	gacggtgggg	caaactctga	420
tttccgtggg	ggaatgtcat	ggtcttgctt	tactaagttt	tgagactggc	aggtagtgaa	480
actcattagg	ctgagaacct	tgtggaatgc	acttgaccca	setgatagag	gaagtagcca	540
ggtgggagcc	tttcccagtg	ggtgtgggac	atatctggca	agattttgtg	gcactcctgg	600
ttacagatac	tggggcagca	aataaaactg	aattcttg			637

<210> 308

<211> 647

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(647)

<223> n = A,T,C or G

<400> 308

acgattttca	ttatcatgta	aatcgggtca	ctcaaggggc	caaccacagc	tgggagccac	60
tgctcagggg	aaggttcata	tgggactttc	tactgcccac	ggttctatac	aggatataaa	120
ggngcctcac	agtatagatc	tggtagcaaa	gaagaagaaa	caaacactga	tctctttctg	180
ccacccctct	gacccttttg	aactcctctg	accctttaga	acaagcctac	ctaatatctg	240
ctagagaaaa	gaccaacaac	ggcctcaaag	gatctcttac	catgaaggtc	tcagctaatt	300
cttggttaag	atgtgggttc	cacattaggt	tctgaatatg	gggggaaggg	tcaatttgct	360
catttttgtg	gtggataaag	tcaggatgcc	caggggccag	agcagggggc	tgcttgcttt	420
gggaacaatg	gctgagcata	taacctatag	ttatggggaa	caaaacaaca	tcaaagtcac	480
tgtatcaatt	gccatgaaga	cttgagggac	ctgaatctac	cgattcatct	taaggcagca	540
ggaccagttt	gagtggcaac	aatgcagcag	cagaatcaat	ggaaacaaca	gaatgattgc	600
aatgtccttt	ttttctcct	gcttctgact	tgataaaagg	ggaccgt		647

<210> 309

<211> 460

<212> DNA

<213> Homo sapien

<400> 309

actttatagt	ttaggctgga	cattggaaaa	aaaaaaaaagc	cagaacaaca	tgtgatagat	60
aatatgattg	gctgcacact	tccagactga	tgaatgatga	acgtgatgga	ctattgtatg	120
gagcacatct	tcagcaagag	ggggaaatac	tcattcatttt	tggccagcag	ttgtttgatc	180
accaaaccatc	atgccagaat	actcagcaaa	ccttcttagc	tcttgagaag	tcaaagtccg	240
ggggaattta	ttcctggcaa	ttttaattgg	actccttatg	tgagagcagc	ggctaccacg	300
ctggggtggt	ggagcgaaac	cgtcactagt	ggacatgcag	tggcagagct	cctggtaacc	360
acctagagga	atacacaggc	acatgtgtga	tgccaagcgt	gacacctgta	gcactcaaat	420
ttgtcttggt	tttgtctttc	ggtgtgtaag	attcttaagt			460

<210> 310

<211> 539

<212> DNA

<213> Homo sapien

<400> 310

acgggactta	tcaaataaag	ataggaaaag	aagaaaactc	aaatattata	ggcagaaatg	60
ctaaagggtt	taaaatatgt	caggattgga	agaaggcatg	gataaagaac	aaagttcagt	120
taggaaagag	aaacacagaa	ggaagagaca	caataaaagt	cattatgtat	tctgtgagaa	180
gtcagacagt	aagattttgt	ggaaatgggt	tggtttgttg	tatggtatgt	attttagcaa	240
taatctttat	ggcagagaaa	gctaaaatcc	tttagcttgc	gtgaatgatc	acttgctgaa	300
ttcctcaagg	taggcatgat	gaaggagggt	ttagaggaga	cacagacaca	atgaactgac	360
ctagatagaa	agccttagta	tactcagcta	ggaatagtga	ttctgagggc	acactgtgac	420
atgattatgt	cattacatgt	atggtagtga	tggggatgat	aggaaggaag	aacttatggc	480
atattttcac	ccccacaaaa	gtcagttaaa	tattgggaca	ctaaccatcc	aggtcaaga	539

<210> 311

<211> 526

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature



<222> (1)...(526)

<223> n = A,T,C or G

<400> 311

caaatttgag	ccaatgacat	agaattttac	aatcaagaa	gcttattctg	gggccatttc	60
ttttgacgtt	ttctctaaac	tactaaagag	gcattaatga	tccataaatt	atattatcta	120
catttacagc	atttaaaatg	tggtcagcat	gaaatattag	ctacagggga	agctaaataa	180
attaacatg	gaataaagat	ttgtccttaa	atataatcta	caagaagact	ttgatatttg	240
tttttcacaa	gtgaagcatt	cttataaagt	gtcataacct	ttttggggaa	actatgggaa	300
aaaatgggga	aactctgaag	ggttttaagt	atcttacctg	aagctacaga	ctccataacc	360
tctctttaca	gggagctcct	gcagccccta	cagaaatgag	tggtgagat	tcttgattgc	420
acagcaagag	cttctcatct	aaaccctttc	cctttttagt	atctgtgtat	caagtataaa	480
agttctataa	actgtagtnt	acttatttta	atccccaaag	cacagt		526

<210> 312

<211> 500

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(500)

<223> n = A,T,C or G

<400> 312

cctctctctc	cccaccccct	gactctagag	aactgggttt	tctccagta	ctccagcaat	60
tcattttctga	aagcagttga	gccactttat	tccaaagtac	actgcagatg	ttcaaactct	120
ccattttctct	ttcccttcca	cctgccagtt	ttgctgactc	tcaacttgct	atgagtgtaa	180
gcattaagga	cattatgctt	cttcgattct	gaagacaggc	cctgctcatg	gatgactctg	240
gcttcttagg	aaaatatattt	tcttccaaaa	tcagtaggaa	atctaaactt	atccctctt	300
tgcagatgtc	tagcagcttc	agacatttgg	ttaagaacct	atgggaaaaa	aaaaaatcct	360
tgctaagtgt	gtttcctttg	taaaccanga	ttcttatttg	nctggtagat	aatatcagct	420
ctgaacgtgt	ggtaaagatt	tttggtttg	aatataggag	aatcagttt	gctgaaaagt	480
tagtcttaat	tatctattgg					500

<210> 313

<211> 718

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(718)

<223> n = A,T,C or G

<400> 313

ggagatttgt	gtggtttgca	gccgagggag	accaggaaga	totgcatggt	gggaaggacc	60
tgatgataca	gaggtgagaa	ataagaaagg	ctgctgactt	taccatctga	ggccacacat	120
ctgctgaaat	ggagataaatt	aacatcacta	gaaacagcaa	gatgacaata	taatgtctaa	180
gtagtacat	gtttttgcac	atttccagcc	cttttaata	tccacacaca	caggaagcac	240
aaaaggaagc	acagagatcc	ctgggagaaa	tgcccgccg	ccatcttggg	tcatcgatga	300
gcctcgccct	gtgcctgntc	ccgcttggtga	gggaaggaca	ttagaaaatg	aattgatgtg	360
ttccttaaag	gatggcagga	aaacagatcc	tggtgtggat	atttatttga	acgggattac	420
agatttgaaa	tgaagtcaca	aagtgagcat	taccaatgag	aggaaaacag	acgagaaaat	480
cttgatgggt	cacaagacat	gcaacaaaca	aatggaata	ctgtgatgac	acgagcagcc	540
aactggggag	gagataccac	ggggcagagg	tcaggattct	ggccctgctg	cctaactgtg	600
cgttatacca	atcattttcta	tttctaccct	caaacaagct	gtngaataac	tgacttacgg	660
ttcttntggc	ccacattttc	atnatccacc	ccntentttt	aannttantc	caaantgt	718

<210> 314  
 <211> 358  
 <212> DNA  
 <213> Homo sapien

<400> 314  
 gtttattttac attacagaaa aaacatcaag acaatgtata ctattttcaaa tatatccata 60  
 cataatcaaa tatagctgta gtacatgttt tcattgggtgt agattaccac aaatgcaagg 120  
 caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg tgtagtccaa 180  
 gctctcggtg gtccagccac tgtgaaacat gctcccttta gattaacctc gtggacgctc 240  
 ttgttgattt gctgaactgt agtgccctgt attttgcttc tgtctgtgaa ttctgttgct 300  
 tctggggcat ttccttggtg tgcagaggac caccacacag atgacagcaa tctgaatt 358

<210> 315  
 <211> 341  
 <212> DNA  
 <213> Homo sapien

<400> 315  
 taccacctcc ccgctggcac tgatgagccg catcaccatg gtcaccagca ccatgaaggc 60  
 ataggtgatg atgaggacat ggaatgggcc cccaaggatg gtctgtccaa agaagcgagt 120  
 gacccccatt ctgaagatgt ctggaacctc taccagcagg atgatgatag cccaatgac 180  
 agtcaccagc tccccgacca gccggatata gtccttaggg gtcattgtagg ctctctgaag 240  
 tagcttctgc tgtaagaggg tgttgctccg ggggctcgtg cggttattgg tctggggctt 300  
 gagggggcgg tagatgcagc acatggtgaa gcagatgatg t 341

<210> 316  
 <211> 151  
 <212> DNA  
 <213> Homo sapien

<400> 316  
 agactgggca agactcttac gcccacact gcaatttggt cttgttgccg tatccattta 60  
 tgtgggcctt tctcgagttt ctgattataa acaccactgg agcgatgtgt tgactggact 120  
 cattcagga gctctggttg caatattagt t 151

<210> 317  
 <211> 151  
 <212> DNA  
 <213> Homo sapien

<400> 317  
 agaactagtg gatacctaag aaataacctga aacatatatt ggcatttatc aatggctcaa 60  
 atcttcattt atctctggcc ttaacctgg ctctgaggc tgccggccagc agatcccagg 120  
 ccagggtctt gttcttgcca cacctgcttg a 151

<210> 318  
 <211> 151  
 <212> DNA  
 <213> Homo sapien

<400> 318  
 actggtggga ggcgctgttt agttggctgt ttccagaggg gtcttttcgga gggacctcct 60  
 gctgcaggct ggagtgtctt tattcctggc gggagaccgc acattccact gctgaggctg 120  
 tgggggacgt ttatcaggca gtgataaaca t 151

<210> 319

<211> 151  
 <212> DNA  
 <213> Homo sapien

<400> 319  
 aactagtggg tccagagcta taggtacagt gtgatctcag ctttgcaaac acattttcta 60  
 catagatagt actaggtatt aatagatatg taaagaaaga aatcacacca ttaataatgg 120  
 taagattggg tttatgtgat tttagtgggt a 151

<210> 320  
 <211> 150  
 <212> DNA  
 <213> Homo sapien

<400> 320  
 aactagtggg tccactagtc cagtgtgggt gaattccatt gtgttggggg tctagatcgc 60  
 gagcggtgc cctttttttt tttttttttg ggggggaatt tttttttttt aatagttatt 120  
 gagtgttcta cagcttacag taaataccat 150

<210> 321  
 <211> 151  
 <212> DNA  
 <213> Homo sapien

<400> 321  
 agcaactttg tttttcatcc aggttatattt aggttagga tttcctctca cactgcagtt 60  
 tagggtggca ttgtaaccag ctatggcata ggtgttaacc aaaggctgag taaacatggg 120  
 tgccctctgag aaatcaaagt cttcatacac t 151

<210> 322  
 <211> 151  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(151)  
 <223> n = A,T,C or G

<400> 322  
 atccagcadc ttctcctggt tcttgccctc ctttttcttc ttcttasatt ctgcttgagg 60  
 tttgggcttg gtcagtttgc cacagggctt ggagatgggt acagtcttct ggcattcggc 120  
 attgtgcagg gctcgcttca nacttccagt t 151

<210> 323  
 <211> 151  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(151)  
 <223> n = A,T,C or G

<400> 323  
 tgaggacttg tkttcttttt ctttatattt aatcctctta ctttgtaa atattgccta 60  
 nagactcant tactaccag tttgtgggtt twtgggagaa atgtaactgg acagttagct 120  
 gttcaatyaa aaagacactt ancccatgtg g 151

<210> 324  
 <211> 461  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(461)  
 <223> n = A,T,C or G

<400> 324  
 acctgtgtgg aatttcagct ttccatcatgc aaaaggattt tgtatccccg gcctacttga 60  
 agaagtgggc agctaaagga atccagggtt ttgggtggac tgtaataacc tttgatgaaa 120  
 agagttacta cgaatcccat ctgggttcca gctatatcac tgacagcatg gtagaagact 180  
 gcgaacctca cttctagact ttcacgggtg gacgaaacgg gttcagaaac tgccaggggc 240  
 ctcatcacagg gatatacaaaa taccctttgt gctaccacagg ccctgggggaa tcagggtgact 300  
 cacacaaatg caatagttgg tcaactgcatt tttacctgaa ccaaagctaa acccgggtgtt 360  
 gccaccatgc accatggcat gccagagttc aacactgttg ctcttgaaaa ttgggtctga 420  
 aaaaacgcac aagagcccct gccctgccct agctgangca c 461

<210> 325  
 <211> 400  
 <212> DNA  
 <213> Homo sapien

<400> 325  
 aaactgtttc catgttatgt ttctacacat tgctacctca gtgctcctgg aaacttagct 60  
 tttgatgtct ccaagtagtc caccttcatt taactctttg aaactgtatc atctttgcca 120  
 agtaagagtg gtggcctatt tcagctgctt tgacaaaatg actggctcct gacttaacgt 180  
 tctataaatg aatgtgctga agcaaagtgc ccatggtggc ggcaagaag agaaagatgt 240  
 gttttgtttt ggactctctg tgggtccctc caatgctgtg gggtttccaa caggggaagg 300  
 gtcccttttg cattgccaaag tgccataacc atgagcacta cgctaccatg gttctgcctc 360  
 ctggccaagc aggtctggtt gcaagaatga aatgaatgat 400

<210> 326  
 <211> 1215  
 <212> DNA  
 <213> Homo sapien

<400> 326  
 ggaggactgc agcccgcact cgcagccctg gcaggcggca ctggtcatgg aaaacgaatt 60  
 gttctgctcg ggcgtcctgg tgcacccgca gtgggtgctg tcagccgcac actgtttcca 120  
 gaactcctac accatcgggc tgggcctgca cagtcttgag gccgaccaag agccaggag 180  
 ccagatgggtg gaggccagcc tctccgtacg gcacccagag tacaacagac ccttgctcgc 240  
 taacgacctc atgctcatca agttggacga atccgtgtcc gactctgaca ccatccggag 300  
 catcagcatt gcttcgcagt gccctaccgc ggggaactct tgectcgttt ctggctgggg 360  
 tctgctggcg aacggcagaa tgectaccgt gctgcagtgc gtgaacgtgt cgggtggtgtc 420  
 tgaggaggtc tgacgtaagc tctatgacct gctgtaccac ccagcatgt tctgcgccgg 480  
 cggaggggca gaccagaagg actcctgcaa cgggtgactc ggggggcccc tgatctgcaa 540  
 cgggtacttg cagggccttg tgtctttcgg aaaagccccg tgtggccaag ttggcgtgcc 600  
 aggtgtctac accaaccctc gcaaattcac tgagtggata gagaaaaccg tccaggccag 660  
 ttaactctgg ggaactgggaa cccatgaaat tgacccccaa atacatcctg cggaaggaa 720  
 tcaggaatat ctgttcccag cccctcctcc ctccaggcca ggagtccagg ccccagccc 780  
 ctctccctc aaaccaaggg tacagatccc cageccctcc tccctcagac ccaggagtcc 840  
 agacccccca gccctcctc cctcagacct aggagtccag cccctcctcc ctccagacca 900  
 ggagtccaga cccccagcc cctcctcctc cagaccaggg ggtccaggcc cccaaccct 960  
 cctccctcag actcagaggt ccaagcccc aaccctcct tcccagacc cagaggtcca 1020

```

gggtcccagcc cctcctccct cagaccacgc ggtccaatgc cacctagact ctccctgtac 1080
acagtgcgcc cttgtggcac gttgacccaa ccttaccagt tggtttttca tttttgtcc 1140
ctttcccta gatccagaaa taaagtctaa gagaagcgca aaaaaaaaaa aaaaaaaaaa 1200
aaaaaaaaa aaaaaa 1215

```

<210> 327  
 <211> 220  
 <212> PRT  
 <213> Homo sapien

<400> 327

```

Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met
1      5      10      15
Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
20     25     30
Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly
35     40     45
Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu
50     55     60
Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala
65     70     75     80
Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp
85     90     95
Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn
100    105    110
Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro
115    120    125
Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu Val Cys
130    135    140
Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly
145    150    155    160
Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro
165    170    175
Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala
180    185    190
Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys
195    200    205
Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
210    215    220

```

<210> 328  
 <211> 234  
 <212> DNA  
 <213> Homo sapien

<400> 328

```

cgctcgtctc tggtagctgc agccaaatca taaacggcga ggactgcagc ccgcactcgc 60
agccctggca ggcggcactg gtcattgaaa acgaattgtt ctgctcgggc gtcctgggtgc 120
atccgcagtg ggtgctgtca gccacacact gtttccagaa ctctacacc atcgggctgg 180
gcctgcacag tcttgaggcc gaccaagagc caggagacca gatggtggag gcca 234

```

<210> 329  
 <211> 77  
 <212> PRT  
 <213> Homo sapien

<400> 329

```

Leu Val Ser Gly Ser Cys Ser Gln Ile Ile Asn Gly Glu Asp Cys Ser

```

1	5	10	15
Pro His Ser Gln	Pro Trp Gln Ala	Ala Leu Val Met Glu Asn	Glu Leu
20	25	30	
Phe Cys Ser Gly	Val Leu Val His	Pro Gln Trp Val	Leu Ser Ala Thr
35	40	45	
His Cys Phe Gln	Asn Ser Tyr Thr	Ile Gly Leu Gly	Leu His Ser Leu
50	55	60	
Glu Ala Asp Gln	Glu Pro Gly Ser	Gln Met Val	Glu Ala
65	70	75	

<210> 330  
 <211> 70  
 <212> DNA  
 <213> Homo sapien

<400> 330  
 cccaacacaa tggcccgatc ccatccctga ctccgccctc aggatcgctc gtctctggta 60  
 gctgcagcca 70

<210> 331  
 <211> 22  
 <212> PRT  
 <213> Homo sapien

<400> 331  
 Gln His Asn Gly Pro Ile Pro Ser Leu Thr Pro Pro Ser Gly Ser Leu  
 1 5 10 15  
 Val Ser Gly Ser Cys Ser  
 20

<210> 332  
 <211> 2507  
 <212> DNA  
 <213> Homo sapien

<400> 332  
 tgggtgcgct gcagccggca gagatggttg agctcatgtt cccgctgttg ctccctccttc 60  
 tgcccttcct tctgtatatg gctgcgcccc aaatcaggaa aatgctgtcc agtgggggtgt 120  
 gtacatcaac tgttcagctt cctgggaaag tagttgtggt cacaggagct aatacaggta 180  
 tcgggaagga gacagccaaa gagctggctc agagaggagc tcgagtatat ttagcttgcc 240  
 gggatgtgga aaagggggaa ttggtggcca aagagatcca gaccacgaca gggaaccagc 300  
 aggtgttggg gcggaaactg gacctgtctg atactaagtc tattcgagct tttgctaagg 360  
 gcttcttagc tgaggaaaag cacctccacg ttttgatcaa caatgcagga gtgatgatgt 420  
 gtccgtactc gaagacagca gatggctttg agatgcacat aggagtcaac cacttgggtc 480  
 acttcctcct aacccatctg ctgctagaga aactaaagga atcagcccca tcaaggatag 540  
 taaatgtgtc ttccctcgca catcacctgg gaaggatcca ctcccataac ctgcagggcg 600  
 agaaattcta caatgcaggc ctggcctact gtcacagcaa gctagccaac atcctcttca 660  
 cccaggaact ggcccggaaga ctaaaaggct ctggcggttac gacgtattct gtacaccctg 720  
 gcacagtcca atctgaactg gttcggcact catctttcat gagatggatg tgggtggcttt 780  
 tctccttttt catcaagact cctcagcagg gagcccagac cagcctgcac tgtgccttaa 840  
 cagaagggtct tgagattcta agtgggaatc atttcagtga ctgtcatgtg gcatgggtct 900  
 ctgcccgaagc tcgtaatgag actatagcaa ggcggctgtg ggacgtcagt tgtgacctgc 960  
 tgggcctccc aatagactaa caggcagtgc cagttggacc caagagaaga ctgcagcaga 1020  
 ctacacagta cttcttgtca aaatgattct ccttcaagggt tttcaaaacc tttagcacia 1080  
 agagagcaaa accttcagc cttgcctgct tgggtgtccag ttaaaactca gtgtactgcc 1140  
 agattcgtct aaatgtctgt catgtccaga tttactttgc ttctgttact gccagagtta 1200  
 ctagagatat cataatagga taagaagacc ctcatatgac ctgcacagct cattttcctt 1260  
 ctgaaagaaa ctactaccta ggagaatcta agctatagca gggatgattt atgcaaatth 1320

gaactagctt	ctttgttcac	aattcagttc	ctcccaacca	accagtcttc	acttcaagag	1380
ggccacactg	caacctcagc	ttaacatgaa	taacaaagac	tggctcagga	gcagggcttg	1440
cccaggcatg	gtggatcacc	ggagggtcagt	agttcaagac	cagcctggcc	aacatgggtga	1500
aaccccacct	ctactaaaaa	ttgtgtatat	ctttgtgtgt	cttcctgttt	atgtgtgcca	1560
agggagtatt	ttcacaaagt	tcaaaacagc	cacaataatc	agagatggag	caaaccagtg	1620
ccatccagtc	tttatgcaaa	tgaatgctg	caaagggaag	cagattctgt	atatgttggt	1680
aactaccac	caagagcaca	tgggtagcag	ggaagaagta	aaaaaagaga	aggagaatac	1740
tggaagataa	tgcacaaaat	gaagggacta	gttaaggatt	aactagccct	ttaaggatta	1800
actagttaag	gattaatagc	aaaagayatt	aaatatgcta	acatagctat	ggaggaattg	1860
agggcaagca	cccaggactg	atgaggctct	aacaaaaacc	agtgtggcaa	aaaaaaaaaa	1920
aaaaaaaaaa	aaaaatccta	aaaacaaaca	aacaaaaaaa	acaattcttc	attcagaaaa	1980
attatcttag	ggactgatat	tggttaattat	ggtcaattta	ataatatttt	ggggcatttc	2040
cttacattgt	cttgacaaga	ttaaaatgtc	tgtgccaaaa	ttttgtattt	tatttgagaga	2100
cttccttatca	aaagtaatgc	tgccaaagga	agtctaagga	attagtagtg	ttcccatcac	2160
ttgtttggag	tgtgctattc	taaaagattt	tgatttcctg	gaatgacaat	tatattttaa	2220
ctttggtggg	ggaaagagtt	ataggaccac	agtcttcact	tctgatactt	gtaaattaat	2280
cttttattgc	acttgttttg	accattaagc	tatatgttta	gaaatggtca	ttttacggaa	2340
aaattagaaa	aattctgata	atagtgcaga	ataaatgaat	taatgtttta	cttaatttat	2400
attgaactgt	caatgacaaa	taaaaattct	ttttgattat	ttttgtttt	catttaccag	2460
aataaaaacg	taagaattaa	aagtttgatt	acaaaaaaa	aaaaaaa		2507

&lt;210&gt; 333

&lt;211&gt; 3030

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 333

gcaggcgact	tgcgagctgg	gagcgattta	aaacgctttg	gattcccccg	gcctgggtgg	60
ggagagcgag	ctgggtgcc	cctagattcc	ccgccccgc	acctcatgag	ccgaccctcg	120
gctccatgga	gcccggcaat	tatgccacct	tggatggagc	caaggataac	gaaggcttgc	180
tgggagcggg	agggggcg	aatctggtcg	cccactcccc	tctgaccagc	caccagcgg	240
cgcctaogct	gatgcctgct	gtcaactatg	cccccttggg	tctgccaggc	tcggcgagc	300
cgccaaagca	atgccaccca	tgccctgggg	tgccccaggg	gacgtcccca	gctcccgtgc	360
cttatggtta	ctttggaggc	gggtactact	cctgccgagt	gtcccggagc	tcgctgaaac	420
cctgtgcccc	ggcagccacc	ctggccgcgt	accccgcgga	gactcccacg	gccggggaag	480
agtacccag	ycgccccact	gagtttgct	tctatccggg	atatccggga	acctaccagc	540
ctatggccag	ttacctggac	gtgtctgtgg	tgcagactct	gggtgctcct	ggagaaccgc	600
gacatgactc	cctgttgct	gtggacagtt	accagtcttg	ggctctcgct	ggtggctgga	660
acagccagat	gtgttgccag	ggagaacaga	accaccagg	tcccttttgg	aaggcagcat	720
ttgcagactc	cagcgggcag	cacctctctg	acgcctgcgc	ctttcgtcgc	ggccgcaaga	780
aacgcattcc	gtacagcaag	gggcagttgc	gggagctgga	gcgggagtat	gcggctaaca	840
agttcatcac	caaggacaag	aggcgcaaga	tctcggcagc	caccagcctc	tcggagcgcc	900
agattaccat	ctggtttcag	aaccgcggg	tcaaagagaa	gaaggttctc	gccaaggtga	960
agaacagcgc	tacccttaaa	gagatctcct	tgccctgggtg	ggaggagcga	aagtgggggt	1020
gtcctgggga	gaccaggaac	ctgccaaagc	caggctgggg	ccaaggactc	tgctgagagg	1080
ccctagaga	caacaccctt	cccaggccac	tggctgctgg	actgttcctc	aggagcggcc	1140
tgggtaccca	gtatgtgcag	ggagacggaa	ccccatgtga	cagcccactc	caccagggtt	1200
cccaaagaac	ctggcccagt	cataatcatt	catectgaca	gtggcaataa	tcacgataac	1260
cagtactagc	tgccatgatc	gttagcctca	tattttctat	ctagagctct	gtagagcact	1320
ttagaaaccg	ctttcatgaa	ttgagctaata	tatgaataaaa	tttggaaggc	gatccctttg	1380
cagggaagct	ttctctcaga	cccccttcca	ttacacctct	caccctggta	acagcaggaa	1440
gactgaggag	aggggaacgg	gcagattcgt	tgtgtggctg	tgatgtccgt	ttagcatttt	1500
tctcagctga	cagctgggta	ggtggacaat	tgtagaggct	gtctcttctc	ccctccttgt	1560
ccaccccata	gggtgtaccc	actggtcttg	gaagcaccca	tccttaatac	gatgattttt	1620
ctgtcgtgtg	aaaatgaagc	cagcaggctg	cccctagtca	gtccttctct	ccagagaaaa	1680
agagatttga	gaaagtgcct	gggttaattca	ccattaattt	cctcccccaa	actctctgag	1740
tcttccctta	atatttctgg	tggttctgac	caaagcaggt	catggtttgt	tgagcatttg	1800
ggatcccagt	gaagtagatg	ttttagtcct	tgcatactta	gcccttccca	ggcacaaaacg	1860

gagtggcaga	gtggtgccaa	ccctgttttc	ccagtccacg	tagacagatt	cacagtgcgg	1920
aattctggaa	gctggagaca	gacgggctct	ttgcagagcc	gggactctga	gagggacatg	1980
agggcctctg	cctctgtgtt	cattctctga	tgtcctgtac	ctgggctcag	tgcccgggtg	2040
gactcatctc	ctggccgcgc	agcaaagcca	gcggttcgt	gctggtcctt	cctgcacctt	2100
aggctggggg	tggggggcct	gccggcgcat	tctccacgat	tgagcgca	ggcctgaagt	2160
ctggacaacc	cgcagaaccg	aagctccgag	cagcggtcgc	gtggcgagta	gtggggtcgg	2220
tggcgagcag	ttggtggtgg	gccggggccg	ccactacctc	gaggacattt	ccctcccgga	2280
gccagctctc	ctagaaaccc	cgcggcgccg	gccgcagcca	agtgtttatg	gcccgcggtc	2340
gggtgggagc	ctagccctgt	ctcctctcct	gggaaggagt	gaggggtggga	cgtgacttag	2400
acacctacaa	atctattttac	caaagaggag	cccgggactg	agggaaaagg	caaagagtg	2460
tgagtgcattg	cggactgggg	gttcaggggg	agaggacgag	gaggaggaag	atgaggtcga	2520
tttctgtatt	taaaaaatcg	tccaagcccc	gtggtccagc	ttaaggctct	cggttacatg	2580
cgcgcctcag	agcaggtcac	tttctgcctt	ccacgtcctc	cttcaaggaa	gccccatgtg	2640
ggtagctttc	aatatcgag	gttcttactc	ctctgcctct	ataagctcaa	acccaccaac	2700
gatcgggcaa	gtaaaccccc	tccctcgccg	acttcggaac	tggcgagagt	tcagcgacga	2760
tgggcctgtg	gggagggggc	aagatagatg	agggggagcg	gcattggtgcg	gggtgacccc	2820
ttggagagag	gaaaaaggcc	acaagagggg	ctgccaccgc	cactaacgga	gatggccctg	2880
gtagagacct	ttgggggtct	ggaacctctg	gactccccat	gctctaactc	ccacactctg	2940
ctatcagaaa	cttaaaacttg	aggattttct	ctgtttttca	ctcgcaataa	aytcagagca	3000
aacaaaaaaa	aaaaaaaaaa	aaaactcgag				3030

&lt;210&gt; 334

&lt;211&gt; 2417

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 334

ggcgccgct	ctagagctag	tgggatcccc	cgggctgcac	gaattcggca	cagtgagtt	60
ggagttttac	ctgtattgtt	ttaatttcaa	caagcctgag	gactagccac	aaatgtaccc	120
agtttacaaa	tgaggaaaca	ggtgcaaaaa	ggttgttacc	tgtcaaagg	cgtatgtggc	180
agagccaaga	tttgagccca	gttatgtctg	atgaacttag	cctatgctct	ttaaacttct	240
gaatgctgac	cattgaggat	atctaaactt	agatcaattg	cattttccct	ccaagactat	300
ttacttatca	atacaataat	accaccttta	ccaatctatt	gttttgatac	gagactcaaa	360
tatgccagat	atatgtaaaa	gcaacctaca	agctctctaa	tcattgctcac	ctaaaagatt	420
cccgggatct	aatagggtca	aagaaacttc	ttctagaaat	ataaaagaga	aaattggatt	480
atgcaaaaat	tcattattaa	tttttttcat	ccatccttta	attcagcaaa	catttatctg	540
ttgttgactt	tatgcagtat	ggccttttaa	ggattggggg	acaggtgaag	aacggggtgc	600
cagaatgcat	cctcctacta	atgaggtcag	tacacatttg	cattttaaaa	tgccctgtcc	660
agctgggcat	ggtggatcat	gcctgtaatc	tcaacatttg	aaggccaagg	caggaggatt	720
gcttcagccc	aggagttcaa	gaccagcctg	ggcaacatag	aaagacccca	tctctcaatc	780
aatcaatcaa	tgccctgtct	ttgaaaataa	aactctttta	gaaaggttta	atgggcaggg	840
tgtggtagct	catgcctata	atacagcact	ttgggaggct	gaggcaggag	gatcacttta	900
gccagaagt	tcaagaccag	cctgggcaac	aagtgcaccc	tcattctcaat	tttttaataa	960
aatgaataca	tacataagga	aagataaaaa	gaaaagttaa	atgaaagaat	acagtataaa	1020
acaaatctct	tggacctaaa	agtatttttg	ttcaagccaa	atattgtgaa	tcacctctct	1080
gtgttgagga	tacagaatat	ctaagcccag	gaaactgagc	agaaagttca	tgtactaact	1140
aatcaaccgg	aggcaaggca	aaaatgagac	taactaatca	atccgaggca	aggggcaaat	1200
tagacggaac	ctgactctgg	tctattaagc	gacaactttc	cctctgttgt	atttttcttt	1260
tattcaatgt	aaaaggataa	aaactctcta	aaactaaaaa	caatgtttgt	caggagttac	1320
aaacctgac	caactaatta	tggggaatca	taaaatatga	ctgtatgaga	tcttgatggg	1380
ttacaaagt	taccactgt	taatcacttt	aaacattaat	gaacttaaaa	atgaatttac	1440
ggagattgga	atgtttcttt	cctgttgtat	tagttggctc	aggctgccat	aacaaaatac	1500
cacagactgg	gaggcttaag	taacagaaat	tcatttctca	cagttctggg	ggctggaagt	1560
ccacgatcaa	ggtgcaggaa	aggcaggctt	cattctgagg	ccctctctct	ggctcacatg	1620
tggccaccct	cccactgcgt	gctcacatga	cctcttttgt	ctcctggaaa	gaggggtgtg	1680
gggacagagg	gaaagagaa	gagaggggaa	tctctggtgt	ctcgtctttc	aaggacccta	1740
acctgggcca	ctttggccca	ggcactgtgg	ggtgggggtg	tgtggctgct	ctgctctgag	1800
tggccaagat	aaagcaacag	aaaaatgtcc	aaagctgtgc	agcaaagaca	agccaccgaa	1860



cagggatctg	ctcatcagt	tggggacctc	caagtcggcc	accctggagg	caagccccc	1920
cagagcccat	gcaaggtggc	agcagcagaa	gaagggaatt	gtccctgtcc	ttggcacatt	1980
cctcacogac	ctggtgatgc	tggacactgc	gatgaatggt	aatgtggatg	agaatatgat	2040
ggactcccag	aaaaggagac	ccagctgctc	aggtggctgc	aatcattac	agccttcac	2100
ctggggagga	actggggggc	tggttctggg	tcagagagca	gcccagtgag	ggtgagagct	2160
acagcctgtc	ctgccagctg	gatccccagt	cccggtcaac	cagtaatcaa	ggctgagcag	2220
atcaggcttc	ccggagctgg	tcttgggaag	ccagccctgg	ggtgagttgg	ctcctgctgt	2280
ggtactgaga	caatattgtc	ataaattcaa	tgcgcccttg	tatccctttt	tcttttttat	2340
ctgtctacat	ctataatcac	tatgcatact	agtctttgtt	agtgtttcta	ttcmacttaa	2400
tagagatatg	ttatact					2417

<210> 335  
 <211> 2984  
 <212> DNA  
 <213> Homo sapien

<400> 335

atccctcctt	ccccactctc	ctttccagaa	ggcacttggg	gtcttatctg	ttggactctg	60
aaaacacttc	aggcgccctt	ccaaggcttc	cccaaacc	taagcagccg	cagaagcgct	120
cccagactgc	cttctccac	actcaggtga	tcgagttgga	gaggaagttc	agccatcaga	180
agtacctgtc	ggccctgaa	cgggcccacc	tggccaagaa	cctcaagctc	acggagaccc	240
aagtgaagat	atggttccag	aacagacgct	ataagactaa	gcgaaagcag	ctctcctcgg	300
agctgggaga	cttggaaga	cactcctctt	tgcggccct	gaaagaggag	gccttctccc	360
gggctccct	ggtctccgtg	tataacagct	atccttacta	cccatacctg	tactgcgtgg	420
gcagctggag	cccagctttt	tggtaatgcc	agctcaggtg	acaaccatta	tgatcaaaaa	480
ctgccttccc	cagggtgtct	ctatgaaaag	cacaaggggc	caaggtcagg	gagcaagagg	540
tgtgcacacc	aaagctattg	gagatttgcg	tggaaatctc	asattcttca	ctggtgagac	600
aatgaaacaa	cagagacagt	gaaagtttta	atacctaagt	cattccccca	gtgcatactg	660
taggtcattt	tttttgcttc	tggctacctg	tttgaagggg	agagagggaa	aatcaagtgg	720
tattttccag	cactttgtat	gattttggat	gagctgtaca	cccaaggatt	ctgttctgca	780
actccatcct	cctgtgtcac	tgaatatcaa	ctctgaaaga	gcaaaccctaa	caggagaaag	840
gacaaccagg	atgaggatgt	caccaactga	attaaactta	agtccagaag	cctcctgttg	900
gccttggaat	atggccaagg	ctctctctgt	ccctgtaaaa	gagaggggca	aatagagagt	960
ctccaagaga	acgccctcat	gctcagcaca	tatttgcatg	ggagggggag	atgggtggga	1020
ggagatgaaa	atatcagctt	ttcttattcc	tttttattcc	ttttaaaatg	gtatgccaac	1080
ttaagtattt	acagggtggc	ccaaatagaa	caagatgcac	tcgctgtgat	tttaagacaa	1140
gctgtataaa	cagaactcca	ctgcaagagg	gggggcccgg	ccaggagaat	ctccgcttgt	1200
ccaagacagg	ggcctaagga	gggtctccac	actgctgcta	ggggtgttg	cattttttta	1260
ttagtagaaa	gtggaaaggc	ctcttctcaa	cttttttccc	ttgggctgga	gaatttagaa	1320
tcagaagttt	cctggagttt	tcaggctatc	atatatactg	tatcctgaaa	ggcaacataa	1380
ttcttccctc	cctcctttta	aaattttgtg	ttcctttttg	cagcaattac	tcactaaagg	1440
gcttcatttt	agtccagatt	tttagtctgg	ctgcacctaa	cttatgcctc	gcttatttag	1500
cccagatctc	ggtctttttt	tttttttttt	tttttccgtc	tcccaaaagc	tttatctgtc	1560
ttgacttttt	aaaaaagttt	gggggcagat	tctgaatttg	ctaaaagaca	tgcattttta	1620
aaactagcaa	ctcttatttc	tttcctttta	aaatacatag	cattaaatcc	caaatoctat	1680
ttaaagacct	gacagcttga	gaaggtcact	actgcattta	taggaccttc	tgggtggttct	1740
gctgttacgt	ttgaagtctg	acaatccttg	agaatccttg	catgcagagg	aggtaagagg	1800
tattggattt	tcacagagga	agaacacagc	gcagaatgaa	gggccaggct	tactgagctg	1860
tccagtggag	ggctcatggg	tgggacatgg	aaaagaaggc	agcctaggcc	ctggggagcc	1920
cagtccactg	agcaagcaag	ggactgagtg	agccttttgc	aggaaaaggc	taagaaaaag	1980
gaaaaccatt	ctaaaacaca	acaagaaact	gtccaaatgc	tttgggaact	gtgtttattg	2040
cctataatgg	gtccccaaaa	tgggtaacct	agacttcaga	gagaatgagc	agagagcaaa	2100
ggagaaatct	ggctgtcctt	ccattttcat	tctgttatct	cagggtgagct	ggtagagggg	2160
agacattaga	aaaaaatgaa	acaacaaaac	aattactaat	gagggtacgt	gaggcctggg	2220
agtctcttga	ctccactact	taattccgtt	tagtgagaaa	ccttttcaatt	ttcttttatt	2280
agaagggcc	gottactgtt	ggtggcaaaa	ttgccaacat	aagttaatat	aaagttggcc	2340
aatttcaccc	cattttctgt	ggtttgggct	ccacattgca	atgttcaatg	ccacgtgctg	2400
ctgacaccga	ccggagtact	agccagcaca	aaaggcaggg	tagcctgaat	tgctttctgc	2460

```

tctttacatt tcttttaaaa taagcattta gtgctcagtc cctactgagt actctttctc 2520
tccccctctc tgaatttaat tctttcaact tgcaatttgc aaggattaca catttcactg 2580
tgaatgtatat tgtgttgcaa aaaaaaaaaa aagtgtcttt gtttaaaatt acttgggttg 2640
tgaatccatc ttgctttttc cccattggaa ctagtcatc acccatctct gaactggtag 2700
aaaaacatct gaagagctag tctatcagca tctgacaggt gaattggatg gttctcagaa 2760
ccatttcacc cagacagcct gtttctatcc tgtttaataa attagtttgg gttctctaca 2820
tgcataacaa accctgctcc aatctgtcac ataaaagtct gtgacttgaa gtttagtcag 2880
cacccccacc aaactttatt tttctatgtg ttttttgcaa catatgagtg ttttgaaaat 2940
aaagtaccca tgtctttatt agaaaaaaaa aaaaaaaaaa aaaa 2984

```

<210> 336  
 <211> 147  
 <212> PRT  
 <213> Homo sapien

<400> 336

```

Pro Ser Phe Pro Thr Leu Leu Ser Arg Arg His Leu Gly Ser Tyr Leu
1          5          10          15
Leu Asp Ser Glu Asn Thr Ser Gly Ala Leu Pro Arg Leu Pro Gln Thr
20          25          30
Pro Lys Gln Pro Gln Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln
35          40          45
Val Ile Glu Leu Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala
50          55          60
Pro Glu Arg Ala His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln
65          70          75          80
Val Lys Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln
85          90          95
Leu Ser Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala
100          105          110
Leu Lys Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn
115          120          125
Ser Tyr Pro Tyr Tyr Pro Tyr Leu Tyr Cys Val Gly Ser Trp Ser Pro
130          135          140
Ala Phe Trp
145

```

<210> 337  
 <211> 9  
 <212> PRT  
 <213> Homo sapien

<400> 337

```

Ala Leu Thr Gly Phe Thr Phe Ser Ala
1          5

```

<210> 338  
 <211> 9  
 <212> PRT  
 <213> Homo sapien

<400> 338

```

Leu Leu Ala Asn Asp Leu Met Leu Ile
1          5

```

<210> 339  
 <211> 318

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 339

```

Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Leu Pro Phe Leu
 1           5           10           15
Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val
          20          25          30
Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
          35          40          45
Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg
          50          55          60
Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu
65          70          75          80
Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val Leu Val
          85          90          95
Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys
          100         105         110
Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala
          115         120         125
Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met
          130         135         140
His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His Leu Leu
145         150         155         160
Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn Val Ser
          165         170         175
Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu Gln Gly
          180         185         190
Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys Leu Ala
          195         200         205
Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly
          210         215         220
Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu Leu Val
225         230         235         240
Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe
          245         250         255
Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys Ala Leu
          260         265         270
Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His
          275         280         285
Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg
          290         295         300
Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp
305         310         315

```

&lt;210&gt; 340

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 340

```

gccgaggtct gccttcacac ggaggacacg agactgcttc ctcaaggggt cctgcctgcc      60
tggacactgg tgggaggcgc tgtttagtgt gctgttttca gaggggtctt tcggagggac      120
ctcctgctgc aggctggagt gtctttattc ctggcgggag accgcacatt ccaactgctga      180
ggttgtgggg gcggtttatc aggcagtgat aaacataaga tgtcatttcc ttgactccgg      240
ccttcaattt tctctttggc tgacgacgga gtccgtggtg tcccgatgta actgaccct      300
gctccaaacg tgacatcact gatgctcttc tcgggggtgc tgatggcccg cttggtcacg      360
tgctcaatct cgccattcga ctcttgctcc aaactgtatg aaagacacctg actgcacgtt      420

```

ttttctgggc ttccagaatt taaagtgaag ggcagcactc ctaagctccg actccgatgc 480  
ctg 483

<210> 341  
<211> 344  
<212> DNA  
<213> Homo sapien

<400> 341  
ctgctgctga gtcacagatt tcattataaa tagcctccct aaggaaaata cactgaatgc 60  
tatttttact aaccattcta tttttataga aatagctgag agtttctaaa ccaactctct 120  
gctgccttac aagtattaaa tattttactt ctttccataa agagtagctc aaaatatgca 180  
attaatttaa taatttctga tgatggtttt atctgcagta atatgtatat catctattag 240  
aatttactta atgaaaaact gaagagaaca aaatttgtaa ccactagcac ttaagtactc 300  
ctgattctta acattgtctt taatgaccac aagacaacca acag 344

<210> 342  
<211> 592  
<212> DNA  
<213> Homo sapien

<400> 342  
acagcaaaaa agaaactgag aagcccaaty tgctttcttg ttaacatcca cttatccaac 60  
caatgtggaa acttcttata cttgggtcca ttatgaagtt ggacaattgc tgctatcaca 120  
cctggcaggt aaaccaatgc caagagagtg atggaaacca ttggcaagac tttgttgatg 180  
accaggattg gaattttata aaaatatgtg tgatgggaag ttgctaaagg gtgaattact 240  
tccctcagaa gagtgtaaag aaaagtcaga gatgctataa tagcagctat tttaatgggc 300  
aagtgccact gtggaaaagag ttcctgtgtg tgctgaagtt ctgaagggca gtcaaattca 360  
tcagcatggg ctgttttgtg caaatgcaaa agcacaggtc tttttagcat gctggctctc 420  
cccgtgtcct tatgcaaata atcgtcttct tctaaatttc tctagggctt cattttccaa 480  
agttcttctt ggtttgtgat gtcttttctg ctttccatta attctataaa atagtatggc 540  
ttcagccacc cactcttcgc cttagcttga ccgtgagtct cggctgccgc tg 592

<210> 343  
<211> 382  
<212> DNA  
<213> Homo sapien

<400> 343  
ttcttgacct cctcctcctt caagctcaaa caccacctcc cttattcagg accggcactt 60  
cttaattgtt gtgcttttct ctccagctc tcttaggagg ggtaatggtg gagttggcat 120  
cttgtaactc tcctttctcc tttcttcccc tttctctgcc cgcctttccc atcctgctgt 180  
agacttcttg attgtcagtc tgtgtcacat ccagtgattg ttttggtttc tgttcccttt 240  
ctgactgccc aaggggctca gaaccccagc aatcccttcc tttcactacc ttcttttttg 300  
ggggtagttg gaagggactg aaattgtggg gggaaggtag gaggcacatc aataaagagg 360  
aaaccaccaa gctgaaaaaa aa 382

<210> 344  
<211> 536  
<212> DNA  
<213> Homo sapien

<400> 344  
ctgggcctga agctgtaggg taaatcagag gcaggcttct gagtgatgag agtcctgaga 60  
caataggcca cataaacttg gctggatgga acctcacaat aaggtggtca cctcttgttt 120  
gtttaggggg atgccaagga taaggccagc tcagttatat gaagagaagc agaacaaaca 180  
agtctttcag agaaatggat gcaatcagag tgggatcccg gtcacatcaa ggtcacactc 240  
caccttcatg tgcctgaatg gttgccaggt cagaaaaatc cacccttac gagtgcggct 300

```

tcgaccctat atcccccgcc cgcgtccctt tctccataaa attcttctta gtagctatta 360
ccttcttatt atttgatcta gaaattgccc tccttttacc cctaccatga gccctacaaa 420
caactaacct gccactaata gttatgtcat ccctcttatt aatcatcatc ctagccctaa 480
gtctggccta tgagtgacta caaaaaggat tagactgagc cgaataacaa aaaaaa 536

```

```

<210> 345
<211> 251
<212> DNA
<213> Homo sapien

```

```

<400> 345
accttttgag gtctctctca ccacctccac agccaccgtc accgtgggat gtgctggatg 60
tgaatgaagc ccccatcttt gtgcctcctg aaaagagagt ggaagtgtcc gaggactttg 120
gcgtagggcca ggaaatcaca tcctacactg cccaggagcc agacacattt atggaacaga 180
aaataacata tcggatttgg agagacactg ccaactggct ggagattaat ccggacactg 240
gtgccatttc c 251

```

```

<210> 346
<211> 282
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(282)
<223> n = A,T,C or G

```

```

<400> 346
cgcgtctctg acactgtgat catgacaggg gttcaaacag aaagtgcctg ggccctcctt 60
ctaagtcttg ttaccaaaaa aaggaaaaag aaaagatctt ctcaattaca aattctggga 120
agggagacta tacctggctc ttgccctaag tgagaggtct tccctccgcg accaaaaaat 180
agaaaggctt tctatttcac tggcccagggt agggggaagg agagtaactt tgagtctgtg 240
ggtctcattt cccaagggtg cttcaatgct catnaaaacc aa 282

```

```

<210> 347
<211> 201
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(201)
<223> n = A,T,C or G

```

```

<400> 347
acacacataa tattataaaa tgccatctaa ttggaaggag ctttctatca ttgcaagtca 60
taaataatac ttttaaaana ntactancag cttttaccta ngctcctaaa tgcttgtaaa 120
tctgagactg actggacca cccagacca gggcaaagat acatgttacc atatcatctt 180
tataaagaat ttttttttgt c 201

```

```

<210> 348
<211> 251
<212> DNA
<213> Homo sapien

```

```

<400> 348
ctgttaatca caacatttgt gcatacttg tgccaagtga gaaaatgttc taaaatcaca 60
agagagaaca gtgccagaat gaaactgacc ctaagtccca ggtgcccttg ggcaggcaga 120

```

aggagacact	cccagcatgg	aggaggggtt	atcttttcat	cctaggtcag	gtctacaatg	180
ggggaaggtt	ttattataga	actccaaca	gccacctca	ctcctgccac	ccacccgatg	240
gccctgcctc	c					251

<210> 349  
 <211> 251  
 <212> DNA  
 <213> Homo sapien

<400> 349						
taaaaatcaa	gccatttaat	tgtatctttg	aaggtaaaca	atatatggga	gctggatcac	60
aacccttgag	gatgccagag	ctatgggtcc	agaacatggt	gtggtattat	caacagagtt	120
cagaagggtc	tgaactctac	gtgttaccag	agaacataat	gcaattcatg	cattccactt	180
agcaattttg	taaaatacca	gaaacagacc	ccaagagtct	ttcaagatga	ggaaaattca	240
actcctgggt	t					251

<210> 350  
 <211> 908  
 <212> DNA  
 <213> Homo sapien

<400> 350						
ctggacactt	tgcgagggct	tttgcctggc	gtcgtcgtc	cccgatcatg	tactcatcgt	60
agcccgcccg	gtgaagctcg	ctgctttccc	tacctcctta	agtgactgcc	aaacgcccac	120
cggctggaat	tgctctgggt	atgatgacag	agaaaatgat	ctcttcctct	gtgacaccaa	180
cacctgtaaa	tttgatgggg	aatgtttaag	aattggagac	actgtgactt	gcgtctgtca	240
gttcaagtgc	aacaatgact	atgtgcctgt	gtgtggctcc	aatggggaga	gctaccagaa	300
tgagtgttac	ctgcgacagg	ctgcatgcaa	acagcagagt	gagatacttg	tggtgtcaga	360
aggatcatgt	gccacagtcc	atgaaggctc	tggagaaact	agtcaaaagg	agacatccac	420
ctgtgatatt	tgccagtttg	gtgcagaatg	tgacgaagat	gccgaggatg	tctgggtgtg	480
gtgtaatatt	gactgttctc	aaaccaactt	caatccccct	tgcgcttctg	atgggaaatc	540
ttatgataat	gcatgccaaa	tcaaagaagc	atcgtgtcag	aaacaggaga	aaattgaagt	600
catgtctttg	ggtcogatgtc	aagataaac	aactacaact	actaagtctg	aagatgggca	660
ttatgcaaga	acagattatg	cagagaatgc	taacaaatta	gaagaaagtg	ccagagaaca	720
ccacatacct	tgtccggaac	attacaatgg	cttctgcatg	catgggaagt	gtgagcattc	780
tatcaatatg	caggagccat	cttgcagggt	tgatgctggg	tatactggac	aacactgtga	840
aaaaaaggac	tacagtgttc	tatacgttgt	tcccggctcc	gtacgatttc	agtatgtctt	900
aatcgacg						908

<210> 351  
 <211> 472  
 <212> DNA  
 <213> Homo sapien

<400> 351						
ccagttatatt	gcaagtggta	agagcctatt	taccataaat	aatactaaga	accaactcaa	60
gtcaaaccct	aatgccattg	ttattgtgaa	ttaggattaa	gtagtaattt	tcaaaattca	120
cattaacttg	attttaaaat	cagwtttgyg	agtcatttac	cacaagctaa	atgtgtacac	180
tatgataaaa	acaaccattg	tattcctgtt	tttctaaaca	gtcctaattt	ctaactgtgt	240
atatatcctt	cgacatcaat	gaactttgtt	ttcttttact	ccagtaataa	agtaggcaca	300
gatctgtcca	caacaaactt	gccctctcat	gccttgccct	tcacatgct	ctgctccagg	360
tcagccccct	tttggcctgt	ttgttttgtc	aaaaacctaa	tctgcttctt	gcttttcttg	420
gtaatatata	tttagggaag	atgttgcttt	gccacacac	gaagcaaagt	aa	472

<210> 352  
 <211> 251  
 <212> DNA  
 <213> Homo sapien

&lt;400&gt; 352

ctcaaagcta atctctcggg aatcaaacca gaaaagggca aggatcttag gcatggtgga	60
tgtggataag gccagggtcaa tggctgcaag catgcagaga aagagggtaca tcggagcgtg	120
caggctgcgt tccgtcctta cgatgaagac cacgatgcag tttccaaaca ttgccactac	180
atacatggaa aggaggggga agccaacca gaaatgggct ttctctaata ctgggatacc	240
aataagcaca a	251

&lt;210&gt; 353

&lt;211&gt; 436

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 353

tttttttttt tttttttttt ttttttataa caatgcagtc atttatttat tgagtatgtg	60
cacattatgg tattattact atactgatta tatttatcat gtgacttcta attaraaaat	120
gtatccaaaa gcaaaacagc agatatacaa aattaaagag acagaagata gacattaaca	180
gataaggcaa cttatacatt gacaatccaa atccaatata tttaaacatt tgggaaatga	240
gggggacaaa tggaagccar atcaaatttg tgtaaaacta ttcagtatgt ttcccttgct	300
tcatgtctga raaggctctc ccttcaatgg ggatgacaaa ctccaaatgc cacacaaatg	360
ttaacagaat actagattca cactggaacg ggggtaaaga agaaattatt ttctataaaa	420
gggctcctaa tgtagt	436

&lt;210&gt; 354

&lt;211&gt; 854

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 354

ccttttctag ttcaccagtt ttctgcaagg atgctgggta gggagtgtct gcaggaggag	60
caagtctgaa accaaatcta ggaaacatag gaaacgagcc aggcacaggg ctggtgggcc	120
atcagggacc accctttggg ttgatatttt gcttaatctg catcttttga gtaagatcat	180
ctggcagtag aagctgttct ccagggtacat ttctctagct catgtacaaa aacatcctga	240
aggactttgt cagggtgcctt gctaaaagcc agatgcgttc ggcacttcct tggctctgagg	300
ttaattgcac acctacagga actgggctca tgctttcaag tattttgtcc tcacttttagg	360
gtgagtgaaa gatccccatt ataggagcac ttgggagaga tcatataaaa gctgactctt	420
gagtacatgc agtaatggg tagatgtgtg tgggtgtgtct tcattcctgc aagggtgctt	480
gttagggagt gtttccagga ggaacaagtc tgaaaccaat catgaaataa atggtaggtg	540
tgaactggaa aactaattca aaagagagat cgtgatataa gtgtgggtga tacaccttg	600
caatatggaa ggctctaatt tgcccatatt tgaaataata attcagcttt ttgtaataca	660
aaataacaaa ggattgagaa tcatggtgtc taatgtataa aagaccagga aaacataaat	720
atatcaactg cataaatgta aaatgcatgt gacccaagaa ggcccaaggg tggcagacaa	780
cattgtaccc attttccctt ccaaaatgtg agcggcgggc ctgctgcttt caaggctgtc	840
acacgggatg tcag	854

&lt;210&gt; 355

&lt;211&gt; 676

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 355

gaaattaagt atgagctaaa ttccctgtta aaacctctag gggtgacaga tctcttcaac	60
cagggtcaaag ctgatctttc tggaatgtca ccaaccaagg gcctatattt atcaaaagcc	120
atccacaagt catacctgga tgtcagcgaa gagggcacgg aggcagcagc agccactggg	180
gacagcatcg ctgtaaaaag cctaccaatg agagctcagt tcaaggcgaa ccaccccttc	240
ctgttcttta taaggcacac tcataccaac acgatcctat tctgtggcaa gcttgccctc	300
ccctaactcag atgggggtga gtaaggctca gagttgcaga tgagggtcag agacaatcct	360
gtgactttcc caccggccaaa aagctgttca cacctcacgc acctctgtgc ctgagtttgc	420

tcattctgcaa	aataggtcta	ggattttcttc	caaccatttc	atgagttgtg	aagctaaggc	480
tttggttaatc	atggaaaaag	gtagacttat	gcagaaagcc	tttctggctt	tcttatctgt	540
ggtgtctcat	ttgagtgtctg	tccagtgcac	tgatcaagtc	aatgagtaaa	attttaaggg	600
attagattttt	cttgacttgt	atgtatctgt	gagatcttga	ataagtgacc	tgacatctct	660
gcttaaagaa	aaccag					676

&lt;210&gt; 356

&lt;211&gt; 574

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 356

tttttttttt	tttttcagga	aaacattctc	ttactttatt	tgcattctcag	caaagggtct	60
catgtggcac	ctgactggca	tcaaaccaaa	gttcgtaggc	caacaaagat	gggccactca	120
caagcttccc	attttagat	ctcagtgcct	atgagtatct	gacacctgtt	cctctcttca	180
gtctcttagg	gaggcttaaa	tctgtctcag	gtgtgctaag	agtgccagcc	caaggkgtc	240
aaaagtccac	aaaactgcag	tctttgctgg	gatagtaagc	caagcagtgc	ctggacagca	300
gagttctttt	cttgggcaac	agataaccag	acaggactct	aatcgtgctc	ttattcaaca	360
ttcttctgtc	tctgcctaga	ctggaataaa	aagccaatct	ctctcgtggc	acagggaagg	420
agatacaagc	tcgtttacat	gtgatagatc	taacaaaggc	atctaccgaa	gtctgggtctg	480
gatagacggc	acaggggagct	cttaggtcag	cgctgctggg	tggaggacat	tcctgagtcc	540
agctttgcag	cctttgtgca	acagtacttt	ccca			574

&lt;210&gt; 357

&lt;211&gt; 393

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 357

tttttttttt	tttttttttt	tttttttttt	tacagaatat	aratgcttta	tcaactgkact	60
taatatggkg	kcttggtcac	tatacttaaa	aatgcaccac	tcataaatat	ttaattcagc	120
aagccacaac	caaracttga	ttttatcaac	aaaaaccct	aaatataaac	ggsaaaaaag	180
atagatataa	ttattccagt	ttttttaaaa	cttaaaarat	attccattgc	cgaattaara	240
araarataag	tggttatatg	aaagaagggc	attcaagcac	actaaaaraa	cctgaggkaa	300
gcataatctg	tacaaaatta	aactgtcctt	tttggcattt	taacaaattt	gcaacgktct	360
tttttttctt	tttctgtttt	tttttttttt	tac			393

&lt;210&gt; 358

&lt;211&gt; 630

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 358

acagggtaaa	caggaggatc	cttgcctctca	cggagcttac	attctagcag	gaggacaata	60
ttaatgttta	taggaaaatg	atgagtttat	gacaaaggaa	gtagatagtg	ttttacaaga	120
gcatagagta	gggaagctaa	tccagcacag	ggaggtcaca	gagacatccc	taagggaagt	180
gagtttaaac	tgagagaagc	aagtgcctta	actgaaggat	gtgttgaaga	agaaggggaga	240
gtagaacaat	ttgggcagag	ggaaccttat	agaccctaag	gtgggaaggt	tcaaagaact	300
gaaagagagc	tagaacagct	ggagccgttc	tccggtgtaa	agaggagtca	aagagataag	360
attaaagatg	tgaagattaa	gatcttggtg	gcattcaggg	attggcactt	ctacaagaaa	420
tcaactgaagg	gagtaatgtg	acattacttt	tcaacttcagg	atggccattc	taactccagg	480
gggtagactg	gactaggtaa	gactggaggc	aggtagacct	cttctaaggc	ctgcgatagt	540
gaaagacaaa	aataagtggg	gaaattcagg	ggatagttaa	aatcagtagg	acttaatgag	600
caagccagag	gttcctccac	aacaaccagt				630

&lt;210&gt; 359

&lt;211&gt; 620

&lt;212&gt; DNA



&lt;213&gt; Homo sapien

&lt;400&gt; 359

acagcattcc	aaaatatata	tctagagact	aarrgtaaat	gctctatagt	gaagaagtaa	60
taattaaaa	atgctactaa	tatagaaaat	ttataatcag	aaaaataaat	attcagggag	120
ctcaccagaa	gaataaagtg	ctctgccagt	tattaaagga	ttactgctgg	tgaattaaat	180
atggcattcc	ccaagggaaa	tagagagatt	cttctggatt	atgttcaata	tttatttcac	240
aggattaact	gttttaggaa	cagatataaa	gcttcgccac	ggaagagatg	gacaaagcac	300
aaagacaaca	tgatacctta	ggaagcaaca	ctaccctttc	aggcataaaa	tttgagagaa	360
tgcaacatta	tgcttcatga	ataatatgta	gaaagaaggt	ctgatgaaaa	tgacatcctt	420
aatgtaagat	aactttataa	gaattctggg	tcaaataaaa	ttctttgaag	aaaacatcca	480
aatgtcattg	acttatcaaa	tactatcttg	gcataatacc	tatgaaggca	aaactaaaca	540
aacaaaaagc	tcacacccaa	caaaaccatc	aacttatttt	gtattctata	acatacgaga	600
ctgtaaagat	gtgacagtgt					620

&lt;210&gt; 360

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 360

aaaaaaaaaa	agccagaaca	acatgtgata	gataaatatga	ttggctgcac	acttccagac	60
tgatgaatga	tgaacgtgat	ggactattgt	atggagcaca	tcttcagcaa	gagggggaaa	120
tactcatcat	ttttggccag	cagttgtttg	atcaccaaac	atcatgccag	aatactcagc	180
aaaccttctt	agctcttgag	aagtcaaaag	ccgggggaat	ttattcctgg	caattttaat	240
tggtactcctt	atgtgagagc	agcggctacc	cagctggggg	ggtggagcga	acccgtcact	300
agtggacatg	cagtggcaga	gctcctggta	accacctaga	ggaatacaca	ggcacatgtg	360
tgatgccaa	cgtagacacct	gtagcactca	aatttgtctt	gtttttgtct	ttcgggtgtg	420
agattcttag	t					431

&lt;210&gt; 361

&lt;211&gt; 351

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 361

acactgattt	ccgatcaaaa	gaatcatcat	ctttaccttg	acttttcagg	gaattactga	60
actttcttct	cagaagatag	ggcacagcca	ttgccttggc	ctcacttgaa	gggtctgcat	120
ttgggtcctc	tggtctcttg	ccaagtttcc	cagccactcg	agggagaaat	atcgggaggt	180
ttgacttcct	ccggggcttt	cccaggggct	tcaccgtgag	ccctgcggcc	ctcagggctg	240
caatcctgga	ttcaatgtct	gaaacctcgc	tctctgcctg	ctggacttct	gaggccgtca	300
ctgccactct	gtcctccagc	tctgacagct	cctcatctgt	ggtcctgttg	t	351

&lt;210&gt; 362

&lt;211&gt; 463

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 362

acttcatcag	gccataatgg	gtgcctcccg	tgagaatcca	agcacctttg	gactgcgcga	60
tgtagatgag	ccggctgaag	atcttgcgca	tgcgcggtt	cagggcggaag	ttcttgggcg	120
ccccggtcac	agaaatgacc	aggttgggtg	ttttcagggt	ccagtgcctg	gtcagcagct	180
cgtaaaggat	ttccgcgtcc	gtgtcgcagg	acagacgtat	atacttccct	ttcttcccca	240
gtgtctcaaa	ctgaatatcc	ccaaaggcgt	cggtaggaaa	ttccttgggt	tgtttcttgt	300
agttccattt	ctcaactttg	ttgatctggg	tgccctccat	gtgctggctc	tgggcatagc	360
cacacttgca	cacattctcc	ctgataagca	cgatgggtgt	gacaggaagg	aaggatttca	420
ttgagcctgc	ttatggaaac	tggtattgtt	agcttaaata	gac		463

<210> 363  
 <211> 653  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(653)  
 <223> n = A,T,C or G

<400> 363  
 acccccagagt ncctgnctgg catactgnga acgaccaacg acacacccaa gctcggcctc 60  
 ctcttgngga ttctgggtga catcttcacg aatggcaacc gtgccagwga ggctgtcctc 120  
 tgggaggcac tacgcaagat gggactgcgt cctgggggtga gacatcctct ccttgagat 180  
 ctaacgaaac ttctcaccta tgagttgtaa agcagaaata cctgnactac agacgagtgc 240  
 ccaacagcaa cccccggaa gtatgagttc ctctrgggcc tccgttccta ccatgagasc 300  
 tagcaagatg naagtgttga gantcattgc agaggttcag aaaagagacc cntcgtgact 360  
 ggtctgcaca gttcatggag gctgcagatg aggccttga tgctctggat gctgctgcag 420  
 ctgaggccga agcccgggt gaagcaagaa cccgcatggg aattggagat gaggtgtgt 480  
 ntgggccctg gagctggat gacattgagt ttgagctgct gacctgggat gaggaaggag 540  
 attttggaga tcentgggtc agaattccat ttacctctg ggccagatac caccagaatg 600  
 cccgctccag attccctcag acctttgccg gtcccattat tggtcstggt ggt 653

<210> 364  
 <211> 401  
 <212> DNA  
 <213> Homo sapien

<400> 364  
 actagaggaa agacgttaaa ccactctact accacttgtg gaactctcaa agggtaaagt 60  
 acaaagccaa tgaatgactc taaaaacaat atttacattt aatggtttgt agacaataaa 120  
 aaaacaaggt ggatagatct agaattgtaa cattttaaga aaaccatagc atttgacaga 180  
 tgagaaagct caattataga tgcaaagtta taactaaact actatagtag taaagaaata 240  
 catttcacac cttcatata aattcactat cttggcttga ggactccat aaaatgtatc 300  
 acgtgcatag taaatcttta tatttgctat ggcgttgac tagaggactt ggactgcaac 360  
 aagtggatgc gcggaaaatg aaatcttctt caatagccca g 401

<210> 365  
 <211> 356  
 <212> DNA  
 <213> Homo sapien

<400> 365  
 ccagtgtcat atttgggctt aaaatttcaa gaagggcact tcaaatggct ttgcatttgc 60  
 atgtttcagt gctagagcgt aggaatagac cctggcgtcc actgtgagat gttcttcagc 120  
 taccagagca tcaagtctct gcagcaggtc attcttgggt aaagaaatga cttccacaaa 180  
 ctctccatcc cctggctttg gcttcggcct tgcgttttcg gcatcatctc cgtaaatggt 240  
 gactgtcacg atgtgtatag tacagtttga caagcctggg tccatacaga ccgctggaga 300  
 acattcggca atgtcccctt tgtagccagt ttcttcttcg agtcccggga gagcag 356

<210> 366  
 <211> 1851  
 <212> DNA  
 <213> Homo sapien

<400> 366  
 tcataccat tgccagcagc ggcaccgtta gtcaggtttt ctgggaatcc cacatgagta 60  
 cttccgtgtt cttcattctt cttcaatagc cataaatctt ctagctctgg ctggctgttt 120

tcacttcctt	taagcctttg	tgactcttcc	tctgatgtca	gctttaagtc	ttgttctgga	180
ttgctgtttt	cagaagagat	ttttaacatc	tggttttctt	tgtagtcaga	aagtaactgg	240
caaattacat	gatgatgact	agaaacagca	tactctctgg	ccgtctttcc	agatcttgag	300
aagatacatc	aacattttgc	tcaagtagag	ggctgactat	acttgctgat	ccacaacata	360
cagcaagtat	gagagcagtt	cttccatata	tatccagcgc	atttaaattc	gcttttttct	420
tgattaaaaa	tttcaaccact	tgctgttttt	gctcatgtat	accaagtagc	agtgggtgta	480
ggccatgctt	gttttttgat	tcgatatacag	caccgtataa	gagcagtgct	ttggccatta	540
atttatcttc	attgtagaca	gcatagtgta	gagtgggtatt	tccatactca	tctggaatat	600
ttggatcagt	gccatgttcc	agcaacatta	acgcacattc	atcttctctg	cattgtacgg	660
cctttgtcag	agctgtcctc	tttttgttgt	caaggacatt	aagttgacat	cgtctgtcca	720
gcacgagttt	tactacttct	gaattcccat	tggcagaggc	cagatgtaga	gcagtcctct	780
tttgctgtc	cctctgttcc	acatccgtgt	ccctgagcat	gacgatgaga	tcctttctgg	840
ggactttacc	ccaccaggca	gctctgtgga	gcttgtccag	atcttctcca	tggaactggg	900
acctgggac	catgaaggcg	ctgtcatcgt	agtctcccca	agcgaccacg	ttgctcttgc	960
cgctccctg	cagcagggga	agcagtgcca	gcaccacttg	cacctcttgc	tccaagcgt	1020
cttcacagag	gagtcgttgt	ggtctccaga	agtgcaccag	ttgctcttgc	cgctccctct	1080
gtccatccag	ggaggaagaa	atgcaggaaa	tgaaagatgc	atgcacgatg	gtatactcct	1140
cagccatcaa	acttctggac	agcaggtcac	ttccagcaag	gtggagaaaag	ctgtccaccc	1200
acagaggatg	agatccagaa	accacaatat	ccattcacia	acaaacactt	ttcagccaga	1260
cacaggtact	gaaatcatgt	catctgcggc	aacatggtgg	aacctaccca	atcacacatc	1320
aagagatgaa	gacactgcag	tatatctgca	caacgtaata	ctcttcatcc	ataacaaaat	1380
aataataatt	tcctctggag	ccatatggat	gaactatgaa	ggaagaactc	cccgaagaag	1440
ccagtcgcag	agaagccaca	ctgaagctct	gtcctcagcc	atcagcgcca	cggacaggag	1500
tgtgtttctt	ccccagtgat	gcagcctcaa	gttatcccca	agctgccgca	gcacacgggtg	1560
gctcctgaga	aacaccccag	ctcttccggg	ctaacacagg	caagtcaata	aatgtgataa	1620
tcacataaac	agaattaaaa	gcaaagtcac	ataagcatct	caacagacac	agaaaaggca	1680
tttgacaaaa	tccagcatcc	ttgtatttat	tggtgcagtt	ctcagaggaa	atgcttctaa	1740
cttttcccca	tttagtatta	tggtggctgt	gggcttgtca	taggtgggtt	ttattacttt	1800
aaggtatgtc	ccttctatgc	ctgttttgct	gagggtttta	attctcgtgc	c	1851

&lt;210&gt; 367

&lt;211&gt; 668

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 367

cttgagcttc	caaataaygga	agactggccc	ttacacasgt	caatgtttaa	atgaatgcat	60
ttcagtat	tgaagataaa	atrrgtagat	ctataccttg	ttttttgatt	cgatatcagc	120
accrtataag	agcagtgcct	tggccattaa	tttatctttc	atrrtagaca	gcrtagtgga	180
gagtgggtatt	tccatactca	tctggaatat	ttggatcagt	gccatgttcc	agcaacatta	240
acgcacattc	atcttctctg	cattgtacgg	cctgtcagta	ttagacccaa	aaacaaatta	300
catatcttag	gaattcaaaa	taacattcca	cagctttcac	caactagtta	tatttaaagg	360
agaaaactca	tttttatgcc	atgtattgaa	atcaaaccac	cctcatgctg	atatagtttg	420
ctactgcata	cctttatcag	agctgtcctc	tttttgttgt	caaggacatt	aagttgacat	480
cgtctgtcca	gcaggagttt	tactacttct	gaattcccat	tggcagaggc	cagatgtaga	540
gcagtcctat	gagagtgaga	agacttttta	ggaaattgta	gtgcactagc	tacagccata	600
gcaatgattc	atgtaactgc	aaacactgaa	tagcctgcta	ttactctgcc	ttcaaaaaaa	660
aaaaaaa						668

&lt;210&gt; 368

&lt;211&gt; 1512

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 368

gggtcgccca	ggggsgcgt	gggctttcct	cgggtgggtg	tgggttttcc	ctgggtgggg	60
tgggctgggc	trgaatccc	tgctgggggt	ggcaggtttt	ggctgggatt	gacttttytc	120
ttcaaacaga	ttggaaccc	ggagttacct	gctagttggt	gaaactgggt	ggtagacgcg	180

atctgttggc	tactactggc	ttctcctggc	tgttaaaagc	agatgggtgg	tgaggttgat	240
tccatgccgg	ctgcttcttc	tgtgaagaag	ccatttggtc	tcaggagcaa	gatgggcaag	300
tggtgctgcc	gttgcttccc	ctgctgcagg	gagagcggca	agagcaacgt	gggcacttct	360
ggagaccacg	acgactctgc	tatgaagaca	ctcaggagca	agatgggcaa	gtggtgccgc	420
cactgcttcc	cctgctgcag	ggggagtggc	aagagcaacg	tgggcgcttc	tggagaccac	480
gacgaytctg	ctatgaagac	actcaggaac	aagatgggca	agtgggtgctg	ccactgcttc	540
ccctgctgca	gggggagcrg	caagagcaag	gtgggcgctt	ggggagacta	cgatgacagt	600
gccttcatgg	agcccaggta	ccacgtccgt	ggagaagatc	tggacaagct	ccacagagct	660
gcctggtggg	gtaaagtccc	cagaaaggat	ctcatcgtca	tgctcaggga	cactgacgtg	720
aacaagaagg	acaagcaaaa	gaggactgct	ctacatctgg	cctctgccaa	tgggaattca	780
gaagtagtaa	aactcstgct	ggacagacga	tgtcaactta	atgtccttga	caacaaaaag	840
aggacagctc	tgayaaaggc	cgtacaatgc	caggaagatg	aatgtgcgctt	aatgttgctg	900
gaacatggca	ctgatccaaa	tattccagat	gagtatggaa	ataccactct	rcactaygct	960
rtctayaatg	aagataaatt	aatggccaaa	gcactgctct	tataygggtgc	tgatatcgaa	1020
tcaaaaaaca	aggtatagat	ctactaattt	tatcttcaaa	atactgaaat	gcattcattt	1080
taacattgac	gtgtgtaagg	gccagtcttc	cgtatttggg	agctcaagca	taacttgaat	1140
gaaaatattt	tgaaatgacc	taattatctm	agactttatt	ttaaataattg	ttattttcaa	1200
agaagcatta	gagggtacag	tttttttttt	ttaaatgcac	ttctggtaaa	tacttttgtt	1260
gaaaacactg	aatttgtaaa	aggtaatact	tactattttt	caatttttcc	ctcctaggat	1320
ttttttcccc	taatgaatgt	aagatggcaa	aatttgccct	gaaatagggtt	ttacatgaaa	1380
actccaagaa	aagttaacaa	tgtttcagtg	aatagagatc	ctgctccttt	ggcaagttcc	1440
taaaaaacag	taatatgatac	gagggtgatgc	gcctgtcagt	ggcaaggttt	aagatatttc	1500
tgatctcgtg	cc					1512

&lt;210&gt; 369

&lt;211&gt; 1853

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 369

gggtcgccca	gggggsgcgt	gggctttcct	cgggtgggtg	tgggttttcc	ctgggtgggg	60
tgggtcgggc	trgaatcccc	tgctgggggt	ggcaggtttt	ggctgggatt	gacttttytc	120
ttcaaacaga	ttggaaaccc	ggagttacct	gctagttggg	gaaactgggt	ggtagacgcg	180
atctgttggc	tactactggc	ttctcctggc	tgttaaaagc	agatgggtgg	tgaggttgat	240
tccatgccgg	ctgcttcttc	tgtgaagaag	ccatttggtc	tcaggagcaa	gatgggcaag	300
tggtgctgcc	gttgcttccc	ctgctgcagg	gagagcggca	agagcaacgt	gggcacttct	360
ggagaccacg	acgactctgc	tatgaagaca	ctcaggagca	agatgggcaa	gtggtgccgc	420
cactgcttcc	cctgctgcag	ggggagtggc	aagagcaacg	tgggcgcttc	tggagaccac	480
gacgaytctg	ctatgaagac	actcaggaac	aagatgggca	agtgggtgctg	ccactgcttc	540
ccctgctgca	gggggagcrg	caagagcaag	gtgggcgctt	ggggagacta	cgatgacagy	600
gccttcatgg	akcccaggta	ccacgtccrt	ggagaagatc	tggacaagct	ccacagagct	660
gcctggtggg	gtaaagtccc	cagaaaggat	ctcatcgtca	tgctcaggga	cackgaygtg	720
aacaagargg	acaagcaaaa	gaggactgct	ctacatctgg	cctctgccaa	tgggaattca	780
gaagtagtaa	aactcstgct	ggacagacga	tgtcaactta	atgtccttga	caacaaaaag	840
aggacagctc	tgayaaaggc	cgtacaatgc	caggaagatg	aatgtgcgctt	aatgttgctg	900
gaacatggca	ctgatccaaa	tattccagat	gagtatggaa	ataccactct	rcactaygct	960
rtctayaatg	aagataaatt	aatggccaaa	gcactgctct	tataygggtgc	tgatatcgaa	1020
tcaaaaaaca	agcatggcct	cacaccactg	ytacttggtr	tacatgagca	aaaacagcaa	1080
gtsgtgaaat	ttttaatyaa	gaaaaaagcg	aatttaaaat	gcrctggata	gatatggaag	1140
ractgctctc	atacttgctg	tatgtttgtg	atcagcaagt	atagtcagcc	ytctacttga	1200
gcaaaatrtt	gatgtatctt	ctcaagatct	ggaaagacgg	ccagagagta	tgctgtttct	1260
agtcatcatc	atgtaatttg	ccagttactt	tctgactaca	aagaaaaaca	gatgttaaaa	1320
atctcttctg	aaaacagcaa	tccagaacaa	gacttaaaag	tgacatcaga	ggaagagtca	1380
caaaggctta	aaggaagtga	aaacagccag	ccagaggcat	ggaaactttt	aaatttaaac	1440
tttttggttta	atgttttttt	tttttgcctt	aataatatta	gatagtccca	aatgaaatwa	1500
cctatgagac	taggctttga	gaatcaatag	attctttttt	taagaatctt	ttggctagga	1560
gcgggtgtctc	acgcctgtaa	ttccagcacc	ttgagaggct	gagggtgggca	gatcacgaga	1620
tcaggagatc	gagaccatcc	tggctaacac	ggtgaaaccc	catctctact	aaaaatacaa	1680

aaacttagct	gggtgtggtg	gcgggtgcct	gtagtccag	ctactcagga	rgctgaggca	1740
ggagaatggc	atgaacccgg	gaggtggagg	ttgcagtgg	ccgagatccg	ccactacact	1800
ccagcctggg	tgacagagca	agactctgtc	tcaaaaaaaaa	aaaaaaaaaaa	aaa	1853

<210> 370  
 <211> 2184  
 <212> DNA  
 <213> Homo sapien

<400> 370						
ggcacgagaa	ttaaaaccct	cagcaaaaca	ggcatagaag	ggacatacct	taaagtaata	60
aaaaccacct	atgacaagcc	cacagccaac	ataatactaa	atggggaaaa	gttagaagca	120
tttcctctga	gaactgcaac	aataaataca	aggatgctgg	attttgtcaa	atgccttttc	180
tgtgtctgtt	gagatgctta	tgtgactttg	cttttaattc	tgtttatgtg	attatcacat	240
ttattgactt	gcctgtgtta	gaccggaaga	gctgggggtg	ttctcaggag	ccaccgtgtg	300
ctgcggcagc	ttcgggataa	cttgaggctg	catcactggg	gaagaaacac	aytcctgtcc	360
gtggcgctga	tggctgagga	cagagcttca	gtgtggcttc	tctgcgactg	gcttcttcgg	420
ggagttcttc	cttcatagtt	catccatatg	gctccagagg	aaaattatat	tattttgtta	480
tggatgaaga	gtattacgtt	gtgcagatat	actgcagtgt	cttcatctct	tgatgtgtga	540
ttgggtaggt	tccaccatgt	tgccgcagat	gacatgattt	cagtacctgt	gtctggctga	600
aaagtgtttg	tttgtgaatg	gatattgtgg	tttctggatc	tcacacctctg	tgggtggaca	660
gctttctcca	ccttgctgga	agtgacctgc	tgtccagaag	tttgatggct	gaggagtata	720
ccatcgtgca	tgcactcttc	atttcttgca	tttcttctc	cctggatgga	cagggggagc	780
ggcaagagca	acgtgggcac	ttctggagac	cacaacgact	cctctgtgaa	gacgcttggg	840
agcaagaggt	gcaagtgggtg	ctgccactgc	ttcccctgct	gcaggggagc	ggcaagagca	900
acgtggctgc	ttggggagac	tacgatgaca	gcgccttcat	ggatcccagg	taccacgtcc	960
atggagaaga	tctggacaag	ctccacagag	ctgcctgggtg	gggtaaagtc	cccagaaagg	1020
atctcatcgt	catgctcagg	gacacggatg	tgaacaagag	ggacaagcaa	aagaggactg	1080
ctctacatct	ggcctctgcc	aatgggaatt	cagaagtagt	aaaactcgtg	ctggacagac	1140
gatgtcaact	taatgtcctt	gacaacaaaa	agaggacagc	tctgacaaaag	gccgtacaat	1200
gccaggaaga	tgaatgtgcg	ttaatgttgc	tggaacatgg	cactgatcca	aatattccag	1260
atgagtatgg	aaataccact	ctacactatg	ctgtctacaa	tgaagataaa	ttaatggcca	1320
aagcactgct	cttatacggg	gctgatatcg	aatcaaaaaa	caagcatggc	ctcacaccac	1380
tgtactttgg	tatacatgag	caaaaacagc	aagtggtgaa	atttttaatc	aagaaaaaag	1440
cgaatttaaa	tgcgctggat	agatatggaa	gaactgctct	catacttgct	gtatgtttgtg	1500
gatcagcaag	tatagtcagc	cctctacttg	agcaaaatgt	tgatgtatct	tctcaagatc	1560
tggaaagacg	gccagagagt	atgctgtttc	tagtcatcat	catgtaattt	gccagttact	1620
ttctgactac	aaagaaaaac	agatgttaaa	aatctcttct	gaaaacagca	atccagaaca	1680
agacttaaa	ctgacatcag	aggaagagtc	acaaaggctt	aaaggaagtg	aaaacagcca	1740
gccagaggca	tggaaacttt	taaatttaaa	cttttggttt	aatgtttttt	ttttttgcct	1800
taataatatt	agatagtccc	aaatgaaatw	acctatgaga	ctaggctttg	agaatcaata	1860
gattcttttt	ttaagaatct	tttggctagg	agcgggtgtc	cacgcctgta	attccagcac	1920
cttgagaggc	tgaggtgggc	agatcacgag	atcaggagat	cgagaccatc	ctggctaaca	1980
cgggtgaaacc	ccatctctac	taaaaatata	aaaacttagc	tgggtgtggt	ggcgggtgcc	2040
tgtagtccca	gctactcagg	argctgaggc	aggagaatgg	catgaaccgg	ggaggtggag	2100
gttgcaagtga	gccgagatcc	gccactacac	tccagcctgg	gtgacagagc	aagactctgt	2160
ctcaaaaaaa	aaaaaaaaaa	aaaa				2184

<210> 371  
 <211> 1855  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(1855)  
 <223> n = A,T,C or G

&lt;400&gt; 371

tgacgcac	ggccagtg	tgtgccac	acactgac	cccctgag	gtgcacgc	60
cacgcgcac	ttgcacgc	ggcagcggt	tggtggctt	gtaacggctt	gcacgcgcac	120
gccgccccg	cataaccgtc	agactggcct	gtaacggctt	gcaggcgcac	gccgcacgcg	180
cgtaacggct	tggtgcccct	gtaacggctt	gcacgtgcat	gctgcacgcg	cgtaacggc	240
ttggctggca	tgtagccgct	tggttggct	ttgcattytt	tgtkkgctk	ggcgttgkty	300
tcttggttg	acgttccctc	cttgatkg	cgtttccctc	ttggatkgac	gtttcytyty	360
tcgcgttcc	ttgctggact	tgacctttty	tctgctgggt	ttggcattcc	tttgggggtg	420
gctgggtgtt	ttctccgggg	gggktkgccc	ttctgggggt	gggcgtgggk	cgccccagg	480
gggcgtgggc	tttccccggg	tgggtgtggg	ttttcctggg	gtgggggtggg	ctgtgctggg	540
atccccctgc	tgggggttggc	agggattgac	ttttttcttc	aaacagattg	gaaacccgga	600
gtaacntgct	agttggtgaa	actggttgg	agacgcgac	tgctggtact	actgtttctc	660
ctggctgtta	aaagcagatg	gtggctgagg	ttgattcaat	gccggctgct	tcttctgtga	720
agaagccatt	tggctctcagg	agcaagatgg	gcaagtgggtg	cgccactgct	tccccctgtg	780
cagggggagc	ggcaagagca	acgtgggcac	ttctggagac	cacaacgact	cctctgtgaa	840
gacgttggg	agcaagaggt	gcaagtgggtg	ctgcccactg	cttccccctg	tgaggggag	900
cggcaagagc	aacgtggkcg	cttggggaga	ctacgatgac	agcgccctca	tggakccag	960
gtaccacgtc	crtggagaag	atctggacaa	gctccacaga	gctgcctgg	ggggtaaagt	1020
ccccagaaag	gatctcatcg	tcatgctcag	ggacactgay	gtgaacaaga	rggacaagca	1080
aaagaggact	gctctacatc	tggcctctgc	caatgggaat	tcagaagtag	taaaactcgt	1140
gctggacaga	cgatgtcaac	ttaatgtcct	tgacaacaaa	aagaggacag	ctctgacaaa	1200
ggccgtacaa	tgccaggaag	atgaatgtgc	gttaatgttg	ctggaacatg	gcactgatcc	1260
aaatattcca	gatgagtatg	gaaataccac	tctacactat	gctgtctaca	atgaagataa	1320
attaatggcc	aaagcactgc	tcttatacgg	tgctgatatc	gaatcaaaaa	acaaggtata	1380
gatctactaa	ttttatcttc	aaaatactga	aatgcattca	ttttaacatt	gacgtgtgta	1440
agggccagtc	ttccgtattt	ggaagctcaa	gcataaactg	aatgaaaata	ttttgaaatg	1500
acctaattat	ctaagacttt	attttaaaata	ttgttatttt	caaagaagca	ttagagggtg	1560
cagttttttt	tttttaaatg	cacttctggt	aaatactttt	gttgaaaaca	ctgaatttgt	1620
aaaaggtaat	acttactatt	tttcaatttt	tccttcctag	gatttttttc	ccctaataa	1680
tgtaatgag	caaaatttgc	cctgaaatag	gttttacatg	aaaactccaa	gaaaagttaa	1740
acatgtttca	gtgaatagag	atcctgctcc	tttggaagt	tcctaaaaaa	cagtaataga	1800
tacgaggtga	tgccgctgtc	agtggcaagg	tttaagatat	ttctgatctc	gtgcc	1855

&lt;210&gt; 372

&lt;211&gt; 1059

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 372

gcaacgtggg	cacttctgga	gaccacaacg	actcctctgt	gaagacgctt	gggagcaaga	60
ggtgcaagtg	gtgctgcca	ctgcttcccc	tgctgcaggg	gagcggaag	agcaacgtgg	120
gcgcttgrgg	agactmcgat	gacagygcct	tcatggagcc	cagggtaccac	gtccgtggag	180
aagatctgga	caagctccac	agagctgccc	tggtggggta	aagtccccag	aaaggatctc	240
atcgctatgc	tcaggggacac	tgaygtgaac	aagarggaca	agcaaaaagag	gactgctcta	300
catctggcct	ctgccaatgg	gaattcagaa	gtagtaaaac	tcstgctgga	cagacgatgt	360
caacttaatg	tccttgacaa	caaaaagagg	acagctctga	yaaaggccgt	acaatgccag	420
gaagatgaat	gtgcgttaat	gttgctggaa	catggcactg	atccaaatat	tccagatgag	480
tatggaaata	ccactctrca	ctaygctrct	tayaatgaag	ataaattaat	ggccaaagca	540
ctgctcttat	ayggtgctga	tatcgaatca	aaaaacaagg	tatagatcta	ctaattttat	600
cttcaaaata	ctgaaatgca	ttcattttta	cattgacgtg	tgtaagggcc	agtcttccgt	660
atttggagc	tcaagcataa	cttgaatgaa	aatattttga	aatgacctaa	ttatctaaga	720
ctttatttta	aatattgtta	ttttcaaaga	agcattagag	ggtacagttt	ttttttttta	780
aatgcacttc	tggtaaaatac	ttttgttgaa	aacactgaat	ttgtaaaagg	taatacttac	840
tatttttcaa	tttttccctc	ctaggatttt	tttcccctaa	tgaatgtaag	atggcaaaat	900
ttgcctgaa	ataggtttta	catgaaaact	ccaagaaaag	ttaaacatgt	ttcagtgaat	960
agagatcctg	ctccttttgc	aagttcctaa	aaaacagtaa	tagatacgag	gtgatgcgcc	1020
tgtcagtggc	aaggtttaag	atattttctga	tctcgtgcc			1059

<210> 373  
 <211> 1155  
 <212> DNA  
 <213> Homo sapien

<400> 373  
 atggtggttg aggttgattc catgccggct gcctcttctg tgaagaagcc atttgggtctc 60  
 aggagcaaga tgggcaagtg gtgctgccgt tgcttcccct gctgcaggga gagcggcaag 120  
 agcaacgtgg gcacttctgg agaccacgac gactctgcta tgaagacact caggagcaag 180  
 atgggcaagt ggtgccgcca ctgcttcccc tgctgcaggg ggagtggcaa gagcaacgtg 240  
 ggcgcttctg gagaccacga cgactctgct atgaagacac tcaggaacaa gatgggcaag 300  
 tgggtgctgcc actgcttccc ctgctgcagg gggagcggca agagcaagggt gggcgcttgg 360  
 ggagactacg atgacagtgc cttcatggag cccagggtacc acgtccgtgg agaagatctg 420  
 gacaagctcc acagagctgc ctggtggggg aaagtcccca gaaaggatct catcgctcatg 480  
 ctgagggaca ctgacgtgaa caagaaggac aagcaaaaga ggactgctct acatctggcc 540  
 tctgccaatg ggaattcaga agtagtaaaa ctctgctgg acagacgatg tcaacttaat 600  
 gtccttgaca acaaaaagag gacagctctg ataaaggccg tacaatgcca ggaagatgaa 660  
 tgtgcgttaa tggtgctgga acatggcact gatccaaata ttccagatga gtatggaaat 720  
 accactctgc actacgctat ctataatgaa gataaattaa tggccaaagc actgctctta 780  
 tatggtgctg atatcgaatc aaaaaacaag catggcctca caccactgtt acttgggtgta 840  
 catgagcaaa aacagcaagt cgtgaaattt ttaatcaaga aaaaagcgaa tttaaatgca 900  
 ctggatagat atggaaggac tgctctcata cttgctgtat gttgtggatc agcaagtata 960  
 gtcagccttc tacttgagca aaatattgat gtatcttctc aagatctatc tggacagacg 1020  
 gccagagagt atgctgtttc tagtcatcat catgtaattt gccagttact ttctgactac 1080  
 aaagaaaaac agatgctaaa aatctcttct gaaaacagca atccagaaaa tgtctcaaga 1140  
 accagaaata aataa 1155

<210> 374  
 <211> 2000  
 <212> DNA  
 <213> Homo sapien

<400> 374  
 atggtggttg aggttgattc catgccggct gcctcttctg tgaagaagcc atttgggtctc 60  
 aggagcaaga tgggcaagtg gtgctgccgt tgcttcccct gctgcaggga gagcggcaag 120  
 agcaacgtgg gcacttctgg agaccacgac gactctgcta tgaagacact caggagcaag 180  
 atgggcaagt ggtgccgcca ctgcttcccc tgctgcaggg ggagtggcaa gagcaacgtg 240  
 ggcgcttctg gagaccacga cgactctgct atgaagacac tcaggaacaa gatgggcaag 300  
 tgggtgctgcc actgcttccc ctgctgcagg gggagcggca agagcaagggt gggcgcttgg 360  
 ggagactacg atgacagtgc cttcatggag cccagggtacc acgtccgtgg agaagatctg 420  
 gacaagctcc acagagctgc ctggtggggg aaagtcccca gaaaggatct catcgctcatg 480  
 ctgagggaca ctgacgtgaa caagaaggac aagcaaaaga ggactgctct acatctggcc 540  
 tctgccaatg ggaattcaga agtagtaaaa ctctgctgg acagacgatg tcaacttaat 600  
 gtccttgaca acaaaaagag gacagctctg ataaaggccg tacaatgcca ggaagatgaa 660  
 tgtgcgttaa tggtgctgga acatggcact gatccaaata ttccagatga gtatggaaat 720  
 accactctgc actacgctat ctataatgaa gataaattaa tggccaaagc actgctctta 780  
 tatggtgctg atatcgaatc aaaaaacaag catggcctca caccactgtt acttgggtgta 840  
 catgagcaaa aacagcaagt cgtgaaattt ttaatcaaga aaaaagcgaa tttaaatgca 900  
 ctggatagat atggaaggac tgctctcata cttgctgtat gttgtggatc agcaagtata 960  
 gtcagccttc tacttgagca aaatattgat gtatcttctc aagatctatc tggacagacg 1020  
 gccagagagt atgctgtttc tagtcatcat catgtaattt gccagttact ttctgactac 1080  
 aaagaaaaac agatgctaaa aatctcttct gaaaacagca atccagaaca agacttaaaag 1140  
 ctgacatcag aggaagagtc acaaagggtc aaaggcagtg aaaatagcca gccagagaaa 1200  
 atgtctcaag aaccagaaat aaataaggat ggtgatagag aggttgaaga agaaatgaag 1260  
 aagcatgaaa gtaataatgt gggattacta gaaaacctga ctaatgggtg cactgctggc 1320  
 aatggtgata atggattaat tcctcaaagg aagagcagaa cacctgaaaa tcagcaattt 1380  
 cctgacaacg aaagtgaaga gtatcacaga atttgcgaat tagtttctga ctacaaagaa 1440  
 aaacagatgc caaaatactc ttctgaaaac agcaaccag aacaagactt aaagctgaca 1500

tcagaggaag	agtcacaaag	gcttgagggc	agtgaaaatg	gccagccaga	gctagaaaat	1560
tttatggcta	tcgaagaaat	gaagaagcac	ggaagtactc	atgtcgggatt	cccagaaaaac	1620
ctgactaatg	gtgccactgc	tggcaatggt	gatgatggat	taattcctcc	aaggaagagc	1680
agaacacctg	aaagccagca	atttcctgac	actgagaatg	aagagtatca	cagtgcacgaa	1740
caaaatgata	ctcagaagca	atthttgtgaa	gaacagaaca	ctggaatatt	acacgatgag	1800
attctgattc	atgaagaaaa	gcagatagaa	gtgggttga	aaatgaattc	tgagctttct	1860
cttagttgta	agaaagaaaa	agacatcttg	catgaaaata	gtacgttgcg	ggaagaaatt	1920
gccatgctaa	gactggagct	agacacaatg	aaacatcaga	gccagctaaa	aaaaaaaaaa	1980
aaaaaaaaaa	aaaaaaaaaa					2000

<210> 375  
 <211> 2040  
 <212> DNA  
 <213> Homo sapien

<400> 375						
atggtggttg	aggttgattc	catgccggct	gcctcttctg	tgaagaagcc	atttggcttc	60
aggagcaaga	tgggcaagtg	gtgctgccgt	tgcttcccct	gctgcaggga	gagcggcaag	120
agcaacgtgg	gcacttctgg	agaccacgac	gactctgcta	tgaagacact	caggagcaag	180
atgggcaagt	ggtgccgcca	ctgcttcccc	tgctgcaggg	ggagtggcaa	gagcaacgtg	240
ggcgcttctg	gagaccacga	cgactctgct	atgaagacac	tcaggaacaa	gatgggcaag	300
tggtgctgcc	atgcttcccc	ctgctgcagg	gggagcggca	agagcaaggt	ggcgcttgg	360
ggagactacg	atgacagtgc	cttcatggag	cccaggtagc	acgtccgtgg	agaagatctg	420
gacaagctcc	acagagctgc	ctggtggggg	aaagtcccca	gaaaggatct	catcgtcatg	480
ctcagggaca	ctgacgtgaa	caagaaggac	aagcaaaaga	ggactgctct	acatctggcc	540
tctgccaatg	ggaattcaga	agtagtaaaa	ctcctgctgg	acagacgatg	tcaacttaat	600
gtccttgaca	acaaaaagag	gacagctctg	ataaaggccg	tacaatgcca	ggaagatgaa	660
tgtgcgttaa	tggtgctgga	acatggcact	gatccaaata	ttccagatga	gtatggaaat	720
accactctgc	actacgctat	ctataatgaa	gataaattaa	tggccaaagc	actgctctta	780
tatggtgctg	atatcgaatc	aaaaaacaag	catggcctca	caccactggt	acttgggtgta	840
catgagcaaa	aacagcaagt	cgtgaaattt	ttaatcaaga	aaaaagcgaa	tttaaatgca	900
ctggatagat	atggaaggac	tgctctcata	cttgcgtgat	ggtgtggatc	agcaagtata	960
gtcagccttc	tacttgagca	aaatattgat	gtatcttctc	aagatctatc	tggacagacg	1020
gccagagagt	atgctgtttc	tagtcatcat	catgtaattt	gccagttact	ttctgactac	1080
aaagaaaaac	agatgctaaa	aatctcttct	gaaaacagca	atccagaaca	agacttaaa	1140
ctgacatcag	aggaagagtc	acaaagggtc	aaaggcagtg	aaaatagcca	gccagagaaa	1200
atgtctcaag	aaccagaaat	aaataaggat	ggtgatagag	aggttgaaga	agaaatgaag	1260
aagcatgaaa	gtaataatgt	gggattacta	gaaaacctga	ctaattggtg	cactgctggc	1320
aatggtgata	atggattaat	tcctcaaagg	aagagcagaa	cacctgaaaa	tcagcaattt	1380
cctgacaacg	aaagtgaaga	gtatcacaga	atttgogaat	tagtttctga	ctacaaagaa	1440
aaacagatgc	caaaataactc	ttctgaaaac	agcaaccacg	aacaagactt	aaagctgaca	1500
tcagaggaag	agtcacaaag	gcttgagggc	agtgaaaatg	gccagccaga	gaaaagatct	1560
caagaaccag	aaataaataa	ggatggtgat	agagagctag	aaaattttat	ggctatcgaa	1620
gaaatgaaga	agcacggaag	tactcatgtc	ggattcccag	aaaacctgac	taatggtgcc	1680
actgctggca	atggtgatga	tggattaatt	cctccaagga	agagcagaac	acctgaaagc	1740
cagcaatttc	ctgacactga	gaatgaagag	tatcacagtg	acgaacaaaa	tgatactcag	1800
aagcaatttt	gtgaagaaca	gaacactgga	atattacacg	atgagattct	gattcatgaa	1860
gaaaagcaga	tagaagtggg	tgaaaaaatg	aattctgagc	tttctcttag	ttgtaagaaa	1920
gaaaagacga	tcttgcatga	aaatagtacg	ttgcgggaag	aaattgccat	gctaagactg	1980
gagctagaca	caatgaaaca	tcagagccag	ctaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	2040

<210> 376  
 <211> 329  
 <212> PRT  
 <213> Homo sapien

<400> 376  
 Met Asp Ile Val Val Ser Gly Ser His Pro Leu Trp Val Asp Ser Phe



```

      1           5           10           15
Leu His Leu Ala Gly Ser Asp Leu Leu Ser Arg Ser Leu Met Ala Glu
      20           25           30
Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser
      35           40           45
Leu Asp Gly Gln Gly Glu Arg Gln Glu Gln Arg Gly His Phe Trp Arg
      50           55           60
Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val
      65           70           75           80
Val Leu Pro Leu Leu Pro Leu Leu Gln Gly Ser Gly Lys Ser Asn Val
      85           90           95
Val Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr
      100          105          110
His Val His Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp
      115          120          125
Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp
      130          135          140
Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser
      145          150          155          160
Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys
      165          170          175
Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala
      180          185          190
Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly
      195          200          205
Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr
      210          215          220
Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr
      225          230          235          240
Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu
      245          250          255
Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys
      260          265          270
Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu
      275          280          285
Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu
      290          295          300
Glu Gln Asn Val Asp Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu
      305          310          315          320
Ser Met Leu Phe Leu Val Ile Ile Met
      325

```

<210> 377  
 <211> 148  
 <212> PRT  
 <213> Homo sapien

<220>  
 <221> VARIANT  
 <222> (1)...(148)  
 <223> Xaa = Any Amino Acid

```

      <400> 377
Met Thr Xaa Pro Ser Trp Ser Pro Gly Thr Thr Ser Val Glu Lys Ile
      1           5           10           15
Trp Thr Ser Ser Thr Glu Leu Pro Trp Gly Lys Val Pro Arg Lys
      20           25           30
Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Xaa Asp Lys

```

```
<210> 378
<211> 1719
<212> PRT
<213> Homo sapien
```

	<400>	378														
Met 1	Val	Val	Glu	Val	Asp	Ser	Met	Pro	Ala	Ala	Ser	Ser	Val	Lys	Lys	
				5					10					15		
Pro	Phe	Gly	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp	Cys	Cys	Arg	Cys	Phe	
			20					25					30			
Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys	Ser	Asn	Val	Gly	Thr	Ser	Gly	Asp	
		35					40					45				
His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp	
	50					55					60					
Cys	Arg	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	Gly	Lys	Ser	Asn	Val	
65					70					75					80	
Gly	Ala	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Asn	
				85					90					95		
Lys	Met	Gly	Lys	Trp	Cys	Cys	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	
			100					105					110			
Gly	Lys	Ser	Lys	Val	Gly	Ala	Trp	Gly	Asp	Tyr	Asp	Asp	Ser	Ala	Phe	
			115				120					125				
Met	Glu	Pro	Arg	Tyr	His	Val	Arg	Gly	Glu	Asp	Leu	Asp	Lys	Leu	His	
	130					135					140					
Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys	Asp	Leu	Ile	Val	Met	
145					150					155					160	
Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	Lys	Asp	Lys	Gln	Lys	Arg	Thr	Ala	
				165					170					175		
Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	Asn	Ser	Glu	Val	Val	Lys	Leu	Leu	
			180				185						190			
Leu	Asp	Arg	Arg	Cys	Gln	Leu	Asn	Val	Leu	Asp	Asn	Lys	Lys	Arg	Thr	
		195					200					205				
Ala	Leu	Ile	Lys	Ala	Val	Gln	Cys	Gln	Glu	Asp	Glu	Cys	Ala	Leu	Met	
	210					215					220					
Leu	Leu	Glu	His	Gly	Thr	Asp	Pro	Asn	Ile	Pro	Asp	Glu	Tyr	Gly	Asn	
225					230					235				240		
Thr	Thr	Leu	His	Tyr	Ala	Ile	Tyr	Asn	Glu	Asp	Lys	Leu	Met	Ala	Lys	
				245				250						255		
Ala	Leu	Leu	Leu	Tyr	Gly	Ala	Asp	Ile	Glu	Ser	Lys	Asn	Lys	His	Gly	
		260					265						270			
Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys	Gln	Gln	Val	Val	
		275				280						285				

Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr  
 290 295 300  
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile  
 305 310 315 320  
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu  
 325 330 335  
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val  
 340 345 350  
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile  
 355 360 365  
 Ser Ser Glu Asn Ser Asn Pro Glu Asn Val Ser Arg Thr Arg Asn Lys  
 370 375 380  
 Pro Arg Thr His Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser  
 385 390 395 400  
 Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys  
 405 410 415  
 Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly  
 420 425 430  
 Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys  
 435 440 445  
 Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly  
 450 455 460  
 Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys  
 465 470 475 480  
 Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys  
 485 490 495  
 Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp  
 500 505 510  
 Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu  
 515 520 525  
 Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp  
 530 535 540  
 Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln  
 545 550 555 560  
 Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val  
 565 570 575  
 Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn  
 580 585 590  
 Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu  
 595 600 605  
 Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp  
 610 615 620  
 Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys  
 625 630 635 640  
 Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys  
 645 650 655  
 Asn Lys His Gly Leu Thr Pro Leu Leu Gly Val His Glu Gln Lys  
 660 665 670  
 Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala  
 675 680 685  
 Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly  
 690 695 700  
 Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser  
 705 710 715 720  
 Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser  
 725 730 735  
 His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln  
 740 745 750

Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys  
 755 760 765  
 Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser  
 770 775 780  
 Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp  
 785 790 795 800  
 Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly  
 805 810 815  
 Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn  
 820 825 830  
 Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe  
 835 840 845  
 Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser  
 850 855 860  
 Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn  
 865 870 875 880  
 Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu  
 885 890 895  
 Glu Gly Ser Glu Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile  
 900 905 910  
 Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn  
 915 920 925  
 Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro  
 930 935 940  
 Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu  
 945 950 955 960  
 Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe  
 965 970 975  
 Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His  
 980 985 990  
 Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser  
 995 1000 1005  
 Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu  
 1010 1015 1020  
 Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His  
 1025 1030 1035 1040  
 Gln Ser Gln Leu Pro Arg Thr His Met Val Val Glu Val Asp Ser Met  
 1045 1050 1055  
 Pro Ala Ala Ser Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met  
 1060 1065 1070  
 Gly Lys Trp Cys Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys  
 1075 1080 1085  
 Ser Asn Val Gly Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr  
 1090 1095 1100  
 Leu Arg Ser Lys Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys  
 1105 1110 1115 1120  
 Arg Gly Ser Gly Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp  
 1125 1130 1135  
 Ser Ala Met Lys Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His  
 1140 1145 1150  
 Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp  
 1155 1160 1165  
 Gly Asp Tyr Asp Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg  
 1170 1175 1180  
 Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val  
 1185 1190 1195 1200  
 Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys  
 1205 1210 1215

Lys Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly  
 1220 1225 1230  
 Asn Ser Glu Val Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn  
 1235 1240 1245  
 Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys  
 1250 1255 1260  
 Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro  
 1265 1270 1275 1280  
 Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr  
 1285 1290 1295  
 Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp  
 1300 1305 1310  
 Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val  
 1315 1320 1325  
 His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala  
 1330 1335 1340  
 Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala  
 1345 1350 1355 1360  
 Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn  
 1365 1370 1375  
 Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr  
 1380 1385 1390  
 Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr  
 1395 1400 1405  
 Lys Glu Lys Gln Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu  
 1410 1415 1420  
 Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly  
 1425 1430 1435 1440  
 Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn  
 1445 1450 1455  
 Lys Asp Gly Asp Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser  
 1460 1465 1470  
 Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly  
 1475 1480 1485  
 Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu  
 1490 1495 1500  
 Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys  
 1505 1510 1515 1520  
 Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser  
 1525 1530 1535  
 Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu  
 1540 1545 1550  
 Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser  
 1555 1560 1565  
 Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe  
 1570 1575 1580  
 Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe  
 1585 1590 1595 1600  
 Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly  
 1605 1610 1615  
 Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro  
 1620 1625 1630  
 Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln  
 1635 1640 1645  
 Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile  
 1650 1655 1660  
 Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser  
 1665 1670 1675 1680

Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn  
 1685 1690 1695  
 Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr  
 1700 1705 1710  
 Met Lys His Gln Ser Gln Leu  
 1715

<210> 379  
 <211> 656  
 <212> PRT  
 <213> Homo sapien

<400> 379  
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys  
 1 5 10 15  
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe  
 20 25 30  
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp  
 35 40 45  
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp  
 50 55 60  
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val  
 65 70 75 80  
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn  
 85 90 95  
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser  
 100 105 110  
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe  
 115 120 125  
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His  
 130 135 140  
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met  
 145 150 155 160  
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala  
 165 170 175  
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu  
 180 185 190  
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr  
 195 200 205  
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met  
 210 215 220  
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn  
 225 230 235 240  
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys  
 245 250 255  
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly  
 260 265 270  
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val  
 275 280 285  
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr  
 290 295 300  
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile  
 305 310 315 320  
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu  
 325 330 335  
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val  
 340 345 350  
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile

```
<210> 380
<211> 671
<212> PRT
<213> Homo sapien
```

<div> <div>&lt;400&gt;</div> <div>380</div> </div>															
Met	Val	Val	Glu	Val	Asp	Ser	Met	Pro	Ala	Ala	Ser	Ser	Val	Lys	Lys
1				5					10					15	
Pro	Phe	Gly	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp	Cys	Cys	Arg	Cys	Phe
			20					25					30		
Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys	Ser	Asn	Val	Gly	Thr	Ser	Gly	Asp
		35					40					45			
His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp
	50					55					60				
Cys	Arg	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	Gly	Lys	Ser	Asn	Val
65					70					75				80	
Gly	Ala	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Asn
				85					90					95	
Lys	Met	Gly	Lys	Trp	Cys	Cys	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser
			100					105					110		

Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe  
 115 120 125  
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His  
 130 135 140  
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met  
 145 150 155 160  
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala  
 165 170 175  
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu  
 180 185 190  
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr  
 195 200 205  
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met  
 210 215 220  
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn  
 225 230 235 240  
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys  
 245 250 255  
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly  
 260 265 270  
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val  
 275 280 285  
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr  
 290 295 300  
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile  
 305 310 315 320  
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu  
 325 330 335  
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His Val  
 340 345 350  
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile  
 355 360 365  
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu  
 370 375 380  
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys  
 385 390 395 400  
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu  
 405 410 415  
 Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn  
 420 425 430  
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro  
 435 440 445  
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu  
 450 455 460  
 Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu  
 465 470 475 480  
 Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp  
 485 490 495  
 Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu  
 500 505 510  
 Asn Gly Gln Pro Glu Lys Arg Ser Gln Glu Pro Glu Ile Asn Lys Asp  
 515 520 525  
 Gly Asp Arg Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys Lys  
 530 535 540  
 His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly Ala  
 545 550 555 560  
 Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser Arg  
 565 570 575



Thr	Pro	Glu	Ser	Gln	Gln	Phe	Pro	Asp	Thr	Glu	Asn	Glu	Glu	Tyr	His
			580					585						590	
Ser	Asp	Glu	Gln	Asn	Asp	Thr	Gln	Lys	Gln	Phe	Cys	Glu	Glu	Gln	Asn
		595					600					605			
Thr	Gly	Ile	Leu	His	Asp	Glu	Ile	Leu	Ile	His	Glu	Glu	Lys	Gln	Ile
	610					615					620				
Glu	Val	Val	Glu	Lys	Met	Asn	Ser	Glu	Leu	Ser	Leu	Ser	Cys	Lys	Lys
625					630					635					640
Glu	Lys	Asp	Ile	Leu	His	Glu	Asn	Ser	Thr	Leu	Arg	Glu	Glu	Ile	Ala
				645					650					655	
Met	Leu	Arg	Leu	Glu	Leu	Asp	Thr	Met	Lys	His	Gln	Ser	Gln	Leu	
			660					665					670		

&lt;210&gt; 381

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 381

ggagaagcgt	ctgctggggc	aggaaggggt	ttccctgccc	tctcacctgt	ccctcaccaa	60
ggtaacatgc	ttcccctaag	ggtatcccaa	cccaggggcc	tcacatgac	ctctgagggg	120
ccaatatccc	aggagaagca	ttggggagtt	gggggcaggt	gaaggaccca	ggactcacac	180
atcctggggc	tccaaggcag	aggagagggt	cctcaagaag	gtcaggagga	aaatccgtaa	240
caagcagtca	g					251

&lt;210&gt; 382

&lt;211&gt; 3279

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 382

cttctctgcag	cccccatgct	ggtgaggggc	acgggcagga	acagtggacc	caacatggaa	60
atgctggagg	gtgtcaggaa	gtgatcgggc	tctggggcag	ggaggagggg	tggggagtgt	120
cactgggagg	ggacatcctg	cagaaggtag	gagtgcagca	acacccgctg	caggggaggg	180
gagagccctg	cggcacctgg	gggagcagag	ggagcagcac	ctgcccaggc	ctgggaggag	240
gggcctggag	ggcgtgagga	ggagcgaggg	ggctgcatgg	ctggagttag	ggatcagggg	300
cagggcgcga	gatggcctca	cacagggaag	agaggggccc	tcctgcaggg	cctcacctgg	360
gccacaggag	gacactgctt	ttcctctgag	gagtcaggag	ctgtggatgg	tgctggacag	420
aagaaggaca	gggcctggct	caggtgtcca	gaggctgtcg	ctggcttccc	tttgggatca	480
gactgcaggg	agggagggcg	gcagggttgt	ggggggagtg	acgatgagga	tgacctgggg	540
gtggctccag	gccttgcccc	tgctggggcc	ctcaccagc	ctccctcaca	gtctcctggc	600
cctcagtctc	tcccctccac	tccatcctcc	atctggcctc	agtgggtcat	tctgatcact	660
gaactgacca	taccagccc	tgcccacggc	cctccatggc	tccccaatgc	cctggagagg	720
ggacatctag	tcagagagta	gtcctgaaga	ggtggcctct	gcgatgtgcc	tgtgggggca	780
gcacatcctg	gatgggtccc	gccctcatcc	tgctgacctg	tctgcaggga	ctgtcctcct	840
ggaccttgcc	ccttgtgcag	gagctggacc	ctgaagtccc	ctccccatag	gccaagactg	900
gagccttggt	ccctctgttg	gactccctgc	ccatattctt	gtgggagtgg	gttctggaga	960
cattttctgtc	tgttcctgag	agctgggaat	tgctctcagt	catctgcctg	cgcggttctg	1020
agagatggag	ttgcctaggg	agttattggg	gccaatcttt	ctcactgtgt	ctctcctcct	1080
ttacccttag	ggtgattctg	gggggtccact	tgtctgtaat	ggtgtgcttc	aaggtatcac	1140
atcattgggg	cctgagccat	gtgccctgcc	tgaagaagcct	gctgtgtaca	ccaaggtggg	1200
gcattaccgg	aagtggatca	aggacaccat	cgcagccaac	ccctgagtgc	ccctgtccca	1260
ccctacctc	tagtaaat	aagtcacact	cacgttctg	catcacttgg	cctttctgga	1320
tgctggacac	ctgaagcttg	gaactcacct	ggccgaagct	cgagcctcct	gagtcctact	1380
gacctgtgct	ttctgggtgtg	gagtcacagg	ctgctaggaa	aaggaatggg	cagacacagg	1440
tgtatgccaa	tgttttctgaa	atgggtataa	tttcgtcctc	tccttcggaa	cactggctgt	1500
ctctgaagac	ttctcgctca	gtttcagtga	ggacacacac	aaagacgtgg	gtgacctgt	1560
tgtttctggg	gtgcagagat	gggaggggtg	gggcccaccc	tggaagagt	gacagtgaca	1620

```

caaggtggac actctctaca gatcactgag gataagctgg agccacaatg catgaggcac 1680
acacacagca aggttgacgc tgtaaacata gcccacgctg tcctgggggc actgggaagc 1740
ctagataagg cagttagcag aaagaagggg aggatcctcc tatgttggtg aaggagggac 1800
tagggggaga aactgaaagc tgattaatta caggaggttt gttcaggtcc cccaaaccac 1860
cgtcagattt gatgatttcc tagcaggact tacagaaata aagagctatc atgctgtggt 1920
ttattatggt ttgttacatt gataggatac atactgaaat cagcaaacaa aacagatgta 1980
tagattagag tgtggagaaa acagaggaaa acttgcagtt acgaagactg gcaacttggc 2040
tttactaagt tttcagactg gcaggaagtc aaacctatta ggctgaggac cttgtggagt 2100
gtagctgac cagctgatag aggaactagc cagggtggggg cctttccctt tggatggggg 2160
gcatatccga cagttattct ctccaagtgg agacttacgg acagcatata attctccctg 2220
caaggatgta tgataatatg tacaaagtaa ttccaactga ggaagctcac ctgaccta 2280
gtgtccaggg tttttactgg ggggtctgtg gacgagtatg gactacttga ataattgacc 2340
tgaagtccct agacctgagg ttccctagag ttcaaacaga tacagcatgg tccagagtcc 2400
cagatgtaca aaaacagggg ttcatcacia atcccattct tagcatgaag ggtctggcat 2460
ggcccaaggc cccaagtata tcaaggcact tgggcagaac atgccaagga atcaaattgc 2520
atctcccagg agttattcaa gggtagagcc tttacttggg atgtacaggc tttgagcagt 2580
gcagggctgc tgagtcaacc ttttattgta caggggatga gggaaagga gaggatgagg 2640
aagccccctt ggggatttgg tttggtcttg tgatcaggtg gtctatgggg ctatccctac 2700
aaagaagaat ccagaaatag gggcacattg aggaatgata ctgagcccaa agagcattca 2760
atcattgttt tatttgcctt cttttcacac cattggtgag ggagggatta ccacctggg 2820
gttatgaaga tggttgaaca cccacacat agcaccggag atatgagatc aacagtttct 2880
tagccataga gattcacagc ccagagcagg aggacgctgc acaccatgca ggatgacatg 2940
ggggatgcgc tcgggatttg tgtgaagaag caaggactgt tagaggcagg ctttatagta 3000
acaagacggt ggggcaaaact ctgatttccg tgggggaatg tcatggtctt gctttactaa 3060
gttttgagac tggcaggtag tgaaactcat taggctgaga acctgttgga atgcagctga 3120
cccagctgat agaggaagta gccaggtggg agcctttccc agtgggtgtg ggacatatct 3180
ggcaagattt tgtggcactc ctggttacag atactggggc agcaaataaa actgaatctt 3240
gttttcagac cttaaaaaaa aaaaaaaaaa aaaagtttt 3279

```

&lt;210&gt; 383

&lt;211&gt; 154

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 383

```

Met Ala Gly Val Arg Asp Gln Gly Gln Gly Ala Arg Trp Pro His Thr
          5                                10                                15

```

```

Gly Lys Arg Gly Pro Leu Leu Gln Gly Leu Thr Trp Ala Thr Gly Gly
          20                                25                                30

```

```

His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln
          35                                40                                45

```

```

Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe
          50                                55                                60

```

```

Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly
          65                                70                                75                                80

```

```

Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala
          85                                90                                95

```

```

Trp Ala Leu Thr Gln Pro Pro Ser Gln Ser Pro Gly Pro Gln Ser Leu
          100                                105                                110

```

```

Pro Ser Thr Pro Ser Ser Ile Trp Pro Gln Trp Val Ile Leu Ile Thr
          115                                120                                125

```

Glu Leu Thr Ile Pro Ser Pro Ala His Gly Pro Pro Trp Leu Pro Asn  
 130 135 140

Ala Leu Glu Arg Gly His Leu Val Arg Glu  
 145 150

<210> 384

<211> 557

<212> DNA

<213> Homo sapiens

<400> 384

```

ggatcctcta gagcgccgc ctactactac taaattcgcg gccgcgtcga cgaagaagag 60
aaagatgtgt ttgttttgg actctctgtg gtcccttcca atgctgtggg tttccaacca 120
ggggaagggt cctttttgca ttgccaagt ccataaccat gagcactact ctaccatggt 180
tctgcctcct ggccaagcag gctggtttgc aagaatgaaa tgaatgattc tacagctagg 240
acttaacctt gaagtggaaa gtcttgcaat cccatttgca ggatccgtct gtgcacatgc 300
ctctgtagag agcagcattc ccagggacct tggaaacagt tggcactgta aggtgcttgc 360
tccccaagac acatcctaaa aggtgttgta atgggtgaaa cgtcttcctt ctttattgcc 420
ccttcttatt tatgtgaaca actgtttgtc tttttttgta tcttttttaa actgtaaagt 480
tcaattgtga aaatgaatat catgcaaata aattatgcga tttttttttc aaagtaaaaa 540
aaaaaaaaaa aaaaaaa 557

```

<210> 385

<211> 337

<212> DNA

<213> Homo sapiens

<400> 385

```

ttcccagggt atgtgcgagg gaagacacat ttactatcct tgatggggct gattccttta 60
gtttctctag cagcagatgg gttaggagga agtgacccaa gtggttgact cctatgtgca 120
tctcaaagcc atctgctgtc ttcgagtacg gacacatcat cactcctgca ttgttgatca 180
aaacgtggag gtgcttttcc tcagctaaga agcccttagc aaaagctcga atagacttag 240
tatcagacag gtccagtttc cgcaccaaca cctgctgggt cctgtcgtg gtctggatct 300
ctttggccac caattcccc ttttccacat cccggca 337

```

<210> 386

<211> 300

<212> DNA

<213> Homo sapiens

<400> 386

```

gggcccgtca ccggcccagg cccgcctcg cgagtctcc tccccgggtg cctgcccga 60
gcccgtcggg ccagaggggt gggcgcgggg ctgcctctac cggtggcggt ctgtaactca 120
gcgaccttgg ccgaaggct ctagcaagga ccacccgacc ccagccgcgg cggcgggcgc 180
gcggaacttg cccggtgtgt gggcgggagc ggactgcgtg tccgcggacg ggcagcgaag 240
atgttagcct tcgctgccag gaccgtggac cgatcccagg gctgtggtgt aacctcagcc 300

```

<210> 387

<211> 537

<212> DNA

<213> Homo sapiens

<400> 387

```

gggcccagtc gggcaccaag ggactctttg caggcttctt tctcggatc atcaaggctg 60
ccccctctg tgccatcatg atcagcacct atgagttcgg caaaagcttc ttccagaggc 120

```

```

tgaaccagga ccggettctg ggcggctgaa aggggcaagg aggcaaggac cccgtctctc 180
ccacggatgg ggagagggca ggaggagacc cagccaagtg ccttttcctc agcactgagg 240
gagggggctt gtttcccttc cctcccgcg acaagctcca gggcagggct gtccctctgg 300
gcggcccagc acttctcag acacaacttc ttctgtctgc tccagtcgtg gggatcatca 360
cttaccacc cccaagttc aagaccaa atctccagctg ccccttctgt gtttccctgt 420
gtttgtgta gctgggcatg tctccaggaa ccaagaagcc ctcagcctgg tgtagtctcc 480
ctgacccttg ttaattcctt aagtctaaag atgatgaact tcaaaaaaaaa aaaaaaa 537

```

&lt;210&gt; 388

&lt;211&gt; 520

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 388

```

aggataattt ttaaaccaat caaatgaaaa aaacaaacaa acaaaaaagg aaatgtcatg 60
tgaggttaaa ccagtttgca ttccccta atgtggaaaa taagaggact actcagcact 120
gtttgaagat tgctcttct acagcttctg agaattgtgt tatttcaact gccaaagtga 180
ggacccctc cccaacatgc ccagcccac ccctaagcat ggtcccttgt caccaggcaa 240
ccaggaaact gctacttgt gacctacca gagaccagga gggtttggtt agctcacagg 300
acttcccca cccagaaga ttagcatccc atactagact cataactcaac tcaactaggc 360
tcataactca ttgatggta ttagacaatt ccatttcttt ctggttatta taaacagaaa 420
atctttctc ttctcattac cagtaaaggc tcttggtatc tttctgttgg aatgatttct 480
atgaacttgt cttattttaa tgggtgggtt ttttctggt 520

```

&lt;210&gt; 389

&lt;211&gt; 365

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 389

```

cgttgcccc gtttgacaga aggaaaggcg gagcttattc aaagtctaga gggagtggag 60
gagttaaggc tggatttcag atctgcctgg ttccagccgc agtgtgccct ctgctcccc 120
aacgactttc caaataatct caccagcgcc ttccagctca ggcgtcctag aagcgtcttg 180
aagcctatgg ccagctgtct ttgtgttccc tctcaccgc ctgtcctcac agctgagact 240
cccaggaaac cttcagacta ccttctctg ccttcagcaa ggggcgttgc ccacattctc 300
tgagggtcag tggaagaacc tagactccca ttgctagagg tagaaagggg aagggtgctg 360
gggag 365

```

&lt;210&gt; 390

&lt;211&gt; 221

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(221)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 390

```

tgctctcca tcttgcccc gacttctctg tcaggaaagt ggggatggac cccatctgca 60
tacacggnnt ctcatgggtg tggaacatct ctgcttgcgg tttcagggaag gcctctggct 120
gctctangag tctgancnga ntctgtgccc cantntgaca naaggaaagg cggagcttat 180
tcaaagtcta gagggagtgg aggagttaag gctggatttc a 221

```

&lt;210&gt; 391

&lt;211&gt; 325

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(325)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 391

```

tggagcaggt cccgaggcct ccctagagcc tggggccgac tctgtgncga tgcangcttt 60
ctctcgcgcc cagcctggag ctgctcctgg catctaccaa caatcagncg aggcgagcag 120
tagccagggc actgctgcc aacagccagtc cnnataccat catgtnaccc ggtgngctct 180
naanttngat ntccanagcc ctaccccatcn tagttctgct ctcccaccgg ntaccagccc 240
cactgcccag gaatcctaca gccagtaccc tgtcccgcag tctctaccta ccagtacgat 300
gagacctccg gctactacta tgacc                                     325

```

&lt;210&gt; 392

&lt;211&gt; 277

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(277)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 392

```

atattgttta actccttcoct ttatatcttt taacattttc atggngaaaag gttcacatct 60
agtctcactt ngcnagngn ctccacttg agtctcttcc ccggcctggn ccagtnghaa 120
antaccanga accgncatgn cttaanaacn ncctgggttn tgggttnntc aatgactgca 180
tgcagtgcac caccctgtcc actacgtgat gctgtaggat taaagtctca cagtgggagg 240
ctgaggatac agcgccgcgt cctgtgttgc tgggggaa                                     277

```

&lt;210&gt; 393

&lt;211&gt; 566

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 393

```

actagtccag tgtggtggaa ttgcgggccc cgtcgacgga caggtcagct gtctggctca 60
gtgatctaca ttctgaagtt gtctgaaaat gtcttcatga ttaaattcag cctaaacggt 120
ttgccgggaa cactgcagag acaatgctgt gagtttccaa ccttagccca tctgcgggca 180
gagaaggctc agtttgtcca tcagcattat catgatatac ggactgggta cttggttaag 240
gaggggtcta ggagatctgt cccttttaga gacaccttac ttataatgaa gtatttgga 300
gggtggtttt caaaaagtaga aatgtcctgt attccgatga tcatcctgta aacattttat 360
catttattaa tcatccctgc ctgtgtctat tattatattc atatctctac gctggaaact 420
ttctgcctca atgtttactg tgcctttgtt tttgctagtt tgtgttggtg aaaaaaaaaa 480
cattctctgc ctgagtttta atttttgtcc aaagttattt taatctatac aattaaaagc 540
ttttgcctat caaaaaaaaaa aaaaaa                                     566

```

&lt;210&gt; 394

&lt;211&gt; 384

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(384)

&lt;223&gt; n = A,T,C or G

<400> 394  
gaacatacat gtcccggcac ctgagctgca gtctgacatc atcgccatca cgggcctcgc 60  
tgcaaattng gaccgggcca aggctggact gctggagcgt gtgaaggagc tacaggccna 120  
gcaggaggac cgggctttta ggagttttta gctgagtgtc actgtagacc ccaaatacca 180  
tccaagatt atcgggagaa agggggcagt aattacccaa atccggttg agcatgacgt 240  
gaacatccag tttoctgata aggaogatgg gaaccagccc caggaccaa ttaccatcac 300  
agggtacgaa aagaacacag aagctgccag ggatgctata ctgagaattg tgggtgaact 360  
tgagcagatg gtttctgagg acgt 384

<210> 395  
<211> 399  
<212> DNA  
<213> Homo sapiens

<400> 395  
ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat cagaagtgc 60  
tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg atgagccagt 120  
tatcagaggt ttcattcattg cggaaattgt ggagtctaag gaaatcatgg cctctgaagt 180  
attcacgtct ttccagtacc ctgagttctc tatagagttg cctaacacag gcagaattgg 240  
ccagctactt gtctgcaatt gtatcttcaa gaataccctg gccatccctt tgactgacgt 300  
caagttctct ttggaaagcc tgggcatctc ctactacag acctctgacc atgggacggt 360  
gcagcctggt gagaccatcc aatcccaaat aaaatgcac 399

<210> 396  
<211> 403  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(403)  
<223> n = A,T,C or G

<400> 396  
tggagttntc agtgcaaaca agccataaag cttcagtagc aaattactgt ctcacagaaa 60  
gacattttca acttctgctc cagctgctga taaaacaaat catgtgttta gcttgactcc 120  
agacaaggac aacctgttcc ttcataactc tctagagaaa aaaaggagtt gttagtagat 180  
actaaaaaaaa gtggatgaat aatctggata tttttcctaa aaagattcct tgaaacacat 240  
taggaaaatg gagggcctta tgatcagaat gctagaatta gtccattgtg ctgaagcagg 300  
gtttagggga gggagtggag gataaaagaa ggaaaaaag aagagtgaga aaacctattt 360  
atcaaagcag gtgctatcac tcaatgttag gccctgctct ttt 403

<210> 397  
<211> 100  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(100)  
<223> n = A,T,C or G

<400> 397  
actagtnacg tgtgggtggaa ttcgcggccg cgtcgacctc naanccatct ctatagcaaa 60  
tccatccccg ctctggttg gtnacagaat gactgacaaa 100

<210> 398  
<211> 278

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(278)

<223> n = A,T,C or G

<400> 398

```
gcggccgcgt cgacagcagt tccgccagcg ctcgcccctg ggtggggatg tgctgcacgc 60
ccacctggac atctggaagt cagcggcctg gatgaaagag cggacttcac ctggggcgat 120
tcaactactgt gcctcgacca gtgaggagag ctggaccgac agcgagggtg actcatcatg 180
ctccggggcag cccatccacc tgtggcagtt cctcaaggag ttgctactca agccccacag 240
ctatggccgc ttcat tangt ggctcaacaa ggagaagg 278
```

<210> 399

<211> 298

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(298)

<223> n = A,T,C or G

<400> 399

```
acggagggtg aggaagcgnc cctgggatcg anaggatggg tcctgncatt gaccncctcn 60
gggggtgccng catggagcgc atgggcgcgg gcctgggcca cggcatggat cgcgtgggct 120
ccgagatcga gcgcatgggc ctggtcatgg accgcatggg ctccgtggag cgcgtgggct 180
ccggcattga gcgcatgggc ccgctgggccc tcgaccacat ggccctccanc attganccga 240
tgggccagac catggagcgc attggctctg gcgtggagcn catgggtgcc ggcattggg 298
```

<210> 400

<211> 548

<212> DNA

<213> Homo sapiens

<400> 400

```
acatcaacta ctctctcatt ttaaggtatg gcagttccct tcatccctt ttctgcctt 60
gtacatgtac atgtatgaaa tttccttctc ttaccgaact ctctccacac atcacaagg 120
caaagaacca cagccttaga agggtaagag ggcaccctat gaaatgaaat ggtgatttct 180
tgagtctctt ttttccacgt ttaaggggcc atggcaggac ttagagttgc gagttaagac 240
tgcagagggc tagagaatta tttcatacag gctttgaggc caccatgtc acttatccc 300
tataccctct caccatcccc ttgtctactc tgatgcccc aagatgcaac tgggcagcta 360
gttggcccca taattctggg cttttgttgt ttgttttaat tacttgggca tcccaggaag 420
ctttccagtg atctcctacc atgggcccc ctctgggat caagccctc ccaggccctg 480
tccccagccc ctctgcccc agcccacccg cttgccttgg tgctcagccc tccattggg 540
agcaggtt 548
```

<210> 401

<211> 355

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(355)

<223> n = A,T,C or G

<400> 401  
actgtttcca tgttatgttt ctacacattg ctacctcagt gtccttgaa acttagcttt 60  
tgatgtctcc aagtagtcca ctttcattta actctttgaa actgtatcat ctttgccaag 120  
taagagtggg ggcctatttc agctgctttg acaaaatgac tggctcctga cttaacgttc 180  
tataaatgaa tgtgctgaag caaagtgcc atggtggcgg cgaagaagan aaagatgtgt 240  
tttgttttgg actctctgtg gtcccttcca atgctgnngg tttccaacca ggggaagggt 300  
cccttttgca ttgccaagtg ccataaccat gagcactact ctaccatggn tctgc 355

<210> 402

<211> 407

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(407)

<223> n = A,T,C or G

<400> 402  
atggggcaag ctggataaag aaccaagacc cactggagta tgctgtcttc aagaaaccca 60  
tctcacatgc ggtggcatac ataggctcaa aataaaggaa tggagaaaaa tatttcaagc 120  
aaatggaaaa cagaaaaaag cagggtgttc actcctactt tctgacaaaa cagactatgc 180  
gaataaagat aaaaaagaga aggacattac aaaggtggtc ctgacctttg ataaatctca 240  
ttgcttgata ccaacctggg ctgttttaat tgcccaaacc aaaaggataa tttgctgagg 300  
ttgtggagct tctccctgc agagagtccc tgatctccca aaatttggtt gagatgtaag 360  
gntgattttg ctgacaactc cttttctgaa gttttactca tttccaa 407

<210> 403

<211> 303

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (1)...(303)

<223> n = A,T,C or G

<400> 403  
cagtatttat agccnaactg aaaagctagt agcaggcaag tctcaaattcc aggcacccaa 60  
tcctaagcaa gagccatggc atggtgaaaa tgcaaaagga gagtctggcc aatctacaaa 120  
tagagaacaa gacctactca gtcataaaca aaaaggcaga caccaacatg gatctcatgg 180  
gggattggat attgtaatta tagagcagga agatgacagt gatcgtcatt tggcacaaca 240  
tcttaacaac gaccgaaacc cattattttac ataaacctcc attcggtaac catgttgaaa 300  
gga 303

<210> 404

<211> 225

<212> DNA

<213> Homo sapiens

<400> 404

aagtgttaact tttaaaaatt tagtggattt tgaaaattct tagaggaaag taaaggaaaa 60  
attgttaatg cactcattta cctttacatg gtgaaagttc tctcttgatc ctacaaacag 120  
acattttcca ctctgttttc catagtgtt aagtgtatca gatgtgttgg gcatgtgaat 180  
ctccaagtgc ctgtgtaata aataaagtat ctttatttca ttcatt 225

<210> 405



<211> 334  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(334)  
<223> n = A,T,C or G

<400> 405  
gagctgttat actgtgagtt ctactaggaa atcatcaaat ctgaggggttg tctggaggac 60  
ttcaatacac ctccccccat agtgaatcag cttccagggg gtccagtccc tctccttact 120  
tcatccccat cccatgccaa aggaagaccc tccctccttg gctcacagcc ttctctaggc 180  
ttcccagtcg ctccaggaca gagtgggtta tgttttcagc tccatccttg ctgtgagtgt 240  
ctggtgcggt tgtgcctcca gcttctgctc agtgcttcat ggacagtgtc cagcccatgt 300  
cactctccac tctctcanng tggatccac ccct 334

<210> 406  
<211> 216  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(216)  
<223> n = A,T,C or G

<400> 406  
tttcatacct aatgagggag ttganatnac atnnaaccag gaaatgcatg gatctcaang 60  
gaaacaaaca cccaataaac tcggagtggc agactgacaa ctgtgagaca tgcacttgct 120  
acnaaacaca aatttnatgt tgcacccttg tttctacacc tgtgggttat gacaaagaca 180  
actgccaaag aatnttcaag aaggaggact gccant 216

<210> 407  
<211> 413  
<212> DNA  
<213> Homo sapiens

<400> 407  
gctgacttgc tagtatcatc tgcattcatt gaagcacaag aacttcatgc cttgactcat 60  
gtaaatgcaa taggattaaa aaataaattt gatatcacat ggaaacagac aaaaaatatt 120  
gtacaacatt gcacccagtg tcagattcta cacctggcca ctcaggaagc aagagttaat 180  
cccagaggtc tatgtcctaa tgtgttatgg caaatggatg tcatgcacgt accttcattt 240  
ggaaaattgt catttgtcca tgtgacagtt gatacttatt cacatttcat atgggcaacc 300  
tgccagacag gagaaagtct tcccatgtta aaagacattt attatcttgt tttcctgtca 360  
tgggagttcc agaaaaagtt aaaacagaca atgggccagg ttctgtagta aag 413

<210> 408  
<211> 183  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(183)  
<223> n = A,T,C or G

<400> 408

```

ggagctngcc ctcaattcct ccatntctat gttancatat ttaatgtctt ttgnnattaa 60
tncttaacta gttaatcctt aaagggctan ntaatcctta actagtccct ccattgtgag 120
cattatcctt ccagtattcn ccttctnttt tatttactcc ttcttggtta cccatgtact 180
ntt 183

```

```

<210> 409
<211> 250
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(250)
<223> n = A,T,C or G

```

```

<400> 409
cccacgcatg ataagctctt tatttctgta agtcctgcta ggaaatcatc aaatctgacg 60
gtgggttggg ggacctgaac aaacctcctg taattaatca gctttcagtt tctcccccta 120
gtccctcctt caacaacata ggaggatcct ccccttcttt ctgctcacgg ccttatctag 180
gcttcccagt gccccagga cagcgtgggc tatgtttaca gcgcntcctt gctggggggg 240
ggccttatgc 250

```

```

<210> 410
<211> 306
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(306)
<223> n = A,T,C or G

```

```

<400> 410
ggctgggttg caagaatgaa atgaatgatt ctacagctag gacttaacct tgaaatggaa 60
agtcttgcaa tcccatgtgc aggatccgtc tgtgcacatg cctctgtaga gagcagcatt 120
cccagggacc ttggaaacag ttggcaactgt aagggtgcttg ctcccccaaga cacatcctaa 180
aagggtgttg aatgggtgaaa accgcttcct tctttattgc cccttcttat ttatgtgaac 240
nactgggttg ctttttttgn atctttttta aactggaaag ttcaattgng aaaatgaata 300
tcntgc 306

```

```

<210> 411
<211> 261
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(261)
<223> n = A,T,C or G

```

```

<400> 411
agagatattn cttaggtnaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaagtgc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240
cttctctcaa ggngaggcaa a 261

```

```

<210> 412

```

<211> 241  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(241)  
 <223> n = A,T,C or G

<400> 412  
 gttcaatggt acctgacatt tctacaacac ccactcacc gatgtattcg ttgccagtg 60  
 ggaacatacc agcctgaatt tggaaaaaat aattgtgttt cttgccagg aaatactacg 120  
 actgactttg atggctccac aaacataacc cagtgtaaaa acagaagatg tggaggggag 180  
 ctgggagatt tcaactggta cattgaattc ccaactacc cangcaatta ccagccaac 240  
 a 241

<210> 413  
 <211> 231  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(231)  
 <223> n = A,T,C or G

<400> 413  
 aactcttaca atccaagtga ctcatctgtg tgcttgaatc ctttccactg tctcatctcc 60  
 ctcatccaag tttctagtac cttctctttg ttgtgaagga taatcaaact gaacaacaaa 120  
 aagttttact tcctcatttg gaacctaaaa actctcttct tcttgggtct gaggggtcca 180  
 agaatccttg aatcanttct cagatcattg gggacaccan atcaggaacc t 231

<210> 414  
 <211> 234  
 <212> DNA  
 <213> Homo sapiens

<400> 414  
 actgtccatg aagcactgag cagaagctgg aggcacaacg caccagacac tcacagcaag 60  
 gatggagctg aaaacataac ccactctgtc ctggaggcac tgggaagcct agagaaggct 120  
 gtgagccaag gagggagggt cttccttttg catgggatgg ggatgaagta aggagagggg 180  
 ctggaccccc tggaaagctga ttcactatgg ggggaggtgt attgaagtcc tcca 234

<210> 415  
 <211> 217  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(217)  
 <223> n = A,T,C or G

<400> 415  
 gcataggatt aagactgagt atcttttcta cattctttta acttttctaag gggcacttct 60  
 caaacacag accaggtagc aaatctccac tgctctaagg ntctcaccac cactttctca 120  
 cacctagcaa tagtagaatt cagtctact totgaggcca gaagaatggt tcagaaaaat 180  
 antggattat aaaaaataac aattaagaaa aataatc 217

<210> 416  
 <211> 213  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(213)  
 <223> n = A,T,C or G

<400> 416  
 atgcatatnt aaagganact gcctcgcttt tagaagacat ctggngctgct ctctgcatga 60  
 ggcacagcag taaagctctt tgattcccag aatcaagaac tctccccttc agactattac 120  
 cgaatgcaag gtgggttaatt gaaggccact aattgatgct caaatagaag gatattgact 180  
 atattggaac agatggagtc tctactacaa aag 213

<210> 417  
 <211> 303  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(303)  
 <223> n = A,T,C or G

<400> 417  
 nagtcttcag gcccatcagg gaagttcaca ctggagagaa gtcatacata tgtactgtat 60  
 gtgggaaagg ctttactctg agttcaaatc ttcaagccca tcagagagtc cactactggag 120  
 agaagccata caaatgcaat gagtgtggga agagcttcag gagggattcc cattatcaag 180  
 ttcacttagt ggtccacaca ggagagaaac cctataaatg tgagatatgt gggaagggct 240  
 tcantcaaag ttcgtatctt caaatccatc ngaaggncca cagtatanan aaacctttta 300  
 agt 303

<210> 418  
 <211> 328  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(328)  
 <223> n = A,T,C or G

<400> 418  
 tttttggcgg tggtggggca gggacgggac angagtctca ctctgttgcc caggctggag 60  
 tgcacaggca tgatctcggc tcactacaac ccctgcctcc catgtccaag cgattcttgt 120  
 gcctcagcct tccctgtagc tagaattaca ggcacatgcc accacaccca gctagttttt 180  
 gtatttttag tagagacagg gtttcaccat gttggccagg ctggtctcaa actcctnacc 240  
 tcagnggtca ggctgggtctc aaactcctga cctcaagtga tctgccacc tcagcctccc 300  
 aaagtgctan gattacaggc cgtgagcc 328

<210> 419  
 <211> 389  
 <212> DNA  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(389)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 419

```

cctcctcaag acggcctgtg gtcgcctcc cggcaaccaa gaagcctgca gtgccatatg 60
acccctgagc catggactgg agcctgaaag gcagcgtaca ccctgctcct gatcttgctg 120
cttgtttccct ctctgtggct ccattcatag cacagttgtt gcactgaggc ttgtgcaggc 180
cgagcaaggc caagctggct caaagagcaa ccagtcaact ctgccacggg gtgccaggca 240
ccggttctcc agccaccaac ctcaactcgt cccgcaaata gcacatcagt tcttctaccc 300
taaaggtagg accaaagggc atctgctttt ctgaagtcc ctgctctatc agccatcacg 360
tggcagccac tcnggctgtg tcgacgcgg 389

```

&lt;210&gt; 420

&lt;211&gt; 408

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 420

```

gttcctccta actcctgcc aaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgacttttgt gtttcggcat ggagaccgaa 180
gtccattga cactttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg aagtgcctatg acaaacctgg caagcccg 408

```

&lt;210&gt; 421

&lt;211&gt; 352

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(352)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 421

```

gctcaaaaat ctttttactg atnngcatgg ctacacaatc attgactatt acggaggcca 60
gaggagaatg aggcctggcc tgggagccct gtgcctacta naagcacatt agattatcca 120
ttcactgaca gaacaggctt tttttgggtc cttcttctcc accacnata acttgacgtc 180
ctccttcttg aagattcttt ggcagttgtc tttgtcataa cccacagggt tagaaacaag 240
ggtgcaacat gaaatttctg tttcgtagca agtgcattgc tcacaagttg gcangtctgc 300
cactccgagt ttattgggtg tttgtttcct ttgagatcca tgcatttctc gg 352

```

&lt;210&gt; 422

&lt;211&gt; 337

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 422

```

atgccaccat gctggcaatg cagcggggcg tcgaaggcct gcatatccag cccaagctgg 60
cgatgatcga cggcaaccgt tgcccgaagt tgccgatgcc agccgaagcg gtggtcaagg 120
gogatagcaa ggtgccggcg atcgcgcgcg cgtcaatcct ggccaaggct agccgtgatc 180
gtgaaatggc agctgtcgaa ttgatctacc cgggttatgg catcggcggg cataagggct 240
atccgacacc ggtgcacctg gaagccttgc agcggctggg gccgacgccg attcaccgac 300
gcttcttccg ccggtacggc tggcctatga aaattat 337

```

<210> 423  
 <211> 310  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(310)  
 <223> n = A,T,C or G

<400> 423  
 gctcaaaaat ctttttactg atatggcatg gctacacaat cattgactat tagaggccag 60  
 aggagaatga ggcctggcct gggagccctg tgcctactan aagcncatta gattatccat 120  
 tcaactgacag aacaggctctt ttttgggtcc ttcttctcca ccacgatata cttgcagtcc 180  
 tccttcttga agattctttg gcagttgtct ttgtcataac ccacaggtgt anaaacaagg 240  
 gtgcaacatg aaatttctgt ttcgtagcaa gtgcatgtct cacagttgtc aagtctgccc 300  
 tccgagttaa 310

<210> 424  
 <211> 370  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(370)  
 <223> n = A,T,C or G

<400> 424  
 gctcaaaaat ctttttactg ataggcatgg ctacacaatc attgactatt agaggccaga 60  
 ggagaatgag gcctggcctg ggagccctgt gcctactaga agcacattag attatccatt 120  
 cactgacaga acaggctctt tttgggtcct tcttctccac cacgatatac ttgcagtcct 180  
 ccttcttgaa gattcttttg cagttgtctt tgtcataacc cacaggtgta gaaacatcct 240  
 gggtgaatct cctggaactc cctcattagg tatgaaatag catgatgcat tgcataaagt 300  
 cacgaagggtg gcaaagatca caacgctgcc cagganaaca ttcattgtga taagcaggac 360  
 tccgtcgacg 370

<210> 425  
 <211> 216  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(216)  
 <223> n = A,T,C or G

<400> 425  
 aattgctatn ntttattttg ccaactcaaaa taattaccaa aaaaaaaaaa tnttaaataga 60  
 taacaacnca acatcaaggc aaananaaca ggaatggntg actntgcata aatnggccga 120  
 anattatcca ttatnttaag ggttgacttc aggntacagc acacagacaa acatgcccag 180  
 gaggnntntca ggaccgctcg atgtntntng aggagg 216

<210> 426  
 <211> 596  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 426

```

cttccagtga ggataaccct gttgccccgg gccgagggttc tccattaggc tctgattgat 60
tggcagtcag tgatggaagg gtgttctgat cattccgact gccccagggt tcgctggcca 120
gctctctgtt ttgctgagtt ggcagtagga cctaatttgt taattaagag tagatgggtga 180
gctgtccttg tattttgatt aacctaatgg ccttcccagc acgactcgga ttcagctgga 240
gacatcacgg caacttttaa tgaaatgatt tgaagggcca ttaagaggca cttcccgtta 300
ttaggcagtt catctgcaact gataacttct tggcagctga gctggtcgga gctgtggccc 360
aaacgcacac ttggcttttg gttttgagat acaactctta atcttttagt catgcttgag 420
ggtggatggc cttttcagct ttaacccaat ttgcaactgcc ttggaagtgt agccaggaga 480
atacactcat atactcgtgg gcttagaggc cacagcagat gtcattggtc tactgcctga 540
gtcccgtggt tcccatccca ggaccttcca tcggcgagta cctgggagcc cgtgct 596

```

&lt;210&gt; 427

&lt;211&gt; 107

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(107)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 427

```

gaagaattca agttagggtt attcaaaggc cttacngaga atcctanacc caggnccag 60
cccgggagca gccttanaga gctcctgtt gactgcccgg ctcagng 107

```

&lt;210&gt; 428

&lt;211&gt; 38

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(38)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 428

```

gaacttcna anaangactt tattcactat ttacatt 38

```

&lt;210&gt; 429

&lt;211&gt; 544

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 429

```

ctttgctgga cggaataaaa gtggacgcaa gcatgacctc ctgatgaggg cgctgcattt 60
attgaagagc ggctgcagcc ctgcggttca gattaaaatc cgagaattgt atagacgccg 120
atatccacga actcttgaag gactttctga tttatccaca atcaaatcat cggttttcag 180
tttggttggt ggctcatcac ctgtagaacc tgacttggcc gtggctggaa tccactcgtt 240
gccttcactc tcagttacac ctcaactcacc atcctctcct gttggttctg tgctgcttca 300
agatactaag cccacatttg agatgcagca gccatctccc ccaattcctc ctgtccatcc 360
tgatgtgcag ttaaaaaatc tgccctttta tgatgtcctt gatgttctca tcaagcccac 420
gagtttagtt caaagcagta ttcagcgatt tcaagagaag ttttttattt ttgctttgac 480
acctcaacaa gttagagaga tatgcatatc cagggatttt ttgccagggtg gtaggagaga 540
ttat 544

```

&lt;210&gt; 430

<211> 507  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(507)  
<223> n = A,T,C or G

<400> 430  
cttatcncaa tggggctccc aaacttggt gtgcagtgga aactccgggg gaattttgaa 60  
gaacactgac acccatcttc caccocgaca ctctgattta attgggctgc agtgagaaca 120  
gagcatcaat ttaaaaagct gcccagaatg ttntcctggg cagcgttggt atctttgcn 180  
ccttcgtgac tttatgcaat gcatcatgct atttcatacc taatgaggga gttccaggag 240  
attcaaccag gatgtttcta cncctgtggg ttatgacaaa gacaactgcc aaagaatntt 300  
caagaaggag gactgcaagt atatcgtggt ggagaagaag gacccaaaaa agacctgttc 360  
tgtcagtga tggataatct aatgtgcttc tagtaggcac agggctccca ggccaggcct 420  
cattctcttc tggcctctaa tagtcaatga ttgtgtagcc atgcctatca gtaaaaagat 480  
ttttgagcaa aaaaaaaaaa aaaaaaa 507

<210> 431  
<211> 392  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(392)  
<223> n = A,T,C or G

<400> 431  
gaaaattcag aatggataaa aacaaatgaa gtacaaaata tttcagattt acatagcgat 60  
aaacaagaaa gcacttatca ggaggactta caaatggaag tacactctan aaccatcatc 120  
tatcatggct aaatgtgaga ttagcacagc tgtattattt gtacattgca aacacctaga 180  
aagagatggg aaacaaaatc ccaggagttt tgtgtgtgga gtcctgggtt ttccaacaga 240  
catcattcca gcattctgag attagggnga ttggggatca ttctggagtt ggaatgttca 300  
acaaaagtga tgttgtagg taaaatgtac aacttctgga tctatgcaga cattgaaggt 360  
gcaatgagtc tggtttttac tctgctgttt ct 392

<210> 432  
<211> 387  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(387)  
<223> n = A,T,C or G

<400> 432  
ggtatcanta cataatcaaa tatagctgta gtacatgttt tcattggngt agattaccac 60  
aaatgcaagg caacatgtgt agatctcttg tottattctt ttgtctataa tactgtattg 120  
ngtagtccaa gctctcgna gtccagccac tngnaaacat gtcctctta gattaacctc 180  
gtggacnctn ttgttgnatt gtctgaactg tagngccctg tattttgctt ctgtctgnga 240  
attctgttgc ttctggggca ttctcttng atgcagagga ccaccacaca gatgacagca 300  
atctgaattg ntccaatcac agctgcgatt aagacatact gaaatcgta aggaccggga 360  
acaacgtata gaacactgga gtccttt 387



<210> 433  
 <211> 281  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(281)  
 <223> n = A,T,C or G

<400> 433  
 ttcaactagc anagaanact gcttcagggg gtgtaaaatg aaaggcttcc acgcagttat 60  
 ctgattaaag aacactaaga gagggacaag gctagaagcc gcaggatgtc tacactatag 120  
 caggcnctat ttgggttggc tggaggagct gtggaaaaca tggagagatt ggcgctggag 180  
 atcgccgtgg ctattcctcn ttgntattac accagnagg ntctctgtnt gccactggt 240  
 tnnaaaaccg ntatacaata atgatagaat aggacacaca t 281

<210> 434  
 <211> 484  
 <212> DNA  
 <213> Homo sapiens

<400> 434  
 ttttaaaata agcatttagt gctcagtcct tactgagtag tctttctctc cctcctctctg 60  
 aatttaattc tttcaacttg caatttgcaa ggattacaca tttcactgtg atgtatattg 120  
 tgttgcaaaa aaaaaaaagt gtctttgttt aaaattactt ggtttgtgaa tccatcttgc 180  
 tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa acatctgaag 240  
 agctagtcta tcagcatctg acaggtgaat tggatggttc tcagaaccat ttcacccaga 300  
 cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca taacaaaccc 360  
 tgctccaatc tgtcacataa aagtctgtga cttgaagttt agtcagcacc cccaccaaac 420  
 tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataaag taccatgtc 480  
 tttta 484

<210> 435  
 <211> 424  
 <212> DNA  
 <213> Homo sapiens

<400> 435  
 ggcgcgctca gagcaggtca ctttctgcct tccacgtcct ccttcaagga agccccatgt 60  
 gggtagcttt caatatcgca ggttcttact cctctgcctc tataagctca aaccaccaa 120  
 cgatcgggca agtaaaccct ctcctcgcgc gacttcggaa ctggcgagag ttcagcgcag 180  
 atgggcctgt ggggaggggg caagatagat gagggggagc ggcattggtgc ggggtgaccc 240  
 cttggagaga ggaaaaaggc cacaagaggg gctgccaccg ccactaacgg agatggcct 300  
 ggtagagacc tttgggggtc tggaacctct ggactcccca tgctctaact cccacactct 360  
 gctatcagaa acttaaactt gaggattttc tctgtttttc actcgcaata aattcagagc 420  
 aaac 424

<210> 436  
 <211> 667  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(667)  
 <223> n = A,T,C or G

&lt;400&gt; 436

```

accttgggaa nactctcaca atataaaggg tcgtagactt tactccaaat tccaaaaagg 60
tcctggccat gtaatcctga aagttttccc aaggtagcta taaaatcctt ataagggtgc 120
agcctcttct ggaattcctc tgatttcaaa gtctcactct caagttcttg aaaacgaggg 180
cagttcctga aaggcaggta tagcaactga tcttcagaaa gaggaactgt gtgcaccggg 240
atgggctgcc agagtaggat aggattccag atgctgacac cttctggggg aaacagggct 300
gccaggtttg tcatagcact catcaaagtc cgtcaacgt ctgtgcttog aatataaacc 360
tgttcatgtt tataggactc attcaagaat tttctatatc tctttcttat atactctcca 420
agttcataat gctgctccat gccagctgg gtgagttggc caaatccttg tggccatgag 480
gattccttta tggggtcagt gggaaagtg tcaatgggac ttcggtctcc atgccgaaac 540
accaaagtca caaacttcaa ctcttggtc agtacacttc ggtctagcca gaaaaaagc 600
agaaacaaga agccaaggct aaggcttgct gccctgccag gaggaggggt gcagctctca 660
tgttgag 667

```

&lt;210&gt; 437

&lt;211&gt; 693

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 437

```

ctacgtctca accctcattt ttaggtaagg aatcttaagt ccaaagatat taagtgactc 60
acacagccag gtaaggaaag ctggattggc aactaggac tctaccatac cgggttttgt 120
taaagctcag gttaggaggc tgataagctt ggaaggaact tcagacagct ttttcagatc 180
ataaaagata attcttagcc catgttcttc tccagagcag acctgaaatg acagcacagc 240
aggtactcct ctattttcac ccctcttgct tctactctct ggcagtcaga cctgtgggag 300
gccatgggag aaagcagctc tctggatgtt tgtacagatc atggactatt ctctgtggac 360
catttctcca ggttacccta ggtgtcacta ttggggggac agccagcatc tttagctttc 420
atgtgagttt ctgtctgtct tcagtagagg aaacttttgc tcttcacact tcacatctga 480
acacctaaact gctgttgctc ctgaggtggg gaaagacaga tatagagctt acagtattta 540
tcctattttct aggcactgag ggctgtgggg taccttgtgg tgccaaaaca gatcctgttt 600
taaggacatg ttgcttcaga gatgtctgta actatctggg ggctctgttg gctctttacc 660
ctgcatcatg tgctctcttg gctgaaaatg acc 693

```

&lt;210&gt; 438

&lt;211&gt; 360

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 438

```

ctgcttatca caatgaatgt tctcctgggc agcgttggtga tctttgccac cttcgtgact 60
ttatgcaatg catcatgcta tttcatacct aatgagggag ttccaggaga ttcaaccagg 120
atgtttctac acctgtgggt tatgacaaag acaactgcc aagaatcttc aagaaggagg 180
actgcaagta tatctggttg agaagaagga cccaaaaaag acctgttctg tcagtgaatg 240
gataatctaa tgtgcttcta gtaggcacag ggctcccagg ccaggcctca ttctcctctg 300
gcctctaata gtcaataatt gtgtagccat gcctatcagt aaaaagattt ttgagcaaac 360

```

&lt;210&gt; 439

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(431)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 439

```

gttcctnnta actcctgcc aaacagctc tcctcaacat gagagctgca cccctcctcc 60

```

```

tggccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgacttttgg gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtccctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag t                                     431

```

&lt;210&gt; 440

&lt;211&gt; 523

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 440

```

agagataaag cttagggtcaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaattgtc tgaattggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttacccat cagttccagc 240
cttctctcaa ggagaggcaa agaaaggaga tacagtggag acatctggaa agttttctcc 300
actggaaaac tgctactatc tgtttttata tttctgttaa aatatatgag gctacagaac 360
taaaaattaa aacctctttg tgtcccttgg tcttggaaac tttatgttcc ttttaaagaa 420
acaaaaatca aactttacag aaagatttga tgtatgtaac acatatagca gctcttgaag 480
tatatatatc atagcaaata agtcatctga tgagaacaag cta                                     523

```

&lt;210&gt; 441

&lt;211&gt; 430

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 441

```

gttcctccta actcctgcc aaaaacagctc tcttcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgacttttgg gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtccctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag                                     430

```

&lt;210&gt; 442

&lt;211&gt; 362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 442

```

ctaaggaatt agtagtggtc ccatcacttg tttggagtgt gctattctaa aagattttga 60
tttcttgga tgacaattat attttaactt tgggtgggga aagagttata ggaccacagt 120
cttcacttct gatacttgta aattaatctt ttattgcact tgttttgacc attaagctat 180
atgtttagaa atggtcattt tacggaaaaa ttagaaaaat tctgataata gtgcagaata 240
aatgaattaa tgttttactt aatttatatt gaactgtcaa tgacaaataa aaattctttt 300
tgattatttt ttgttttcat ttaccagaat aaaaactaag aattaaaagt ttgattacag 360
tc                                     362

```

&lt;210&gt; 443

&lt;211&gt; 624

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(624)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 443

```

ttttttttttt gcaacacaaat atacatcaca gtgaaatgtg taatccttgc aaattgcaag 60
ttgaaagaat taaattcaga ggaggggaga gaaagagtac tcagtaggga ctgagcacta 120
aatgcttatt ttaaaagaaa tgtaaagagc agaaagcaat tcaggctacc ctgccttttg 180
tgctggctag tactccggtc ggtgtcagca gcacgtggca ttgaacattg caatgtggag 240
cccaaaccac agaaaatggg gtgaaattgg ccaactttct attaacttgg cttcctggtt 300
tataaaatat tgtgaataat atcacctact tcaaagggca gttatgaggc ttaaataaac 360
taacgcctac aaaacactta aacatagata acataggtgc aagtactatg tatctggtag 420
atggtaaaca tccttattat taaagtcaac gctaaaaatga atgtgtgtgc atatgcta 480
agtacagaga gagggcactt aaaccaacta agggcctgga gggaagggtt cctggaaaga 540
ngatgcttgt gctgggtcca aatcttggtc tactatgacc ttggccaaat tatttaaact 600
ttgtccctat ctgctaaaca gatc 624

```

&lt;210&gt; 444

&lt;211&gt; 425

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(425)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 444

```

gcacatcatt nntcttgcatt tctttgagaa taagaagatc agtaaatagt tcagaagtgg 60
gaagctttgt ccaggcctgt gtgtgaaccc aatgttttgc ttagaaatag aacaagtaag 120
ttcattgcta tagcataaca caaaatttgc ataagtgttg gtcagcaaat ccttgaatgc 180
tgcttaatgt gagaggttgg taaaatcctt tgtgcaacac tctaactccc tgaatgtttt 240
gctgtgctgg gacctgtgca tgccagacaa ggccaagctg gctgaaagag caaccagcca 300
cctctgcaat ctgccacctc ctgctggcag gatttgtttt tgcacctgt gaagagccaa 360
ggaggcacca gggcataagt gagtagactt atggctcgacg cggccgcgaa ttagtagta 420
gtaga 425

```

&lt;210&gt; 445

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(414)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 445

```

catgtttatg nttttggatt actttgggca cctagtgttt ctaaactcgtc tatcattctt 60
ttctgttttt caaaagcaga gatggccaga gtctcaacaa actgtatctt caagtctttg 120
tgaaattctt tgcattgtggc agattattgg atgtagtttc ctttaactag catataaatc 180
tggtgtgttt cagataaatg aacagcaaaa tgtggtggaa ttaccatttg gaacattgtg 240
aatgaaaaat tgtgtctcta gattatgtaa caaataacta tttcctaacc attgatcttt 300
ggatttttat aatcctactc acaaataact aggccttctc tcttgtattt tgaagcagtg 360
tggtgtgctg attgataaaa aaaaaaaaaa tcgacgcggc cgcaattta gtag 414

```

&lt;210&gt; 446

<211> 631  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(631)  
 <223> n = A,T,C or G

<400> 446  
 acaaattaga anaaagtgcc agagaacacc acataccttg tccggaacat tacaatggct 60  
 tctgcatgca tgggaagtgt gagcattcta tcaatatgca ggagccatct tgcaggtgtg 120  
 atgctgggta tactggacaa cactgtgaaa aaaaggacta cagtgttcta tacgttggtc 180  
 ccggtcctgt acgatttcag tatgtcttaa tcgcagctgt gattggaaca attcagattg 240  
 ctgtcatctg tgtgggtggtc ctctgcatca caagggccaa actttaggta atagcattgg 300  
 actgagattt gtaaaccttc caaccttcca ggaaatgccc cagaagcaac agaattcaca 360  
 gacagaagca aaatacaggg cactacagtt cagacaatac aacaagagcg tccacgaggt 420  
 taatctaaag ggagcatggt tcacagtggc tggactaccg agagcttgga ctacacaata 480  
 cagtattata gacaaaagaa taagacaaga gatctacaca tgttgccctg catttggtgtg 540  
 aatctacacc aatgaaaaca tgtactacag ctatatttga ttatgtatgg atatatttga 600  
 aatagtatac attgtcttga tgttttttct g 631

<210> 447  
 <211> 585  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(585)  
 <223> n = A,T,C or G

<400> 447  
 ccttgaggaaa antntcacia tataaagggt cgtagacttt actccaaatt ccaaaaagggt 60  
 cctggccatg taatcctgaa agttttccca aggtagctat aaaatcctta taagggtgca 120  
 gcctcttctg gaattcctct gatttcaaag tctcactctc aagttcttga aacagagggc 180  
 agttcctgaa aggcaggtat agcaactgat cttcagaaag aggaactgtg tgcaccggga 240  
 tgggctgcca gagtaggata ggattccaga tgctgacacc ttctggggga aacagggctg 300  
 ccagggttgt catagcactc atcaaagtcc ggtcaacgtc tgtgcttcga atataaacct 360  
 gttcatgttt ataggactca ttcaagaatt ttctatatct ctttcttata tactctccaa 420  
 gttcataatg ctgtcccatg cccagctggg tgagttggcc aaatccttgt ggccatgagg 480  
 attcctttat ggggtcagtg ggaaagggtg caatgggact tcggtctcca tgccgaaaca 540  
 ccaaagtcac aaacttcaac tccttggtca gtacacttcg gtcta 585

<210> 448  
 <211> 93  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(93)  
 <223> n = A,T,C or G

<400> 448  
 tgctcgtggg tcattctgan ncccgaactg accntgccag ccctgccgan gggccnccat 60  
 ggctccctag tgccctggag agganggggc tag 93

<210> 449  
 <211> 706  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(706)  
 <223> n = A,T,C or G

<400> 449  
 ccaagttcat gctntgtgct ggacgctgga cagggggcaa aagcnnttgc tcgtgggtca 60  
 ttctganeac cgaactgacc atgccagccc tgccgatggg cctccatggc tccctagtc 120  
 cctggagagg aggtgtctag tcagagagta gtccctggaag gtggcctctg ngaggagcca 180  
 cggggacagc atcctgcaga tggtcgggag cgctccattc gccattcagg ctgcgcaact 240  
 gtggggaag gcgatcggtg cgggcctctt cgctattacg ccagctggcg aaagggggat 300  
 gtgctgcaag gcgattaagt tgggtaacgc caggggtttc ccagtcncca cgttgtaaaa 360  
 cgacggccag tgaattgaat ttaggtgacn ctatagaaga gctatgacgt cgcatgcacg 420  
 cgtacgtaag cttggatcct ctagagcggc cgccactac tactaaattc gcggccgcgt 480  
 cgacgtggga tccnactga gagagtggag agtgacatgt gctggacnct gtccatgaag 540  
 cactgagcag aagctggagg cacaacgcnc cagacactca cagctactca ggaggctgag 600  
 aacaggttga acctgggagg tggagggttg aatgagctga gatcaggccn ctgcncccca 660  
 gcatggatga cagagtgaat ctccatctta aaaaaaaaaa aaaaaa 706

<210> 450  
 <211> 493  
 <212> DNA  
 <213> Homo sapiens

<400> 450  
 gagacggagt gtcactctgt tgcccaggct ggagtgcagc aagacactgt ctaagaaaaa 60  
 acagttttta aaggtaaaaa aacataaaaa gaaatatcct atagtggaaa taagagagtc 120  
 aaatgaggct gagaacttta caaagggatc ttacagacat gtgcgcaata tcaactgcatg 180  
 agcctaagta taagaacaac ctttggggag aaaccatcat ttgacagtga ggtacaattc 240  
 caagtcagggt agtgaaatgg gtggaattaa actcaaatta atcctgccag ctgaaacgca 300  
 agagacactg tcagagagtt aaaaagttag ttctatccat gaggtgattc cacagtcttc 360  
 tcaagtcaac acatctgtga actcacagac caagttctta aaccactgtt caaactctgc 420  
 tacacatcag aatcacctgg agagctttac aaactcccat tgccgagggt cgacgcggcc 480  
 gcgaatttag tag 493

<210> 451  
 <211> 501  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(501)  
 <223> n = A,T,C or G

<400> 451  
 gggcgcgctc cattcgccat tcaggctgag caactgttgg gaagggcgat cgggtcgggc 60  
 ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaaggcgat taagttgggt 120  
 aacgccaggg ttttccagc cncgacgttg taaaacgacg gccagtgaat tgaatttagg 180  
 tgacnctata gaagagctat gacgtcgcat gcacgcgtac gtaagcttgg atcctctaga 240  
 gcggccgcct actactacta aattcgcggc cgcgtcgacg tgggatccnc actgagagag 300  
 tggagagtga catgtgctgg acnctgtcca tgaagcactg agcagaagct ggaggcacia 360  
 cgcncacagc actcacagct actcaggagg ctgagaacag gttgaacctg ggaggtggag 420

gttgcaatga gctgagatca ggccnctgcn ccccagcatg gatgacagag tgaaactcca 480  
tcttaaaaaa aaaaaaaaaa a 501

<210> 452  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(51)  
<223> n = A,T,C or G

<400> 452  
agacggtttc accntttacaa cnccttttag gatgggnntt ggggagcaag c 51

<210> 453  
<211> 317  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(317)  
<223> n = A,T,C or G

<400> 453  
tacatcttgc tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa 60  
acatctgaag agctagtcta tcagcatctg gcaagtgaat tggatgggtc tcagaaccat 120  
ttcaccana cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca 180  
taacaaaccc tgctccaatc tgtcacataa aagctctgtga cttgaagttt antcagcacc 240  
cccacaaac tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataagg 300  
taccatgtc tttatta 317

<210> 454  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 454  
ttcgaggtag aatcaactct cagagtgtag tttccttcta tagatgagtc agcattaata 60  
taagccacgc cacgctcttg aaggagtctt gaattctcct ctgctcactc agtagaacca 120  
agaagaccaa attcttctgc atcccagctt gcaaacaaaa ttgttcttct aggtctccac 180  
ccttcctttt tcagtgttcc aaagctcctc acaatttcat gaacaacagc t 231

<210> 455  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 455  
taccaaagag ggcataataa tcagtctcac agtaggggtc accatcctcc aagtgaaaaa 60  
cattgttccg aatgggcttt ccacaggcta cacacacaaa acaggaaaca tgccaagttt 120  
gtttcaacgc attgatgact tctccaagga tcttcctttg gcatcgacca cattcagggg 180  
caaagaattt ctcatagcac agctcacaat acagggtctc tttctcctct a 231

<210> 456  
<211> 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 456

```
ttggcaggta cccttacaaa gaagacacca taccttatgc gttattaggt ggaataatca 60
ttccattcag tattatcggt attattcttg gagaaaccct gtctgtttac tgtaaccttt 120
tgcaactcaa ttccctttatc aggaataact acatagccac tatttacaaa gccattggaa 180
cctttttatt tgggtgcagct gctagtcagt ccctgactga cattgccaag t 231
```

&lt;210&gt; 457

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(231)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 457

```
cgaggtagccc aggggtctga aaatctctnn tttantagtc gatagcaaaa ttgttcatca 60
gcattcctta atatgatctt gctataatta gatttttctc cattagagtt catacagttt 120
tatttgattt tattagcaat ctctttcaga agacccttga gatcattaag ctttgtatcc 180
agttgtctaa atcgatgcct catttcctct gaggtgtcgc tggcttttgt g 231
```

&lt;210&gt; 458

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 458

```
aggtcttggtt cccccactt ccactcccct ctactctctc taggactggg ctggggccaag 60
agaagagggg tggtaggga agccgttgag acctgaagcc ccaccctcta ccttccttca 120
acaccctaac cttgggtaac agcatttgga attatcattt gggatgagta gaatttccaa 180
ggtectgggt taggcatttt gggggggccag accccaggag aagaagattc t 231
```

&lt;210&gt; 459

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 459

```
ggtaccgagg ctcgctgaca cagagaaaac ccaacgcgag gaaaggaatg gccagccaca 60
ccttcgcgaa acctgtggtg gccaccagt cctaacggga caggacagag agacagagca 120
gccctgcact gttttccctc caccacagcc atcctgtccc tcattggctc tgtgctttcc 180
actatacaca gtcaccgtcc caatgagaaa caagaaggag caccctccac a 231
```

&lt;210&gt; 460

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 460

```
gcagggtataa catgctgcaa caacagatgt gactaggaac ggccggtgac atgggggaggg 60
cctatcacc cttcttggg ggctgcttct tcacagtgat catgaagcct agcagcaaat 120
cccacctccc cacacgcaca cgccagcct ggagcccaca gaagggtcct cctgcagcca 180
gtggagcttg gtccagcctc cagtccaccc ctaccaggct taaggataga a 231
```



<210> 461  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 461  
cgaggtttga gaagctctaa tgtgcagggg agccgagaag caggcggcct agggagggtc 60  
gcgtgtgctc cagaagagtgt tgtgcatgcc agaggggaaa caggcgcctg tgtgtcctgg 120  
gtggggttca gtgaggagtgt ggaaattggt tcagcagaac caagccgttg ggtgaataag 180  
agggggattc catggcactg atagagccct atagtttcag agctgggaat t 231

<210> 462  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 462  
aggtaccctc attgtagcca tgggaaaatt gatgttcagt ggggatcagt gaattaaatg 60  
gggtcatgca agtataaaaa ttaaaaaaaaa aagacttcat gcccaatctc atatgatgtg 120  
gaagaactgt tagagagacc aacagggttag tggggttagag atttccagag tcttacattt 180  
tctagaggag gtatttaatt tcttctcact catccagtgt tgtatttagg a 231

<210> 463  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 463  
tactccagcc tgggtgacaga gcgagaccct atcaccgccc cccacccccc caaaaaaaaa 60  
actgagtaga cagggtgtcct cttggcatgg taagtcttaa gtccccctcc agatctgtga 120  
catttgacag gtgtcttttc ctctggacct cggtgtcccc atctgagtga gaaaaggcag 180  
tggggagggtg gatcttccag tcgaagcggg atagaagccc gtgtgaaaag c 231

<210> 464  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 464  
gtactctaag attttatcta agttgccttt tctgggtggg aaagttaa cttagtgtgact 60  
aaggacatca catatgaaga atgtttaagt tggagggtggc aacgtgaatt gcaaacaggg 120  
cctgcttcag tgactgtgtg cctgtagtcc cagctactcg ggagtctgtg tgaggccagg 180  
ggtgccagcg caccagctag atgctctgta acttctaggc cccattttcc c 231

<210> 465  
<211> 231  
<212> DNA  
<213> Homo sapiens

<400> 465  
catgttggtg tagctgtggt aatgctggct gcacttcaga cagggttaac ttcagctcct 60  
gtggcaaatt agcaacaaat tctgacatca tttttatggt ttctgtatct ttgttgatga 120  
aggatggcac aatttttgct tgtgttcata atatactcag attagttagc ctccatcaga 180  
taaactggag acatgcagga cattagggta gtgtttagc tctggtaatg a 231

<210> 466  
<211> 231  
<212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 466

```

caggtacctc tttccattgg ataactgtgct agcaagcatg ctctccgggg tttttttaat 60
ggccttcgaa cagaacttgc cacataccca ggtataatag tttctaacat ttgcccagga 120
cctgtgcaat caaatattgt ggagaattcc ctagctggag aagtcacaaa gactataggc 180
aataatggag accagtccca caagatgaca accagtcggt gtgtgcggt g          231

```

&lt;210&gt; 467

&lt;211&gt; 311

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 467

```

gtacaccctg gcacagtcca atctgaactg gttcggcact catctttcat gagatggatg 60
tgggtggcttt tctccttttt catcaagact cctcagcagg gagcccagac cagcctgcac 120
tgtgccttaa cagaaggtct tgagattcta agtgggaatc atttcagtga ctgtcatgtg 180
gcatgggtct ctgcccaagc tcgtaatgag actatagcaa ggcggctgtg ggacgtcagt 240
tgtgacctgc tgggcctccc aatagactaa caggcagtgc cagttggacc caagagaaga 300
ctgcagcaga c          311

```

&lt;210&gt; 468

&lt;211&gt; 3112

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 468

```

cattgtgttg ggagaaaaac agaggggaga tttgtgtggc tgcagccgag ggagaccagg 60
aagatctgca tgggtgggaag gacctgatga tacagagttt gataggagac aattaaaggc 120
tggaaggcac tggatgcctg atgatgaagt ggactttcaa actggggcac tactgaaacg 180
atgggatggc cagagacaca ggagatgagt tggagcaagc tcaataacaa agtggttcaa 240
cgaggacttg gaattgcatg gagctggagc tgaagtttag cccaattgtt tactagttag 300
gtgaatgtgg atgattggat gatcatttct catctctgag cctcaggttc cccatccata 360
aaatgggata cacagtatga tctataaagt gggatatagt atgatctact tcaactgggt 420
atltgaagga tgaattgaga taatttattt cagggtgccta gaacaatgcc cagattagta 480
catttggttg aactgagaaa tggcataaca ccaaatttaa tatatgtcag atgttactat 540
gattatcatt caatctcata gttttgtcat ggcccaattt atcctcactt gtgcctcaac 600
aaattgaact gttaacaaag gaatctcttg tcttggttaa tggctgagca ccactgagca 660
tttccattcc agttggcttc ttgggtttgc tagctgcata actagtcata ttaaataaat 720
gaagttttaa catttctcca gtgatttttt tatctcacct ttgaagatac tatgttatgt 780
gattaaataa agaacttgag aagaacagg ttcattaaac ataaaatcaa ttagacgca 840
aattttcttg atgggcaata cttatgttca caggaaatgc tttaaaatat gcagaagata 900
attaaatggc aatggacaaa gtgaaaaact tagacttttt tttttttttt ggaagtatct 960
ggatgttcct tagtcactta aaggagaact gaaaaatagc agtgagttcc acataatcca 1020
acctgtgaga ttaaggctct ttgtggggaa ggacaaagat ctgtaaattt acagtttcct 1080
tccaaagcca acgtcgaatt ttgaaacata tcaaagctct tcttcaagac aaataatcta 1140
tagtacatct tcttatggg atgcacttat gaaaaatggg ggctgtcaac atctagtcac 1200
tttagctctc aaaatgggtc attttaagag aaagttttag aatctcata tttattcctgt 1260
ggaaggacag cattgtggct tggactttat aaggctttta ttcaactaaa taggtgagaa 1320
ataagaaagg ctgctgactt taccatctga ggccacacat ctgctgaaat ggagataatt 1380
aacatcacta gaaacagcaa gatgacaata taatgtctaa gtagtgacat gtttttgcac 1440
atttccagcc cctttaaata tccacacaca caggaagcac aaaaggaagc acagagatcc 1500
ctgggagaaa tgcccgccg ccatcttggg tcatcgatga gcctogccct gtgcctgggtc 1560
ccgcttgtga gggaaggaca ttagaaaatg aattgatgtg ttccttaaag gatgggcagg 1620
aaaacagatc ctgttgtgga tatttatttg aacgggatta cagatttgaa atgaagtcac 1680
aaagttagca ttaccaatga gaggaaaaca gacgagaaaa tcttgatggc ttcacaagac 1740
atgcaacaaa caaatggaa tactgtgatg acatagggca gccaaagctgg ggaggagata 1800
accacggggc agagggtcag gattctggcc ctgctgccta aactgtgcgt tcataaccaa 1860

```

```

atcatttcat atttctaacc ctcaaaacaa agctgttgta atatctgac tctacgggtc 1920
cttctggggc caacattctc catatatcca gccacactca tttttaatat ttagttccca 1980
gatctgtact gtgaccttct tacaactgtag aataacatta ctcatcttct tcaaagaccc 2040
ttcgtgttgc tgcctaatat gtagctgact gtttttccca aggagtgttc tggcccaggg 2100
gatctgtgaa caggctggga agcatctcaa gatctttcca gggttatact tactagcaca 2160
cagcatgac attacggagt gaattatcta atcaacatca tcctcagtgt ctttgcccat 2220
actgaaattc atttccact tttgtgcca ttctcaagac ctcaaaatgt cattccatta 2280
atatcacagg attaactttt ttttttaacc tggaagaatt caatgttaca tgcagctatg 2340
ggaatttaat tacataattt gttttccagt gcaaagatga ctaagtcctt tatccctccc 2400
ctttgtttga ttttttttcc agtataaagt taaaatgctt agccttgtag tgaggctgta 2460
tacagccaca gcctctcccc atccctccag ccttatctgt catcaccatc aaccctccc 2520
atgcacctaa acaaaatcta acttgaatt ccttgaacat gtcaggcata cattattcct 2580
tctgcctgag aagctcttcc ttgtctctta aatctagaat gatgtaaagt tttgaataag 2640
ttgactatct tacttcatgc aaagaaggga cacatatgag attcatcatc acatgagaca 2700
gcaaatacta aaagtgtaat ttgattataa gagttagat aaatatatga aatgcaagag 2760
ccacagaggg aatgtttatg gggcacgttt gtaagcctgg gatgtgaagc aaaggcaggg 2820
aacctcatag tatcttatat aatatacttc atttctctat ctctatcaca atatccaaca 2880
agcttttcac agaattcatg cagtgc aaat ccccaaaggt aacctttatc catttcatgg 2940
tgagtgcgct ttagaatttt ggcaaatcat actggctact tatctcaact ttgagatgtg 3000
tttgccttg tagttaattg aaagaaatag ggcaactctg tgagccactt tagggttcac 3060
tcctggcaat aaagaattta caaagagcaa aaaaaaaaaa aaaaaaaaaa aa 3112

```

&lt;210&gt; 469

&lt;211&gt; 2229

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 469

```

agctctttgt aaattcttta ttgccaggag tgaaccctaa agtggctcac aagagtgtcc 60
tatttctttc aattaactac aaggacaaac acatctcaaa gttgagataa gtgaccagta 120
tgatttgcca aaattctaaa ggcactcac catgaaatgg ataaaggta cctttgggga 180
tttgactgac atgaattctg tgaaaagctt gttggatatt gtgatagaga tagagaaatg 240
aagtatatta tataagatac tatgagggtc cctgccttg cttcacatcc caggcttaca 300
aacgtgcccc ataaacattc cctctgtggc tcttgcatct catatatatta tctaaactct 360
tataatcaaa tacactttta gtatttgctg tctcatgtga tgatgaatct catatgtgtc 420
ccttctttgc atgaagtaag atagtcaact tattcaaaac tttacatcat tctagattta 480
agagacaagg aagagcttct caggcagaag gaataatgta tgctgacat gttcaaggaa 540
ttacaagtta gattttgttt aggtgcatgg gaggggttga tgggtgatgac agataaggct 600
ggagggatgg ggagaggctg tggctgtata cagcctcagt acaaggctaa gcattttaac 660
tttatactgg aaaaaaatc aaacaaaggg gagggataaa ggacttagtc atctttgcac 720
tgaaaaacaa aatatgtaat taaattccca tagctgcatg taacattgaa ttcttccagg 780
ttaaaaaaaa agttaatcct gtgatattaa tggaatgaca ttttgaggct ttgagaatgg 840
gcacaaaagt gggaaatgaa tttcagtatg ggcaaagaca ctgaggatga tgttgattag 900
ataattcact ccgtaatgat catgctgtgt gctagtaagt ataaccctgg aaagatcttg 960
agatgcttcc cagcctgttc acagatcccc tgggccagaa cactccttag gaaaaacagt 1020
cagctacata ttaggcagca acacgaaggg tctttgaaca aaatgagtaa tgttattcta 1080
cagtgtagaa aggtcacagt acagatctgg gaactaaata ttaaaaatga gtgtggctgg 1140
atatatggag aatgttgggc ccagaaggaa ccgtagagat cagatattac aacagctttg 1200
ttttgagggt tagaaatatg aaatgatatt gttatgaacg cacagtttag gcagcagggc 1260
cagaatcctg accctctgcc ccgtggttat ctctcccca gcttggctgc ctcatgtcat 1320
cacagtattc cattttgttt gttgcatgtc ttgtgaagcc atcaagattt tctcgtctgt 1380
tttctctca ttgtaatgc tcaactttgt acttcatttc aaatctgtaa tcccgttcaa 1440
ataaatatcc acaacaggat ctgttttctt gccatcctt taaggaaacac atcaattcat 1500
tttctaattg ccttccctca caagcgggac caggcacagg gogaggctca tcgatgacc 1560
aagatggcgg ccgggcatct ctcccaggga tctctgtgct tctttttgtg ctctctgtgt 1620
gtgtggatat ttaaaggggc tggaaatgtg caaaaacatg tcaactacta gacattatat 1680
tgtcatcttg ctgtttctag tgatgttaat tatctccatt tcagcagatg tgtggcctca 1740
gatggtaaag tcagcagcct ttcttatttc tcacctggaa atacatacga ccatttgagg 1800

```

```

agacaaatgg caaggtgtca gcataccctg aacttgagtt gagagctaca cacaatatta 1860
ttggtttccg agcatcacia acaccctctc tgtttcttca ctgggcacag aattttaata 1920
cttatttcag tgggctgttg gcaggaacaa atgaagcaat ctacataaag tcactagtgc 1980
agtgcctgac acacaccatt ctcttgaggt cccctctaga gatcccacag gtcatatgac 2040
ttcttgggga gcagtggctc acacctgtaa tcccagcact ttgggaggct gaggcagggtg 2100
ggtcacctga ggtcaggagt tcaagaccag cctggccaat atggtgaaac cccatctcta 2160
ctaaaaatac aaaaattagc tgggcgtgct ggtgcatgcc tgtaatccca gcccacacac 2220
aatggaatt                                     2229

```

&lt;210&gt; 470

&lt;211&gt; 2426

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 470

```

gtaaattctt tattgccagg agtgaaccct aaagtggctc acaagagtgc cctatttctt 60
tcaattaact acaaggacaa acacatctca aagttgagat aagtgaccag tatgatttgc 120
caaaattcta aagcgcactc accatgaaat ggataaagggt tacctttggg gatttgcact 180
gcatgaattc tgtgaaaagc ttgttggata ttgtgataga gatagagaaa tgaagtatat 240
tatataagat actatgaggt tccctgcctt tgcttcacat cccaggctta caaacgtgcc 300
ccataaacat tccctctgtg gctcttgcac ttcatatatt tatctaaact cttataatca 360
aattacactt ttagtatttg ctgtctcatg tgatgatgaa tctcatatgt gtcccttctt 420
tgcatgaagt aagatagtca acttattcaa aactttacat cattctagat ttaagagaca 480
aggaagagct tctcaggcag aaggaataat gtatgcctga catgttcaag gaattacaag 540
ttagattttg tttagggtgca tgggaggggt tgatggtgat gacagataag gctggaggga 600
tggggagagg ctgtggctgt atacagcctc agtacaaggc taagcatttt aactttatac 660
tggaaaaaaa atcaaacaaa ggggagggat aaaggactta gtcatctttg cactggaaaa 720
caaaatatgt aattaaattc ccatagctgc atgtaacatt gaattcttcc aggttaaaaa 780
aaaaagttaa tctgtgata ttaatggaat gacattttga ggtcttgaga atgggcacaa 840
aagtggaaaa tgaatttcag tatgggcaaa gacactgagg atgatgttga ttagataatt 900
cactccgtaa tgatcatgct gtgtgctagt aagtataacc ctggaaagat cttgagatgc 960
ttcccagcct gttcacagat cccctgggcc agaacactcc ttaggaaaaa cagtcagcta 1020
catattagga agcaacacga aggtctttg aacaaaatga gtaattgttat tctacagtgt 1080
agaaaggtca cagtacagat ctgggaacta aatattaaaa atgagtgtgg ctggatatat 1140
ggagaatgtt gggcccagaa ggaaccgtag agatcagata ttacaacagc tttgttttga 1200
gggttagaaa tatgaaatga tttggttatg aacgcacagt ttaggcagca gggccagaat 1260
cctgaccctc tgccccgtgg ttatctcctc cccagcttgg ctgcctcatg tcatcacagt 1320
attccatttt gtttgttgca tgtcttgtga agccatcaag attttctcgt ctgttttctt 1380
ctcattggta atgctcactt tgtgacttca tttcaaactc gtaatcccgt tcaaataaat 1440
atccacaaca ggatctgttt tcctgcccac cttttaagga acacatcaat tcattttcta 1500
atgtccttcc ctcaacagcg ggaccaggca cagggcgagg ctcatcgatg acccaagatg 1560
gcggccgggc atttctccca gggatctctg tgcttcttct tgtgttctct gtgtgtgtgg 1620
atattttaaag gggctggaaa tgtgcaaaaa catgtcacta cttagacatt atattgtcat 1680
cttgctgttt ctagtgtgt taattatctc catttcagca gatgtgtggc ctcataggtt 1740
aaagtcagca gcctttctta tttctcacct ggaaatacat acgaccattt gaggagacaa 1800
atggcaaggt gtcagcatac cctgaacttg agttgagagc tacacacaat attattgggt 1860
tccgagcatc acaaacaccc tctctgtttc ttcactgggc acagaatttt aatacttatt 1920
tcagtgggct gttggcagga acaaatgaag caatctacat aaagtcacta gtgcagtgcc 1980
tgacacacac cattctcttg aggtcccctc tagagatccc acaggtcata tgacttcttg 2040
gggagcagtg gctcacacct gtaatcccag cactttggga ggctgaggca ggtgggtcac 2100
ctgaggtcag gagttcaaga ccagcctggc caatatggtg aaaccccatc tctactaaaa 2160
atacaaaaat tagctgggag tgcctgtgca tgctgtgaa cccagctact tgggaggctg 2220
aggcaggaga attgctggaa catgggaggc ggaggttgca gtgagctgta attgtgccat 2280
tgcactcgaa cctgggcgac agagtggaa cctgtttcca aaaaacaaac aaacaaaaaa 2340
ggcatagtca gataaacgt ggggtgggat tgtaaataga agcaggatat aaagggcagt 2400
gggtgacggg tttgcccac acaatg                                     2426

```

&lt;210&gt; 471

<211> 812  
 <212> DNA  
 <213> Homo sapiens

<400> 471  
 gaacaaaatg agtaatgtta ttctacagtg tagaaaggct acagtacaga tctgggaact 60  
 aaatattaaa aatgagtgtg gctggatata tggagaatgt tgggccaga aggaaccgta 120  
 gagatcagat attacaacag ctttgttttg agggtttaga atatgaaatg atttggttat 180  
 gaacgcacag tttaggcagc agggccagaa tcctgaccct ctgcccctg gttatctcct 240  
 cccagcttg gctgcctcat gtcacacag tattccattt tgtttgttg atgtcttg 300  
 aagccatcaa gattttctcg tctgttttcc tctcattggt aatgctcact ttgtgacttc 360  
 atttcaaate tgtaatcccg ttcaataaaa tatccacaac aggatctgtt ttcctgccc 420  
 tcctttaagg aacacatcaa ttcattttct aatgtccttc cctcacaagc gggaccaggc 480  
 acagggcgag gctcatcgat gacccaagat ggcgccggg catttctccc agggatctct 540  
 gtgttctctt ttgtgttcc tgtgtgtgtg gatattttaa ggggctggaa atgtgcaaaa 600  
 acatgtcact acttagacat tatattgtca tcttgctgtt tctagtgatg ttaattatct 660  
 ccatttcagc agatgtgtgg cctcagatgg taaagtcagc agcctttctt atttctcacc 720  
 tctgtatcat caggctcctc ccaccatgca gatcttctcg gtctcctcg gctgcagcca 780  
 cacaaatctc ccctctgttt ttctgatgcc ag 812

<210> 472  
 <211> 515  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(515)  
 <223> n = A,T,C or G

<400> 472  
 acgggagactt attttctgat attgtctgca tatgtatgtt ttttaagagtc tggaaatagt 60  
 cttatgactt tcttatcatg cttattaata aataatacag cccagagaag atgaaaatgg 120  
 gttccagaat tattggctct tgcagcccgg tgaatctcag caagaggaa caccaactga 180  
 caatcaggat attgaacctg gacaagagag agaaggaaca cctccgatcg aagaacgtaa 240  
 agtagaagggt gattgccagg aaatggatct ggaaaagact cggagtgagc gtggagatgg 300  
 ctctgatgta aaagagaaga ctccacctaa tcctaagcat gctaagacta aagaagcagg 360  
 agatgggcag ccataagtta aaaagaagac aagctgaagc tacacacatg gctgatgtca 420  
 cattgaaaat gtgactgaaa atttgaaaat tctctcaata aagtttgagt tttctctgaa 480  
 gaaaaaaaaa naaaaaaaaa aaanaaaan aaaaa 515

<210> 473  
 <211> 5829  
 <212> DNA  
 <213> Homo sapiens

<400> 473  
 cgcatgccgg ggaagcccaa gctggctcga agagccacca gccacctgtg caagggtggg 60  
 cctggaccag ttggaccagc caccaagctc acctactcaa ggaagcaggg atggccagg 120  
 tgcaacagcc tgagtggctg ccacctgata gctgatggag cagaggcctg aggaaaatca 180  
 gatggcacat ttagctcttt aatggatctt aagttaattt ttctataaag cacatggcac 240  
 cagtccatgc ctccagagctc gtatggcact gcggaccaca gcaggccgag ttcccaggat 300  
 tgccatccag gggggccttc tgtagccctg gccagacctt gcagagggtg ctgggtgctc 360  
 tttgagcgag ctccgctcc ctggcatgca caggccccag gtactgacac gctgctctga 420  
 gtgagcttgt cctgccttgg ctggcaccta actgctgatg gagcagcggc cttaggaaaa 480  
 gcaaatggcg ctgtagccca actttagggt agaagaagat gtaccatgtc cggccgctag 540  
 ttggtgactg gtgcacctgc tctggcgta cccttgca ggtgggtggg tgctctttgg 600  
 ccagcttggc cttgcctggc atgcacaagc ctcatgtcaa caactgtcct acaaatggag 660

acacagagag gaaacaagca gcgggctcag gagcaggggtg tgtgctgcct ttggggctcc 720  
 agtccatgcc tcgggtcgta tggtagtcca ggcttcttgg ttgccaaagag gcggaccaca 780  
 ggccttcttg aggaggactt tacgttcaag tgcagaaagc agccaaaatt accatccatg 840  
 agactaagcc ttctgtggcc ctggcgagac ttaaaatttg tgccaaggca ggacaagctc 900  
 actcggagca gcgtgtcagt agctggggcc tatgcatgcc gggcagggcc gggctggctg 960  
 aaggagcaac cagccacctc tgcaagggtg cgcctagtgc aggcggagca tccaccacct 1020  
 caccgcctcg aggaagtggg gatggccagg tccccacagc ctgagtgtct gccaccttat 1080  
 tgctgatgga gcagaggcct taagaaaagc agatggcact gtggccctac ctttaggggtg 1140  
 gaagaagtga tgtacatgtc cggacgctaa ttggtgactg gtacaccggc tctgctaca 1200  
 cctttgcaga ggtggctggt tgetctttga gccagcttgt ccttgcccgg catgcacaag 1260  
 tttcagtcca acaactttgc cacaatgga gccatataga ggaaacaaga agcaggttca 1320  
 ggagaagggg gtaccctgcc tttggggctc cagttcatgc ctgaggtgtc acatggcact 1380  
 gcgggcttct tgggtgccag gaggcgagc acaggccatc ttggggagga ctttgtgttc 1440  
 aagtgcagaa agcagccagg attgccatcc agggggacct tctatagccc tggccaaacc 1500  
 ttgcaggggt gtctgggttc tctttgagcc ggcttggcct ccctggcatg cacgggcccc 1560  
 aggtgctggc acgctgctcc gagtgtgctt gtctgctctt ggctgccacc tctgcggggg 1620  
 tgcgtctgga ggggtggac cggccacca ccttaccag tcaaggaagt ggatggccat 1680  
 gttcccacag cctgagtggc tgccacctga tggctgatgg agcaaaggcc ttaggaaaag 1740  
 cagatggccc ttggccctac cttttgttta gaagaactga tgttccatgt cctgcagoga 1800  
 gtgaggttgg tggctgtgcc ccagctcctt ggcgcgcctt cgcagaggtg actggttgc 1860  
 ctttggggcc tcttggcctt gccagcatg cacaagcctc agtgctacta ctgtgctaca 1920  
 aatggagcca tataggggaa acgagcagcc atctcaggag caaggtgtat gctgcctttg 1980  
 ggggctccag tcttgcctc aagggtctta tgtcactgtg ggcttcttgg ttgtcaagag 2040  
 gcagaccata ggccgtcttg agagggactt tatgttcaag tgcagaaagc agccaggatt 2100  
 gccaccctcg ggactctgcc ttctgtggcc ctggccaaac ttagaatttg gccgtagaca 2160  
 ggacaggctc acttggagta gcgtgtccgt agctggggtc tgtgcatgcc gggcaaggcc 2220  
 gggctggctc ggggagcaac cagccacctc tgcgggggtg cgcctggagc aggtggagca 2280  
 gccaccagct caccactcc aggaagccgg ggtagccagg ttcccaaggc ctgagtgggt 2340  
 gccacctaat ggctgaagaa acagaggcct tgggaaaacc agatggcact gtggccctac 2400  
 ctttatggta gaagagctga tttagcctga ctggcagcgt gtgggggttg tggctggtct 2460  
 gcctgtgctt ggcgcatccg tgcaaggatg gctgggttgc ctttgagcca gcttgcctt 2520  
 gcccgcatg cgcaagcctc agtgcaacaa ctgtgctgca aatggggcca tatagaggaa 2580  
 aggagcagct ggctctggag catggtgtgc actccctttg ggccttcagt ccatgtctca 2640  
 tgggtcgat gacactgcgg gcttgttggg tgccaagagg cagaccacag gtcattctga 2700  
 ggaggacttt atgttccagt ccagaaagca gccagtggta ccaccaggg gacttgtgct 2760  
 tctgtgcccc ggccagacgt agaatttgac aaagtcagga cggctcctag cagagcggcg 2820  
 tgtcggctcc cggggcctgt gcatgccggg cagggccggg ctggcttggg gagcaagcag 2880  
 ccacctctgt taagggtgtg cctggagcag gtggagcagc caccaacctc acgactgaa 2940  
 agaagcagg atggccagg tccaacatcc tgagtggctg ccacctgatg gctgatggag 3000  
 cagaggcctg aggaaaagca gatggcactg cttttagagt ctgttctttg tctctcttga 3060  
 tctttttcag ttaatgtctg ttttatcaga gactaggatt gcaaaccctg ctcttttttg 3120  
 ctttccattt gcttggtaaa tattcctcca tccctttatt ttaagcctat gtgtgtctt 3180  
 gcacatgaga tgggtctcct gaatacagga caacaatggg tctttactct ttatccaact 3240  
 tgccagtctg tgtcttttaa ctggggcatt tagccattt acatttaagt ttagtattgt 3300  
 tacatgtgaa atttatcctg tcatgatgtt gctagctttt ttttttccc attagtttgc 3360  
 agtttcttta tagtgtcaat ggtctttaca attogatatg tttttgtagt ggctgggtact 3420  
 ggtttttcct tctacgctt agtgtctcct tcaggagctc ttgtaacaca agaattgtga 3480  
 tttatttctt gtaaggtaaa tatgtggatt tatttcttgg gactgtattc tatggcctt 3540  
 acccaagaa tcattacttt ttaaaatgca attcaaatta gcataaaaca tttacagcct 3600  
 atggaaaggc ttgtggcatt agaatcctta tttataggat tttttgtgt ttttttgaga 3660  
 tatggctctt gtcacagag cagaagtgcc gtgggttgat cataattcac cacagccctg 3720  
 aactcttgag tccaagccat cttttgcct taatctccca accagttgga tctgcaggca 3780  
 taaggcatca tgcgtggcta atttttcac gtttttttt tttttttgtc gagattatgg 3840  
 tgtcactgtg ttgctctggc tgatctcaaa tgtttgacct caagggatct tctgccacg 3900  
 gcctcctaaa gtgctaggat tatatgcatg atacaccatg cctattgtag agtattacat 3960  
 ttttttcaaa gtcttattgt aagagccatt tattgccttt ggcctaaata actcaatata 4020  
 atatctctga aacttttttt tgacaaattt tggggcgtga tgatgagaga aggggggttg 4080  
 aaactttcta ataagagtta acttagagcc atttaagaaa ggaaaaaaca caaattatca 4140

```

gaaaaacaac agtaagatca agtgcaaaaag ttctgtggca aagatgatga gagtaaagaa 4200
tatatgtttg tgactcatgg tggctttttac tttgttcttg aatttctgag tacgggttaa 4260
catttaaaga atctacatta tagataacat tttattgcaa gtaaatgtat ttcaaaatth 4320
gttattgggtt ttgtatgaga ttattctcag cctacttcat tatcaagcta tattatttta 4380
ttaatgtagt tcatgatctt tacagcaaag ctgaaagctg tatcttcaaa atatgtctat 4440
ttgactaaaa agttattcaa caggagttat tatctataaa aaaaatacaa caggaatata 4500
aaaaacttga ggataaaaaag atgttggaaa aagtaatat aaatcttaaa aaacatatgg 4560
aaactacaca atgggtgaaga cacattgggtg aagtacaaaa atataaattg gatctagaag 4620
aaagggcaat gcaggcaata gaaaaattag tagaaatccc tttaaagggt agtttgtaaa 4680
atcaggtaag tttattttata atttgctttc atttatttca ctgcaaatta tattttggat 4740
atgtatatat attgtgcttc ctctgcctgt cttacagcaa ttgacctgag agagttctag 4800
gaaaaagggtg gcatgtgttt ttactttcaa aatatttaaa tttccatcat tataacaaaa 4860
tcaatttttc agagtaattga ttctcactgt ggagtcattt gattattaag acccggtggc 4920
ataagattac atcctctgac tataaaaaatc ctggaagaaa acctaggaaa tattcgtctg 4980
gacattgcac ttggcaatga atttatgggt aaccactgat ccacttccag tcaactatcca 5040
tgagttttta tttccagata catgaaatca tatgagttga aactttcttt tgattgagca 5100
gtttggaaac cgtctttttg tagaatctgc aagtggatat ttggaaccct ttgaggccta 5160
tgctgaaaaa agaaatatct tcaactacatg atgaccacca gcagcagctg gggaaaccag 5220
cacctgtgg aattccatac ggtgcataga atacatcttc ccttcagtcg gcttgggtca 5280
acttaggtca tgggccacct ggctgatagc agtttccaca gaaatgcttc aagatgaaag 5340
tggatgaccg ggccaccctc caccactgcc ctgtaagacc atgggacaca caggccacca 5400
gttcttttca tgtggtcatc cctgtttaga tgggagaaaa tacacctgcc tcatttttgt 5460
accttctgtg tgaacattcc acggcagact gtgcgtaaat gtggatgaag aattgaatga 5520
atgaatgaat atgagagaaa atgaataaat ggttcagatc ctgggctgga aggctgtgta 5580
tgaggatggt gggtagagga ggggtctgtt ttcttgcctt taagtcacta attgtcactt 5640
tggggcagga gcacaggctt tgaatgcaga ccgactggac ttttaattctg gctttactag 5700
ttgtgattgt gtgacctgtt gaaagttact taaaccctct gtgcctgttt ctttatctgt 5760
aaaatggaga taataagatg tcaaaggact gtggttaagaa ttaaatgctt taaaaaaaaa 5820
aaaaaaaaa

```

&lt;210&gt; 474

&lt;211&gt; 1594

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 474

```

atztatggat cattaatgcc tcttttagtag tttagagaaa acgtcaaaaag aaatggcccc 60
agaataagct tcttgatttg taaaattcta tgcattggc tcaaatttgt atagtatctc 120
aaaaataaaa tatatagaca tctcagataa tatatttgaa atagcaaatt cctgttagaa 180
aataatagta cttactaga tgagaataac aggtcgccat tatttgaatt gtctcctatt 240
cgtttttcat ttgttgtgtt actcatgttt tacttatgag ggatatatat aacttccact 300
gttttcagaa ttattgtatg cagtcagtat gagaatgcaa ttttaagttc cttgatgctt 360
ttcacactt ctattactag aaataagaat acagtaatat tggcaaagaa aattgaccag 420
ttcaataaaa ttttttagta aatctgattg aaaataaaca ttgcttatgg ctttcttaca 480
tcaatattgt tatgtcctag acaccttatc tgaaattacg gcttcaaaat tctaattatg 540
tgcaaatgtg taaaatatca atactttatg ttcaagctgg ggcctcttca ggcgtcctgg 600
gctgagagag aaagatgcta gctccgcaag ccggagaggg aacaccgcca cattgttaca 660
cggacacacc gccacgtgga cacatgacca gactcacatg tacagacaca cggagacatt 720
accacatgga gacacgttca cacagtccca cggacacact ggcatagtca catggacgga 780
cacacagaca tatggagaaa tcacatggac acaccaaccac actatcacag ggacacagac 840
acacggagac atcaccacat ggacacactg tcacactacc acagggacac gagacatcac 900
actgtcacat ggacacacca tcacacacat gaacacaccg acacactgcc atatggacac 960
tggcacacac actgccacac tgtcacatgg acacacctcc acaccatcac accaccacac 1020
acactgcctg tggacacaag gacacacaga cactgtcaca cagatacaca aaacactgtc 1080
acacggagac atcaccatgc agatacacca ccactctggg gccgtctgaa ttacctgtct 1140
ggggggacag cagtggcata ctcatgccta agtgactggc tttcacccca gtagtgattg 1200
ccctccatca aactgcca cccaggttg gggctacccc agcccatctt taaaaacag 1260
ggcaagggtga actaatggag tgggtggagg agttggaaga aatcccagcg tcagtcaccg 1320

```

```

ggatagaatt  cccaaggaac  cctctttttg  gaggatgggt  tccatttctg  gaggcgatct  1380
gccgacaggg  tgaatgcctt  cttgcttgct  ttctggggaa  tcagagagag  tccgttttgt  1440
ggtgggaaga  gtgtggctgt  gtactttgaa  ctctgtataa  ttctctgact  catgtccaca  1500
aaaccaacag  ttttgtgaat  gtgtctggag  gcaagggag  ggccactcag  gatctatgtt  1560
gaagggaaga  ggcctggggc  tggagtattc  gctt

```

&lt;210&gt; 475

&lt;211&gt; 2414

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (33)

&lt;223&gt; n=A,T,C or G

&lt;400&gt; 475

```

cccaacacaa  tggctttata  agaatgcttc  acntgtgaaa  aacaaatata  aaagtcttct  60
tgtagattat  ttttaaggac  aaatctttat  tccatgttta  atttatttag  ctttccctgt  120
agctaataat  tcatgctgaa  cacattttta  atgctgtaaa  tgtagataat  gtaatttatg  180
tatcattaat  gcctctttag  tagtttagag  aaaacgtcaa  aagaaatggc  cccagaataa  240
gcttcttgat  ttgtaaaatt  ctatgtcatt  ggctcaaatt  tgtatagtat  ctcaaaatat  300
aaatatatag  acatctcaga  taatatattt  gaaatagcaa  attcctgtta  gaaaataata  360
gtacttaact  agatgagaat  aacaggctgc  cattatttga  attgtctcct  attcgttttt  420
catttgttgt  gttactcatg  ttttacttat  ggggggatat  atataaactt  cgctgttttc  480
agaagtattg  tatgcagtca  gtatgagaat  gcaatttaag  tttccttgat  gctttttcac  540
acttctatta  ctagaaataa  gaatacagta  atattggcaa  agaaaattga  ccagttcaat  600
aaaatttttt  agtaaactct  attgaaaata  aacattgctt  atggctttct  tacatcaata  660
ttgttatgtc  ctagacacct  tatctgaaat  tacggcttca  aaattctaata  tatgtgcaaa  720
tgtgtaaaat  atcaatactt  tatgttcaag  ctggggcctc  ttcaggcgtc  ctgggctgag  780
agagaaagat  gtagctccg  caagccgggg  agggaaacac  gccacattgt  tacatggaca  840
caccgccacg  tggacacatg  accagactca  catgtacaga  cacacggaga  cattaccaca  900
tggagacacc  gtacacagct  cacacgagca  cactggcata  gtcacatgga  cggacacaca  960
gacatatgga  gaaatcacac  tgacacacca  ccacactatc  acaggggcac  agacacacgg  1020
agacatcacc  acatggacac  actgtcacac  taccacaggg  acacgagaca  tcacactgtc  1080
acatggacac  accatcacac  acatgaacac  accgacacac  tgccatatgg  acactgccac  1140
acacactgcc  acactgtcac  atggacacac  ctccatacca  tcacaccacc  acacacactg  1200
ccatgtggac  acaaggacac  acagacactg  tcacacagat  acacaaaaca  ctgtcacacg  1260
gagacatcac  catgcagata  caccaccaca  tggacatagc  accagacact  ctgccacaca  1320
gatacaccac  cacacagaaa  tgcggacaca  ctgccacaca  gacaccacca  catcgttgcc  1380
acactttcat  gtgtcagctg  gcggtgtggg  cccacagact  ctgggctcta  atcgagaaat  1440
tacttggaca  tatagtgaag  gcaaaatttt  tttttatttt  ctgggtaacc  aagcgcgact  1500
ctgtctcaaa  aaaagaaaaa  aaaagcaata  tactgtgtaa  tcgttgacag  cataattcac  1560
tattatgtag  atcgggagag  agaggattct  gaatgcatga  acatatcatt  aacatttcaa  1620
tacattactc  ataattactg  atgaactaaa  gagaaaccaa  gaaattatgg  tgatagttat  1680
attgacctgg  agaaatgtag  acacaaaaga  accgtaagat  gagaaatgtg  ttaacacagt  1740
ctataagggc  atgcaagaat  aaaaataggg  gagaaaacag  gagagttttt  caagagcttt  1800
ctggtcatgt  aagtcaactt  gtatcggtta  atttttaaaa  ggtttattta  catgcaataa  1860
actgcacata  cttcaattgt  acattttggt  aattcttggc  attttagct  ctataaaacc  1920
agcaacata  taaaatagca  aacatatcca  ttacctttac  caccaaagtt  ttcttgtgtt  1980
tttttactc  actttttcct  gcctatcccc  ccatctcttc  cacaggtaac  cactgatcca  2040
cttccagtca  ctatccatga  gtttttattt  ccaaatacat  gaaatcatat  gaatttctgg  2100
tttttctgt  tggagcccaa  ggagcaaggg  cagaatgagg  aacatgatgt  ttcttwccga  2160
cagttactca  tgacgtctcc  atccaggact  gaggggggca  tccttctcca  tctaggactg  2220
ggggcatcct  tctccatcca  gtattggggg  tcaccttct  ccacccagta  ttgggggtca  2280
tctctctcca  tccaggacct  gaggggtgtc  cttttctgcg  cttccttgga  tggcagtctt  2340
tcccttcatg  tttatagtra  cttaccatta  aatcactgtg  ccgttttttc  ctaaaataaa  2400
aaaaaaaaaa  aaaa

```



<210> 476  
<211> 3434  
<212> DNA  
<213> Homo sapiens

<400> 476  
ctgtgctgca aatggggcca tatagaggaa aggagcagct ggctctggag catggtgtgc 60  
actccctttg ggccttcagt ccatgtctca tgggtcgtat gacactgagg gcttgttggg 120  
tgccaagagg cagaccacag gtcactctga ggaggacttt atgttccagt ccagaaagca 180  
gccagtggta ccaccagagg gacttgtgct tctgtggccc aggccagacg tagaatttga 240  
caaaagtcagg acggtctcag tcagagcagc atgtcgggtcc ccggggcctg tgcattgccg 300  
gcaggggccag gctggcttaa ggagcaagca gccacctctg ttaggggtgt gcctggagca 360  
ggtggagcag ccaccaacct cacgactga aagaagcagg gatggccagg ttccaacatc 420  
ctgagtggct gccacctgat ggctgatgga gcagaggcct gaggaaaagc agatggcact 480  
gctttgtagt gctgttcttt gtctctcttg atctttttca gttaatgtct gttttatcag 540  
agactaggat tgcaaacctt gctctttttt gctttccatt tgcttggtaa atattcctcc 600  
atccctttat ttttaagccta tgttgtctct tgcacatgag atgggtctcc tgaatacagg 660  
acaacaatgg gtctttactc tttatccaac ttgccagtct gtgtctttta actggggcat 720  
ttagccatt tacatttaag tttagtattt gttacatgtg aaatttatcc tgtcatgatg 780  
ttgctagctt tttatttttc ccattagttt gcagtttctt tatagtgtca atgggtctta 840  
caattcgata tgtttttgta gtggctggta ctggtttttc ctttctacgt ttagtgtctc 900  
cttcaggagc tcttgtaaca caagaatgtg gatttatttc ttgtaaggta aatatgtgga 960  
tttattctgg gactgtattc tatggccttt accccaagaa tcattacttt ttaaaatgca 1020  
attcaaatga gcataaaaca tttacagcct atggaaaggc ttgtggcatt agaatcctta 1080  
tttataggat tattttgtgt ttttttgaga tatggtcttt gtcatcgagg cagaagtgcc 1140  
gtggtttgat cataattcac cacagccctg aactcttgag tccaagccat ctttttgctt 1200  
taatctccca accagttgga tctacaagca taaggcatca tgcgtggcta attttttcac 1260  
gttttttttt tttttgtcga gattatggta tcaactgtgt gctctggctg atctcaaag 1320  
tttgacctca agggatcttt ctgccacagc ctccataaag gctaggatta tatgcatgat 1380  
acaccatgcc tattgtagag tattacatta ttttcaaagt cttattgtaa gagccattta 1440  
ttgcctttgg cctaaataac tcaatataat atctctgaaa cttttttttg acaaattttg 1500  
gggcgtgatg atgagagaag ggggtttgaa actttctaag aagagttaac ttagagccat 1560  
ttaagaaagg aaaaaacaca aattatcaga aaaacaacag taagatcaag tgcaaaagtt 1620  
ctgtggcaaa gatgatgaga gtaaaagaata tatgtttgtg actcatggtg gcttttactt 1680  
tgttcttgaa tttctgagta cgggttaaca tttaaagaat ctacattata gataacattt 1740  
tattgcaagt aaatgtattt caaaatttgt tattggtttt gtatgagatt attctcagcc 1800  
tacttcatta tcaagctata ttattttatt aatgtagttc gatgatctta cagcaaagct 1860  
gaaagctgta tcttcaaaat atgtctattt gactaaaaag ttattcaaca ggagttatta 1920  
tctataaaaa aatacaacag gaatataaaa aacttgagga taaaaagatg ttggaaaaag 1980  
taatattaaa tcttaaaaaa catatggaaa ctacacaatg gtgaagacac attggtgaag 2040  
tacaaaaata taaattggat ctagaagaaa gggcaatgca ggcaatagaa aaattagtag 2100  
aaatcccttt aaaggttagt ttgtaaaatc aggttaagttt atttataatt tgctttcatt 2160  
tatttcactg caaattatat tttggatatg tatatatatt gtgcttcctc tgctgtctt 2220  
acagcaattt gccttgca ga gttctaggaa aaagggtgga tgtgttttta ctttcaaaat 2280  
attttaaattt ccattcattat aacaaaatca atttttcaga gtaatgattc tcaactgtga 2340  
gtcatttgat tattaagacc cgttggcata agattacatc ctctgactat aaaaatcctg 2400  
gaagaaaacc taggaaatat tcgtctggac attgcacttg gcaatgaatt tatgggcgct 2460  
ttggaatcct gcagatataa taatgataat taacaaaaac actcagagaa actgccaacc 2520  
ctaggatgaa gtatattgtt actgtgcttt gggattaaaa taagtaacta cagtttatag 2580  
aacttttata ctgatacaca gacactaaaa agggaaaggg tttagatgag aagctctgct 2640  
atgcaatcaa gactctcagc cactcatttc tttaggggct gcaggagctc cctgtaaaga 2700  
gaggttatgg agctctgagc ttcaggtaag atacttaaaa cccttcagag tttctccatt 2760  
ttttcccata gtttccccaa aaaggttatg acactttata agaatgcttc acttgtgaaa 2820  
aacaatatc aaagtcttct tgtagattat ttttaaggac aaatctttat tccatgttta 2880  
atttatttag ctttccctgt agctaataat tcatgctgaa cacattttta atgctgtaaa 2940  
tgtagataat gtaatttatg tatcattaat gcctctttag tagtttagag aaaacgtcaa 3000  
aagaaatggc ccagaataa gcttcttgat ttgtaaaatt ctatgtcatt ggctcaaatt 3060

```

tgtatagtat ctcaaaatat aaatatatag acatctcaga taatatatatt gaaatagcaa 3120
attcctgtta gaaaataata gtacttaact agatgagaat aacaggtcgc cattatttga 3180
attgtctcct attcgttttt catttggtgt gttactcatg ttttacttat ggggggatat 3240
atataacttc cgtctgtttt agaagtattg tatgcagtca gtatgagaat gcaatttaag 3300
tttcttgat gctttttcac acttctatta ctagaataa gaatacagta atattggcaa 3360
agaaaattga ccagttcaat aaaatttttt agtaaactcg attgaaaata aaaaaaaaaa 3420
aaaaaaaaa aaaa 3434

```

&lt;210&gt; 477

&lt;211&gt; 140

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 477

```

Met Asp Gly His Thr Asp Ile Trp Arg Asn His Met Asp Thr Pro Pro
                    5                      10                      15

```

```

His Tyr His Arg Asp Thr Asp Thr Arg Arg His His His Met Asp Thr
                    20                      25                      30

```

```

Leu Ser His Tyr His Arg Asp Thr Arg His His Thr Val Thr Trp Thr
                    35                      40                      45

```

```

His His His Thr His Glu His Thr Asp Thr Leu Pro Tyr Gly His Trp
                    50                      55                      60

```

```

His Thr His Cys His Thr Val Thr Trp Thr His Leu His Thr Ile Thr
                    65                      70                      75                      80

```

```

Pro Pro His Thr Leu Pro Val Asp Thr Arg Thr His Arg His Cys His
                    85                      90                      95

```

```

Thr Asp Thr Gln Asn Thr Val Thr Arg Arg His His His Ala Asp Thr
                    100                      105                      110

```

```

Pro Pro Leu Trp Cys Arg Leu Asn Tyr Pro Ala Gly Gly Thr Ala Val
                    115                      120                      125

```

```

Ala Tyr Ser Cys Leu Ser Asp Trp Leu Ser Pro Gln
                    130                      135                      140

```

&lt;210&gt; 478

&lt;211&gt; 143

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 478

```

Met Tyr Arg His Thr Glu Thr Leu Pro His Gly Asp Thr Val Thr Gln
                    5                      10                      15

```

```

Ser His Gly His Thr Gly Ile Val Thr Trp Thr Asp Thr Gln Thr Tyr
                    20                      25                      30

```

```

Gly Glu Ile Thr Trp Thr His His His Thr Ile Thr Gly Thr Gln Thr
                    35                      40                      45

```

```

His Gly Asp Ile Thr Thr Trp Thr His Cys His Thr Thr Thr Gly Thr

```

50                      55                      60  
 Arg Asp Ile Thr Leu Ser His Gly His Thr Ile Thr His Met Asn Thr  
 65                      70                      75                      80  
 Pro Thr His Cys His Met Asp Thr Gly Thr His Thr Ala Thr Leu Ser  
 85                      90                      95  
 His Gly His Thr Ser Thr Pro Ser His His His Thr His Cys Leu Trp  
 100                      105                      110  
 Thr Gln Gly His Thr Asp Thr Val Thr Gln Ile His Lys Thr Leu Ser  
 115                      120                      125  
 His Gly Asp Ile Thr Met Gln Ile His His His Ser Gly Ala Val  
 130                      135                      140  
  
 <210> 479  
 <211> 222  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 479  
 Met Tyr Arg His Thr Glu Thr Leu Pro His Gly Asp Thr Val Thr Gln  
 5                      10                      15  
 Ser His Glu His Thr Gly Ile Val Thr Trp Thr Asp Thr Gln Thr Tyr  
 20                      25                      30  
 Gly Glu Ile Thr Leu Thr His His His Thr Ile Thr Gly Thr Gln Thr  
 35                      40                      45  
 His Gly Asp Ile Thr Thr Trp Thr His Cys His Thr Thr Thr Gly Thr  
 50                      55                      60  
 Arg Asp Ile Thr Leu Ser His Gly His Thr Ile Thr His Met Asn Thr  
 65                      70                      75                      80  
 Pro Thr His Cys His Met Asp Thr Ala Thr His Thr Ala Thr Leu Ser  
 85                      90                      95  
 His Gly His Thr Ser Ile Pro Ser His His His Thr His Cys His Val  
 100                      105                      110  
 Asp Thr Arg Thr His Arg His Cys His Thr Asp Thr Gln Asn Thr Val  
 115                      120                      125  
 Thr Arg Arg His His His Ala Asp Thr Pro Pro His Gly His Ser Thr  
 130                      135                      140  
 Arg His Ser Ala Thr Gln Ile His His His Thr Glu Met Arg Thr His  
 145                      150                      155                      160  
 Cys His Thr Asp Thr Thr Thr Ser Leu Pro His Phe His Val Ser Ala  
 165                      170                      175  
 Gly Gly Val Gly Pro Thr Thr Leu Gly Ser Asn Arg Glu Ile Thr Trp

167

180 185 190  
 Thr Tyr Ser Glu Gly Lys Ile Phe Phe Tyr Phe Leu Gly Asn Gln Ala  
 195 200 205

Arg Leu Cys Leu Lys Lys Arg Lys Lys Lys Gln Tyr Thr Val  
 210 215 220

<210> 480  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 480  
 Met Glu Pro Tyr Arg Gly Asn Glu Gln Pro Ser Gln Glu Gln Gly Val  
 5 10 15

Cys Cys Leu Trp Gly Leu Gln Ser Leu Pro Gln Gly Ser Tyr Val Thr  
 20 25 30

Val Gly Phe Leu Val Val Lys Arg Gln Thr Ile Gly Arg Leu Glu Arg  
 35 40 45

Asp Phe Met Phe Lys Cys Arg Lys Gln Pro Gly Leu Pro Pro Ser Gly  
 50 55 60

Leu Cys Leu Leu Trp Pro Trp Pro Asn Leu Glu Phe Gly Arg Arg Gln  
 65 70 75 80

Asp Arg Leu Thr Trp Ser Ser Val Ser Val Ala Gly Val Cys Ala Cys  
 85 90 95

Arg Ala Arg Pro Gly Trp Leu Gly Glu Gln Pro Ala Thr Ser Ala Gly  
 100 105 110

Val Arg Leu Glu Gln Val Glu Gln Pro Pro Ala His Pro Leu Gln Glu  
 115 120 125

Ala Gly Val Ala Arg Phe Pro Arg Pro Glu Trp Val Pro Pro Asn Gly  
 130 135 140

<210> 481  
 <211> 167  
 <212> PRT  
 <213> Homo sapiens

<400> 481  
 Met His Gly Pro Gln Val Leu Ala Arg Cys Ser Glu Cys Ala Cys Pro  
 5 10 15

Ala Leu Ala Ala Thr Ser Ala Gly Val Arg Leu Glu Gly Val Asp Arg  
 20 25 30

```
<210> 482
<211> 143
<212> PRT
<213> Homo sapiens
```

```

<400> 482
Met Glu Pro Tyr Arg Gly Asn Lys Lys Gln Val Gln Glu Lys Gly Val
      5              10              15

Pro Cys Leu Trp Gly Ser Ser Pro Cys Leu Arg Cys His Met Ala Leu
      20              25              30

Arg Ala Ser Trp Leu Pro Gly Gly Gly Pro Gln Ala Ile Leu Gly Arg
      35              40              45

Thr Leu Cys Ser Ser Ala Glu Ser Ser Gln Asp Cys His Pro Gly Gly
      50              55              60

Pro Ser Ile Ala Leu Ala Lys Pro Cys Arg Gly Val Trp Leu Leu Phe
      65              70              75              80

Glu Pro Ala Trp Pro Pro Trp His Ala Arg Ala Pro Gly Ala Gly Thr
      85              90              95

Leu Leu Arg Val Cys Leu Ser Cys Leu Gly Cys His Leu Cys Gly Gly
      100             105             110

Ala Ser Gly Gly Gly Gly Pro Ala Thr Asn Leu Thr Gln Ser Arg Lys
      115              120              125

```

Trp Met Ala Met Phe Pro Gln Pro Glu Trp Leu Pro Pro Asp Gly  
 130 135 140

<210> 483

<211> 143

<212> PRT

<213> Homo sapiens

<400> 483

Met Glu Thr Gln Arg Gly Asn Lys Gln Arg Ala Gln Glu Gln Gly Val  
 5 10 15

Cys Cys Leu Trp Gly Ser Ser Pro Cys Leu Gly Ser Tyr Gly Thr Ala  
 20 25 30

Gly Phe Leu Val Ala Lys Arg Arg Thr Thr Gly Leu Leu Glu Glu Asp  
 35 40 45

Phe Thr Phe Lys Cys Arg Lys Gln Pro Lys Leu Pro Ser Met Arg Leu  
 50 55 60

Ser Leu Leu Trp Pro Trp Arg Asp Leu Lys Phe Val Pro Arg Gln Asp  
 65 70 75 80

Lys Leu Thr Arg Ser Ser Val Ser Val Ala Gly Ala Tyr Ala Cys Arg  
 85 90 95

Ala Gly Pro Gly Trp Leu Lys Glu Gln Pro Ala Thr Ser Ala Arg Val  
 100 105 110

Arg Leu Val Gln Ala Glu His Pro Pro Pro His Pro Leu Glu Glu Val  
 115 120 125

Gly Met Ala Arg Phe Pro Gln Pro Glu Cys Leu Pro Pro Tyr Cys  
 130 135 140

<210> 484

<211> 30

<212> PRT

<213> Homo Sapien

<400> 484

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe  
 1 5 10 15  
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile  
 20 25 30

<210> 485

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 485

gggaagctta tcacctatgt gccgcctctg c

<210> 486  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 486  
gcgaattctc acgctgagta tttggcc

27

<210> 487  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 487  
cccgaattct tagctgcca tccgaacgcc ttcac

36

<210> 488  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 488  
gggaagcttc ttccccggct gcaccagctg tgc

33

<210> 489  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 489  
Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala  
1 5 10 15  
Ser Val Ala

<210> 490  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 490  
Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys

```

1          5          10          15
Leu Ser His Ser
20

<210> 491
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 491
Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
1          5          10          15
Thr Gly Phe Thr
20

<210> 492
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 492
Ala Leu Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr
1          5          10          15
Leu Ala Ser Leu
20

<210> 493
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 493
Tyr Thr Leu Ala Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro
1          5          10          15
Lys Tyr Arg Gly
20

<210> 494
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 494
Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser
1          5          10          15
Leu Met Ile Ser

```



<220>  
<223> Made in a lab

<220>  
<223> Made in a lab

<220>  
<223> Made in a lab

<220>  
<223> Made in a lab

<400> 498  
 Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val  
 1 5 10 15  
 Val Pro Gly Arg  
 20

```

<210> 499
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 499
Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 1             5             10             15
Ser Ala Phe Leu
                20

<210> 500
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 500
Leu Asp Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met
 1             5             10             15
Gly Ser Ile Val
                20

<210> 501
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in a lab

<400> 501
Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met
 1             5             10             15
Val Ser Ala Ala
                20

<210> 502
<211> 414
<212> DNA
<213> Homo Sapien

<220>
<221> misc_feature
<222> (1)...(414)
<223> n=A,T,C or G

<400> 502
caccatggag acaggcctgc gctggctttt cctggctcgt gtgctcaaag gtgtccaatg      60
tcagtcggtg gaggagtccg ggggtcgcct ggtcacgcct gggacacctt tgacantcac      120
ctgtagagtt tttggaatng acctcagtag caatgcaatg agctgggtcc gccaggctcc      180
agggaagggg ctggaatgga tcggagccat tgataattgt ccacantacg cgacctgggc      240

```

```

gaaaggccga ttnatnattt ccaaaacctn gaccacgggtg gatttgaaaa tgaccagtcc 300
gacaaccgag gacacggcca cctatttttg tggcagaatg aatactggta atagtgggtg 360
gaagaatatt tggggcccag gcaccctggt caccgtntcc tcagggaac ctaa 414

```

```

<210> 503
<211> 379
<212> DNA
<213> Homo Sapien

```

```

<220>
<221> misc_feature
<222> (1)...(379)
<223> n=A,T,C or G

```

```

<400> 503
atnccgatggt gcttgggtcaa aggtgtccag tgtcagtcgg tggaggagtc cgggggtcgc 60
ctggtcacgc ctgggacacc cctgacactc acctgcaccg tntctggatt ngacatcagt 120
agctatggag tgagctgggt ccgccaggct ccagggaagg ggctgggnata catcggatca 180
ttagtagtag tggtagattt tacgcgagct gggcgaaagg ccgattcacc atttccaaaa 240
cctngaccac ggtggatttg aaaatcacca gtttgacaac cgaggacacg gccacctatt 300
tntgtgccag aggggggttt aattataaag acatttgggg cccaggcacc ctggtcaccg 360
tntccttagg gcaacctaa 379

```

```

<210> 504
<211> 19
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Made in a lab

```

```

<400> 504
Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp Ser Pro Tyr Phe Lys Glu
 1           5           10           15
Asn Ser Ala

```

```

<210> 505
<211> 20
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Made in a lab

```

```

<400> 505
Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn Asp Asn Val Thr
 1           5           10           15
Asn Thr Ala Asn
 20

```

```

<210> 506
<211> 407
<212> DNA
<213> Homo Sapien

```

```

<400> 506

```

```

atggagacag gcctgcgctg gcttctcctg gtcgctgcgc tcaaaggtgt ccagtgtcag      60
tcgctggagg agtccggggg tcgctgggtc acgcctggga caccctgac actcacctgc      120
accgtctctg gattctccct cagtagcaat gcaatgatct ggggccgcca ggctccaggg      180
aaggggctgg aatacatcgg atacattagt tatggtggta gcgcatacta cgcgagctgg      240
gtgaaaggcc gattcaccat ctccaaaacc tcgaccacgg tggatctgag aatgaccagt      300
ctgacaaccg aggacacggc cacctatttc tgtgccagaa atagtgattt tagtggtatg      360
ttgtggggcc caggcaccct ggtcaccgtc tcctcagggc aacctaa      407

```

<210> 507  
 <211> 422  
 <212> DNA  
 <213> Homo Sapien

```

<400> 507
atggagacag gcctgcgctg gcttctcctg gtcgctgtgc tcaaaggtgt ccagtgtcag      60
tcggtggagg agtccggggg tcgctgggtc acgcctggga caccctgac actcacctgt      120
acagtctctg gattctccct cagcaactac gacctgaact ggggccgcca ggctccaggg      180
aaggggctgg aatggatcgg gatcattaat tatgttggta ggacggacta cgcgaactgg      240
gcaaaaggcc ggttcaccat ctccaaaacc tcgaccaccg tggatctcaa gatcgccagt      300
ccgacaaccg aggacacggc cacctatttc tgtgccagag ggtggaagtg cgatgagctc      360
ggtccgtgct tgcgcatctg gggcccaggc accctggtca ccgtctcctt agggcaacct      420
aa                                                                                   422

```

<210> 508  
 <211> 411  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(411)  
 <223> n=A,T,C or G

```

<400> 508
atggagacag gcctgcgctg cttctcctgg tcgctgtgct caaaggtgtc cagtgtcagt      60
cggtggagga gtccgggggt cgctgggtca cgcctgggac acccctgaca ctcacctgca      120
cagtctcttg aatcgacctc agtagctact gcatgagctg ggtccgccag gctccagggg      180
aggggctgga atggatcggg atcattggta ctctgggtga cacatactac gcgaggtggg      240
cgaaaggccg attcaccatc tccaaaacct cgaccacggg gcatntgaaa atcnccagtc      300
cgacaaccga ggacacggcc acctatttct gtgccagaga tcttcgggat ggtagtagta      360
ctggttatta taaaatctgg ggcccaggca ccctggtcac cgtctccttg g      411

```

<210> 509  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

```

<400> 509
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
 1             5             10             15

```

<210> 510  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 510

Pro	Glu	Tyr	Asn	Arg	Pro	Leu	Leu	Ala	Asn	Asp	Leu	Met	Leu	Ile
1				5					10					15

&lt;210&gt; 511

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 511

Tyr	His	Pro	Ser	Met	Phe	Cys	Ala	Gly	Gly	Gly	Gln	Asp	Gln	Lys
1				5					10					15

&lt;210&gt; 512

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 512

Asp	Ser	Gly	Gly	Pro	Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu
1				5					10					15

&lt;210&gt; 513

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 513

Ala	Pro	Cys	Gly	Gln	Val	Gly	Val	Pro	Asx	Val	Tyr	Thr	Asn	Leu
1				5					10					15

&lt;210&gt; 514

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 514

Leu	Cys	Lys	Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Ala	Ser
1				5					10					15

&lt;210&gt; 515

<211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 515  
 Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg  
 1 5 10 15

<210> 516  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 516  
 Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln  
 1 5 10 15

<210> 517  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 517  
 Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met  
 1 5 10 15

<210> 518  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 518  
 Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly  
 1 5 10 15

<210> 519  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 519  
 Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg Asn Tyr Asp Glu Gly Cys  
 1 5 10 15

Gly

<210> 520  
 <211> 25  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 520  
 Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr  
 1 5 10 15  
 Glu Ala Arg Arg His Tyr Asp Glu Gly  
 20 25

<210> 521  
 <211> 21  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 521  
 Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu  
 1 5 10 15  
 Pro Pro Pro Pro Ala  
 20

<210> 522  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 522  
 Leu Leu Val Val Pro Ala Ile Lys Lys Asp Tyr Gly Ser Gln Glu Asp  
 1 5 10 15  
 Phe Thr Gln Val  
 20

<210> 523  
 <211> 254  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<220>  
 <221> VARIANT  
 <222> (1)...(254)  
 <223> Xaa = any amino acid

<400> 523

Met	Ala	Thr	Ala	Gly	Asn	Pro	Trp	Gly	Trp	Phe	Leu	Gly	Tyr	Leu	Ile
1				5				10					15		
Leu	Gly	Val	Ala	Gly	Ser	Leu	Val	Ser	Gly	Ser	Cys	Ser	Gln	Ile	Ile
			20					25					30		
Asn	Gly	Glu	Asp	Cys	Ser	Pro	His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu
		35					40					45			
Val	Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln
	50					55					60				
Trp	Val	Leu	Ser	Ala	Thr	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly
65					70				75					80	
Leu	Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met
				85					90					95	
Val	Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu
			100					105					110		
Leu	Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu
		115					120					125			
Ser	Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala
	130					135					140				
Gly	Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly	Arg
145					150					155				160	
Met	Pro	Thr	Val	Leu	Gln	Cys	Val	Asn	Val	Ser	Val	Val	Ser	Glu	Glu
				165					170					175	
Val	Cys	Ser	Lys	Leu	Tyr	Asp	Pro	Leu	Tyr	His	Pro	Ser	Met	Phe	Cys
			180					185					190		
Ala	Gly	Gly	Gly	Gln	Xaa	Gln	Xaa	Asp	Ser	Cys	Asn	Gly	Asp	Ser	Gly
			195				200					205			
Gly	Pro	Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu	Val	Ser	Phe	Gly
	210					215					220				
Lys	Ala	Pro	Cys	Gly	Gln	Val	Gly	Val	Pro	Gly	Val	Tyr	Thr	Asn	Leu
225					230					235				240	
Cys	Lys	Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Ala	Ser		
				245					250						

&lt;210&gt; 524

&lt;211&gt; 765

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 524

atggccacag	caggaaatcc	ctggggctgg	ttcctgggggt	acctcatcct	tggtgtcgca	60
ggatcgctcg	tctctggtag	ctgcagccaa	atcataaacg	gcgaggactg	cagcccgcac	120
tcgcagccct	ggcaggcggc	actggtcatg	gaaaacgaat	tggtctgctc	gggcgtcctg	180
gtgcatccgc	agtgggtgct	gtcagccgca	cactgtttcc	agaactccta	caccatcggg	240
ctgggcctgc	acagtcttga	ggccgaccaa	gagccaggga	gccagatggt	ggaggccagc	300
ctctccgtac	ggcaccacaga	gtacaacaga	cccttgctcg	ctaacgacct	catgctcatc	360
aagtgggacg	aatccgtgtc	cgagtctgac	accatccgga	gcatcagcat	tgcttcgcag	420
tgccctaccg	cggggaactc	ttgcctcgtt	tctggctggg	gtctgctggc	gaacggcaga	480
atgcctaccg	tgctgcagtg	cgtgaacgtg	tcgggtggtg	ctgaggaggt	ctgcagtaag	540
ctctatgacc	cgtgtacca	ccccagcatg	ttctgcgccg	gcggagggca	agaccagaag	600
gactcctgca	acggtgactc	tggggggccc	ctgatctgca	acgggtactt	gcagggcctt	660
gtgtctttcg	gaaaagcccc	gtgtggccaa	gttggcgctg	caggtgtcta	caccaacctc	720
tgcaaattca	ctgagtggat	agagaaaacc	gtccaggcca	gttaa		765

&lt;210&gt; 525

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Homo sapien



&lt;400&gt; 525

Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile  
 1 5 10 15  
 Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile  
 20 25 30  
 Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu  
 35 40 45  
 Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln  
 50 55 60  
 Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly  
 65 70 75 80  
 Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met  
 85 90 95  
 Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu  
 100 105 110  
 Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu  
 115 120 125  
 Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala  
 130 135 140  
 Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg  
 145 150 155 160  
 Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu  
 165 170 175  
 Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys  
 180 185 190  
 Ala Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly  
 195 200 205  
 Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly  
 210 215 220  
 Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu  
 225 230 235 240  
 Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser  
 245 250

&lt;210&gt; 526

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 526

atgagttcct gcaacttcac acatgccacc tttgtgctta ttggtatccc aggattagag 60  
 aaagccatt tctgggttgg cttccccctc ctttccatgt atgtagtggc aatgtttgga 120  
 aactgcatcg tggctttcat cgtaaggacg gaacgcagcc tgcacgctcc gatgtacctc 180  
 tttctctgca tgccttgacg cattgacctg gccttatcca catccaccat gcctaagatc 240  
 cttgcccttt tctgggttga ttcccgagag attagctttg aggctgtct taccagatg 300  
 ttctttattc atgccctctc agccattgaa tccaccatcc tgctggccat ggcctttgac 360  
 cgttatgtgg ccatctgcca cccactgcgc catgctgcag tgcctcaaca tacagtaaca 420  
 gccagattg gcatcggtggc tgtggtccgc ggatccctct tttttttccc actgcctctg 480  
 ctgatcaagc ggetggcctt ctgccactcc aatgtcctct cgcactccta ttgtgtccac 540  
 caggatgtaa tgaagttggc ctatgcagac actttgccca atgtggtata tggcttact 600  
 gccattctgc tggctcatggg cgtggacgta atgttcatct ccttgtccta ttttctgata 660  
 atacgaacgg ttctgcaact gccttccaag tcagagcggg ccaaggcctt tggaacctgt 720  
 gtgtcacaca ttggtgtggg actcgccttc tatgtgccac ttattggcct ctcaattgta 780  
 caccgctttg gaaacagcct tcatcccatt gtgcgtgttg tcatgggtga catctacctg 840  
 ctgctgcctc ctgtcatcaa tcccatcatc tatggtgcca aaaccaaaca gatcagaaca 900  
 cgggtgctgg ctatgttcaa gatcagctgt gacaaggact tgcaggctgt gggaggcaag 960  
 tga

181

&lt;210&gt; 527

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 527

Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile  
                                   5                                  10                                  15

Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser  
                                   20                                  25                                  30

Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val  
                                   35                                  40                                  45

Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met  
                                   50                                  55                                  60

Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile  
                                   65                                  70                                  75                                  80

Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys  
                                   85                                  90                                  95

Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr  
                                   100                                  105                                  110

Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro  
                                   115                                  120                                  125

Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly  
                                   130                                  135                                  140

Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu  
                                   145                                  150                                  155                                  160

Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser  
                                   165                                  170                                  175

Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu  
                                   180                                  185                                  190

Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val  
                                   195                                  200                                  205

Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val  
                                   210                                  215                                  220

Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys  
                                   225                                  230                                  235                                  240

Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly  
                                   245                                  250                                  255

Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg  
                                   260                                  265                                  270

Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro  
 275 280 285

Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala  
 290 295 300

Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln Ala Val Gly Gly Lys  
 305 310 315 320

<210> 528  
 <211> 20  
 <212> DNA  
 <213> Homo Sapien

<400> 528  
 actatgggtcc agaggctgtg 20

<210> 529  
 <211> 20  
 <212> DNA  
 <213> Homo Sapien

<400> 529  
 atcacctatg tgccgcctct 20

<210> 530  
 <211> 1852  
 <212> DNA  
 <213> Homo sapiens

<400> 530  
 ggacagagaa ttaaaaccct cagcaaaaaca ggcataaga ggacatacct taaagtaata 60  
 aaaaccacct atgacaagcc cacagccaac ataatactaa atggggaaaa gttagaagca 120  
 tttcctctga gaactgcaac aataaataca aggatgctgg attttgtcaa atgccttttc 180  
 tgtgtctgtt gagatgctta tgtgactttg cttttaattc tgtttatgtg attatcacat 240  
 ttattgactt gcctgtgtta gaccggaaga gctgggggtg ttctcaggag ccaccgtgtg 300  
 ctgcggcagc ttccgggataa cttgaggctg catcactggg gaagaaacac aytccctgtcc 360  
 gtggcgctga tggctgagga cagagcttca gtgtggcttc tctgcgactg gcttcttcgg 420  
 ggagttcttc cttcatagtt catccatatg gctccagagg aaaattatat tattttgtta 480  
 tggatgaaga gtattacgtt gtgcagatat actgcagtg cttcatctct tgatgtgtga 540  
 ttgggtaggt tccaccatgt tgccgcagat gacatgattt cagtacctgt gtctggctga 600  
 aaagtgtttg tttgtgaatg gatattgtgg tttctggatc tcactcctct tgggtggaca 660  
 gctttctcca ccttgctgga agtgacctgc tgtccagaag tttgatggct gaggagtata 720  
 ccactcgtga tgcactcttc atttcttgca tttcttctc cctggatgga cagggggagc 780  
 ggcaagagca acgtgggcac ttctggagac cacaacgact cctctgtgaa gacgcttggg 840  
 agcaagaggt gcaagtgggt ctgccactgc ttccctgct gcagggggag cggcaagagc 900  
 aacgtggctg cttggggaga ctacgatgac agcgccctca tggatcccag gtaccacgtc 960  
 catggagaa atctggacaa gctccacaga gctgcctggt ggggtaaagt cccagaaaag 1020  
 gatctcatcg tcatgtcag ggacacggat gtgaacaaga gggacaagca aaagaggact 1080  
 gctctacatc tggcctctgc caatgggaat tcagaagtag taaaactcgt gctggacaga 1140  
 cgatgtcaac ttaatgtcct tgacaacaaa aagaggacag ctctgacaaa ggccgtacaa 1200  
 tgccaggaag atgaatgtgc gttaatgttg ctggaacatg gcactgatcc aaatattcca 1260  
 gatgagtatg gaaataccac tctacactat gctgtctaca atgaagataa attaattgcc 1320  
 aaagcactgc tcttatacgg tgctgatatc gaatcaaaaa acaagcatgg cctcacacca 1380  
 ctgctacttg gtatacatga gcaaaaacag caagtgggtga aatttttaat caagaaaaaa 1440  
 gcgaatttaa atgcgctgga tagatatgga agaactgctc tcatacttgc tgtatgttgt 1500  
 ggatcagcaa gtatagtcag ccctctactt gagcaaaatg ttgatgtatc ttctcaagat 1560  
 ctggaaagac ggccagagag tatgctgttt ctatgcatca tcatgtaatt tgccagttac 1620

```
<210> 531
<211> 879
<212> DNA
<213> Homo sapiens
```

<400> 531						
atgcatcttt	catttcctgc	attttottoct	ccctggatgg	acaggggggag	cggcaagagc	60
aacgtgggca	cttctggaga	ccacaacgac	tctctgtga	agacgcttgg	gagcaagagg	120
tgcaagtgg	gctgccactg	cttccctgc	tgcaggggga	gcggcaagag	caacgtggtc	180
gcttggggag	actacgatga	cagcgccttc	atggatccca	ggtaccacgt	ccatggagaa	240
gatctggaca	agctccacag	agctgcctgg	tggggtaaag	tccccagaaa	ggatctcatc	300
gtcatgtctca	gggacacgga	tgtgaacaag	agggacaagc	aaaagaggac	tgctctacat	360
ctggcctctg	ccaatgggaa	ttcagaagta	gtaaaactcg	tgctggacag	acgatgtcaa	420
cttaatgtcc	ttgacaacaa	aaagaggaca	gctctgacaa	aggccgtaca	atgccaggaa	480
gatgaatgtg	cgттаатgtt	gctggaacat	ggcactgatc	caaatatcc	agatgagtat	540
ggaaatacca	ctctacacta	tgctgtctac	aatgaagata	aattaatggc	caaagcactg	600
ctcttatacg	gtgctgatat	cgaatcaaaa	aacaagcatg	gcctcacacc	actgctactt	660
ggtatacatg	agcaaaaaa	gcaagtggg	aaatttttaa	tcaagaaaaa	agcgaattta	720
aatgcgctga	atagatatgg	aagaactgct	ctcatacttg	ctgtatgttg	tggatcagca	780
agtagtagtc	gccctctact	tgagcaaaat	gttgatgtat	cttctcaaga	tctggaaaaga	840
cggccagaga	gtatgctgtt	tctagtcatc	atcatgtaa			879

```
<210> 532
<211> 292
<212> PRT
<213> Homo sapiens
```

```

<400> 532
Met His Leu Ser Phe Pro Ala Phe Leu Pro Pro Trp Met Asp Arg Gly
      5              10              15

Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp His Asn Asp Ser Ser
      20              25              30

Val Lys Thr Leu Gly Ser Lys Arg Cys Lys Trp Cys Cys His Cys Phe
      35              40              45

Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val Val Ala Trp Gly Asp
      50              55              60

Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr His Val His Gly Glu
      65              70              75              80

Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg
      85              90              95

Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Arg Asp
      100              105              110

Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser
      115              120              125

Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys Gln Leu Asn Val Leu

```

```
<210> 533
<211> 801
<212> DNA
<213> Homo sapiens
```

<400> 533						
atgtacaagc	ttcagtgtcaa	caactgtgtct	acaaatggag	ccacagagag	gaaacaagca	60
gcagggtcag	gagcagggtta	tgcgtgtcct	tcggtctctc	aatccatgcc	tcagggtctc	120
tatgccactg	cacgattctt	ggttgccaag	aggccaacca	caggccaatct	tgagaaggag	180
tttatgtttc	actgcagaaa	gcagccagga	tcaccatcca	ggggacttgg	tcttctgttg	240
ccctggccag	acatagaatt	tgtgtccaag	caggacaagc	tcactcagag	cagcgtgtta	300
gtacctcaaa	tctgtgcgtg	ccagacaagg	ccaaactggc	tcaatgagca	accagccacc	360
tctgcagggg	tgcgtctgga	ggaggtggac	cagccacca	ccttaccag	tcaaggaagt	420
ggatggccat	gttcccacag	cctgagtggc	tgccacctga	tggctgatat	agcaaaggcc	480
ttaggaaaag	cagatggccc	ttggccctac	ctttttgtta	gaagaactga	tgttccatgt	540
cctgcagcga	gtgaggttg	tggctgtgcc	cccagctcct	ggcacaccct	cgcagaggtg	600
actggttgct	ctttgagccc	tcttagccct	gccagcatg	cacaagcctc	agtgtacta	660
ctgtgctaca	aattggagcca	tataggggaa	acgagcagcc	atctcaggag	caaggtgtat	720
gctgcctttg	ggggctccag	tccttgccct	aagggtctta	tgctactgtg	ggcttcttgg	780
ttgccaaagag	gcagaccata	g				801

```
<210> 534
<211> 266
<212> PRT
<213> Homo sapiens
```

&lt;400&gt; 534

Met Tyr Lys Leu Gln Cys Asn Asn Cys Ala Thr Asn Gly Ala Thr Glu  
                           5                          10                          15

Arg Lys Gln Ala Ala Gly Ser Gly Ala Gly Tyr Ala Leu Pro Ser Ala  
                           20                          25                          30

Leu Gln Ser Met Pro Gln Gly Ser Tyr Ala Thr Ala Arg Phe Leu Val  
                           35                          40                          45

Ala Lys Arg Pro Thr Thr Gly His Leu Glu Lys Glu Phe Met Phe His  
                           50                          55                          60

Cys Arg Lys Gln Pro Gly Ser Pro Ser Arg Gly Leu Gly Leu Leu Trp  
                           65                          70                          75                          80

Pro Trp Pro Asp Ile Glu Phe Val Pro Arg Gln Asp Lys Leu Thr Gln  
                           85                          90                          95

Ser Ser Val Leu Val Pro Gln Ile Cys Ala Cys Gln Thr Arg Pro Asn  
                           100                          105                          110

Trp Leu Asn Glu Gln Pro Ala Thr Ser Ala Gly Val Arg Leu Glu Glu  
                           115                          120                          125

Val Asp Gln Pro Pro Thr Leu Pro Ser Gln Gly Ser Gly Trp Pro Cys  
                           130                          135                          140

Ser His Ser Leu Ser Gly Cys His Leu Met Ala Asp Ile Ala Lys Ala  
                           145                          150                          155                          160

Leu Gly Lys Ala Asp Gly Pro Trp Pro Tyr Leu Phe Val Arg Arg Thr  
                           165                          170                          175

Asp Val Pro Cys Pro Ala Ala Ser Glu Val Gly Gly Cys Ala Pro Ser  
                           180                          185                          190

Ser Trp His Thr Leu Ala Glu Val Thr Gly Cys Ser Leu Ser Pro Leu  
                           195                          200                          205

Ser Leu Ala Gln His Ala Gln Ala Ser Val Leu Leu Leu Cys Tyr Lys  
                           210                          215                          220

Trp Ser His Ile Gly Glu Thr Ser Ser His Leu Arg Ser Lys Val Tyr  
                           225                          230                          235                          240

Ala Ala Phe Gly Gly Ser Ser Pro Cys Leu Lys Gly Leu Met Ser Leu  
                           245                          250                          255

Trp Ala Ser Trp Leu Pro Arg Gly Arg Pro  
                           260                          265

&lt;210&gt; 535

&lt;211&gt; 6082

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 535

```

cctccactat tacagcttat aggaaattac aatccacttt acaggcctca aaggttcatt 60
ctggccgagc ggacaggcgt ggcgcccgga gccccagcat ccctgcttga ggtccaggag 120
cggagcccg cggccactgcc gcctgatcag cgcgaccccg gcccgcgccc gccccgccc 180
gcaagatgct gcccggtgtac caggaggtga agcccaaccc gctgcaggac gcgaacctct 240
gctcacgcgt gttcttcttg tggctcaatc ccttgtttaa aattggccat aaacggagat 300
tagaggaaga tgatatgtat tcagtgtctg cagaagaccg ctcacagcac cttggagagg 360
agttgcaagg gttctgggat aaagaagttt taagagctga gaatgacgca cagaagcctt 420
ctttaacaag agcaatcata aagtgttact ggaaatctta tttagttttg ggaattttta 480
cgtaaatga ggaaagtgcc aaagtaatcc agcccatatt tttgggaaaa attattaatt 540
atthtgaata ttatgatccc atggattctg tggctttgaa cacagcgtac gcctatgcca 600
cgggtgctgac tttttgcacg ctcatthtgg ctatactgca tcacttatat ttttatcaog 660
ttcagtgtgc tgggatgagg ttacgagtag ccatgtgcca tatgatttat cggaaggcac 720
ttcgtcttag taacatggcc atggggaaga caaccacagg ccagatagtc aatctgctgt 780
ccaatgatgt gaacaagttt gatcagggtga cagtgttctt acacttcttg tgggcaggac 840
cactgcaggc gatcgcagtg actgccctac tctggatgga gataggaata tcgtgccttg 900
ctgggatggc agttctaatc attctcctgc ccttgcaaaag ctgttttggg aagttgttct 960
catcactgag gactaaaact gcaactttca cggatgccag gatcaggacc atgaatgaag 1020
ttataactgg tataaggata ataaaaatgt agcctggga aaagtcattt tcaaatctta 1080
ttaccaattt gagaaagaag gagatttcca agattctgag aagttcctgc ctcaggggga 1140
tgaatttggc ttctgttttc agtgcaagca aaatcatcgt gtttgtgacc ttcaccacct 1200
acgtgctcct cggcagtggt atcacagcca gccgcgtgtt cgtggcagtg acgctgtatg 1260
gggtgtgctg gctgacggtt accctcttct tcccctcagc cattgagagg gtgtcagagg 1320
caatcgtcag catccgaaga atccagacct ttttgcact tgatgagata tcacagcgca 1380
accgtcagct gccgtcagat ggtaaaaaga tgggtcatgt gcaggatttt actgcttttt 1440
gggataaggc atcagagacc ccaactctac aaggcctttc ctttactgtc agacctggcg 1500
aattgttagc tgtggtcggc cccgtgggag cagggaagtc atcactgtta agtgccgtgc 1560
tcggggaatt ggcccaagt cacgggctgg tcagcgtgca tggagaatt gcctatgtgt 1620
ctcagcagcc ctgggtgttc tcgggaactc tgaggagtaa tattttattt gggaagaaat 1680
acgaaaagga acgatatgaa aaagtcataa aggtctgtgc tctgaaaaag gatttacagc 1740
tggtggagga tgggtgatctg actgtgatag gagatcggg aaccacgctg agtggagggc 1800
agaaagcacg ggtaaacctt gcaagagcag tgtatcaaga tgctgacatc tatctcctgg 1860
acgatcctct cagtgcagta gatgcggaag ttagcagaca cttgttcgaa ctgtgtattt 1920
gtcaaattht gcatgagaag atcacaatth tagtgactca tcagttgcag tacctcaaag 1980
ctgcaactca gattctgata ttgaaagatg ctaaaatggg gcagaagggg acttacactg 2040
agttcctaaa atctggtata gattttggct ccctttttaa gaaggataat gaggaaagt 2100
aacaacctcc agttccagga actcccacac taaggaaatcg taccttctca gactctcgg 2160
tttgggtctc acaatcttct agacctcct tgaaagatgg tgctctggag agccaagata 2220
cagagaatgt cccagttaca ctatcagagg agaaccgttc tgaaggaaaa gttggttttc 2280
aggcctataa gaattacttc agagctgggt ctcactggat tgtcttcatt ttccttattc 2340
tcctaaacac tgcagctcag gttgcctatg tgcttcaaga ttggtggctt tcatactggg 2400
caaacaacaa aagtatgcta aatgtcactg taaatggagg aggaaatgta accgagaagc 2460
tagatcttaa ctggtactta ggaatttatt caggtttaac tgtagctacc gttctttttg 2520
gcatagcaag atctctattg gtattctacg tccttgthaa ctcttcacaa actttgcaca 2580
acaaaatgtt tgagtcaatt ctgaaagctc cggatattat ctttgataga aatccaatag 2640
gaagaatttt aaatcgtht tccaaagaca ttggacactt ggatgatttg ctgccgctga 2700
cgthttttaga tttcatccag acattgctac aagtggtht tgtggtctct gtggtgtgg 2760
ccgtgattcc ttggatcgca atacccttg tcccccttg aatcatttht atthttcttc 2820
ggcgatattt tttggaaacg tcaagagatg tgaagcgctt ggaatctaca actcgagtc 2880
cagtgttht cacttgtca tcttctctcc aggggctctg gaccatccgg gcatacaaa 2940
cagaagagag gtgtcaggaa ctgtttgatg cacaccagga tttacattca gaggcttgg 3000
tctgttht gacaacgtcc cgtggttg cgtccgtct ggatgccatc tgtgccatgt 3060
ttgtcatcat cgttgcttht ggtccctga tcttgcaaa aactctggat gccgggcagg 3120
ttggtthtggc actgtctat gccctcagc tcatgggat gtttcagtg tgtgtcgac 3180
aaagtgtgta agttgagaat atgatgatc catgagaaag ggtcattgaa tacacagacc 3240
ttgaaaaaga agcaccttg gaatatcaga aacgccacc accagcctgg ccccatgaag 3300
gagtgataat ctttgacaat gtgaacttca tgtacagtc aggtgggct ctggtactga 3360

```

```

agcatctgac agcactcatt aaatcacaag aaaaggttgg cattgtggga agaaccggag 3420
ctggaaaaag ttccctcatc tcagcccttt ttagattgtc agaaccogaa ggtaaaaattt 3480
ggattgataa gatcttgaca actgaaattg gacttcacga tttaaggaaag aaaatgtcaa 3540
tcatacctca ggaacctgtt ttgttcaactg gaacaatgag gaaaaacctg gatcccttta 3600
atgagcacac ggatgaggaa ctgtggaatg ccttacaaga ggtacaactt aaagaaacca 3660
ttgaagatct tcctggtaaa atggatactg aattagcaga atcaggatcc aatttttagtg 3720
ttggacaaaag acaactgggtg tgccttgcca gggcaattct caggaaaaat cagatattga 3780
ttattgatga agcgacggca aatgtggatc caagaactga tgagttaata caaaaaaaat 3840
ccgggagaaa tttgccact gcaccgtgct aaccattgca cacagattga acaccattat 3900
tgacagcgac aagataatgg ttttagattc aggaagactg aaagaatatg atgagccgta 3960
tgttttgctg caaaataaag agagcctatt ttacaagatg gtgcaacaac tgggcaaggc 4020
agaagccgct gccctcactg aaacagcaaa acaggtatac ttcaaaaagaa attatccaca 4080
tattggtcac actgaccaca tggttacaaa cacttccaat ggacagccct cgaccttaac 4140
tattttcgag acagcactgt gaatccaacc aaaatgtcaa gtccgttccg aaggcatttg 4200
ccactagttt ttggactatg taaaccacat tgtacttttt ttacttttg caacaaatat 4260
ttatacatat aagatgctag ttcatittgaa tatttctccc aacttatcca aggatctcca 4320
gctctaacia aatgggtttat ttttatttaa atgtcaatag ttgtttttta aaatccaaat 4380
cagaggtgca ggccaccagt taaatgccgt ctatcagggt ttgtgcctta agagactaca 4440
gagtcaaaagc tcatTTTTTaa aggagtagga cagagttgtc acaggttttt gttgttgttt 4500
ttattgcccc caaaattaca tgTTaatttc catttatatc agggattcta tttacttgaa 4560
gactgtgaag ttgccatttt gtctcattgt tttctttgac ataactagga tccattattt 4620
cccctgaagg cttcttgTTa gaaaatagta cagttacaac caataggaac aacaaaaaga 4680
aaaagtttTgt gacattgtag tagggagtgt gtacccctta ctccccatca aaaaaaaaaa 4740
tggtatacat gTTaaaggat agaagggcaa tattttatca tatgttctaa aagagaagga 4800
agagaaaata ctactttctc aaaatggaag cccttaaagg tgctttgata ctgaaggaca 4860
caaatgtgac cgtccatcct ccttttagag ttgcatgact ggacacggta actgttgag 4920
ttttagactc agcatttgta cacttcccaa gaaggccaaa cctctaaccg acattcctga 4980
aatacgtggc attattcttt tttggatttc tcatTTatgg aaggctaacc ctctgttgac 5040
tgtaagcctt ttggtttggg ctgtattgaa atcctttcta aattgcatga ataggctctg 5100
ctaacgtgat gagacaaact gaaaattatt gcaagcattg actataatta tgcagtacgt 5160
tctcaggatg catccagggg ttcatTTtca tgagcctgtc caggttagtt tactcctgac 5220
cactaatagc attgtcattt gggctttctg ttgaatgaat caacaaacca caatacttcc 5280
tgggaccttt tgtactttat ttgaactatg agtctTTaat tttcctgat gatgggtggc 5340
gtaatatgtt gagttcagtt tactaaaggT tttactatta tggtttgaag tggagtctca 5400
tgacctctca gaataagggt tcacctccct gaaattgcat atatgtatat agacatgcac 5460
acgtgtgcat ttgtttgtat acatatattt gtccttcgta tagcaagttt tttgctcatc 5520
agcagagagc aacagatgtt ttattgagtg aagccttaaa aagcacacac cacacacagc 5580
taactgccaa aatacattga cagtagtagc tgttcaactc ctagtactta gaaatacacg 5640
tatggttaat gttcagtcac acaaaccaca cacagtaaTt gtttattaat agtcatgggt 5700
cgtatttttag gtgactgaaa ttgcaacagt gatcataatg aggtttgtta aaatgatagc 5760
tatattcaaa atgtctatat gtttattttg acttttgagg ttaaagacag tcatataaac 5820
gtcctgtttc tgtttttaat ttatcataga attttttaTt gaaactaaat tcaattgaaa 5880
taaatgatag ttttcatctc caaaaaaaa aaaaaaaagg gcggccgctc gagtctagag 5940
ggcccgTTta aaccgctga tcagcctcga ctgtgccttc tagttgccag ccatctgttg 6000
tttgccctc ccccgTgcct tccttgaccc tggaaggTgc cactccact gtcccttctc 6060
aataaaatga ggaaattgca tc 6082

```

&lt;210&gt; 536

&lt;211&gt; 6140

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(6140)

&lt;223&gt; n=A,T,C or G

&lt;400&gt; 536



```

cagtggcgca gtctcagctc actgcagcct ccacctcctg tgttcaagca gtcctcctgc 60
ctcagccacc agactagcag gtctcccccg cctctttctt ggaaggacac ttgccattgg 120
atntagacc cacttggaata atccaggatg atgtcttcac tccaacatcc tcagtttaat 180
tccatgtgca aatacccttt tcccaaataa cattcaattc tttaccagga aagggtggctc 240
aatcccttgt ttaaaattgg ccataaacgg agattagagg aagatgatat gtattcagtg 300
ctgccagaag accgctcaca gcaccttgga gaggagtgc aagggttctg ggataaagaa 360
gttttaagag ctgagaatga cgcacagaag ccttctttaa caagagcaat cataaagtgt 420
tactggaaat cttatttagt tttgggaatt tttacgttaa ttgaggaaag tgccaaagta 480
atccagccca ttttttggg aaaaattatt aattattttg aaaattatga tcccatggat 540
tctgtggctt tgaacacagc gtacgcctat gccacgggtg tgactttttg cagctcatt 600
ttggctatac tgcatactt atatttttat caggttcagt gtgctgggat gaggttcagg 660
gtagccatgt gccatatgat ttatcggaag gcacttcgtc ttagtaacat ggccatgggg 720
aagacaacca caggccagat agtcaatctg ctgtccaatg atgtgaacaa gtttgatcag 780
gtgacagtgt tcttacactt cctgtgggca ggaccactgc aggcgatcgc agtgactgcc 840
ctactctgga tggagatagg aatatcgtgc cttgctggga tggcagttct aatcattctc 900
ctgcccttgc aaagctgttt tgggaagttg ttctcatcac tgaggagtaa aactgcaact 960
ttcacggatg ccaggatcag gaccatgaat gaagttataa ctggtataag gataataaaa 1020
atgtacgcct gggaaaagtc attttcaaat cttattacca atttgagaaa gaaggagatt 1080
tccaagattc tgagaagttc ctgcctcagg gggatgaatt tggcttcgtt tttcagtgc 1140
agcaaaatca tctgttttgc gaccttcacc acctacgtgc tctcggcag tgtgatcaca 1200
gccagccgct tgttcgtggc agtgacgctg tatggggctg tgcggctgac ggttaccctc 1260
ttcttcccct cagccattga gaggtgtgca gaggcaatcg tcagcatccg aagaatccag 1320
acctttttgc tacttgatga gatatacag cgcaaccgtc agctgccgtc agatggtaaa 1380
aagatggtgc atgtgcagga ttttactgct ttttgggata aggcatacaga gaccccaact 1440
ctacaaggcc tttcctttac tgtcagacct ggcgaattgt tagctgtggt cggccccgtg 1500
ggagcagggg agtcatcact gttaagtgcc gtgctcgggg aattggcccc aagtcacggg 1560
ctggtcagcg tgcattggaag aattgcctat gtgtctcagc agccctgggt gttctcggga 1620
actctgagga gtaataattt atttgggaag aaatacgaaa aggaacgata tgaaaagtgc 1680
ataaaggctt gtgctctgaa aaaggattta cagctggttg aggatggtga tctgactgtg 1740
ataggagatc ggggaaccac gctgagtgga gggcagaaag caggggtaaa ccttgcaaga 1800
gcagtgtatc aagatgctga catctatctc ctggacgata ctctcagtg 1860
gaagttagca gacacttgtt cgaactgtgt atttgtcaaa ttttgcata gaagatcaca 1920
attttagtga ctcatcagtt gcagtacctc aaagctgcaa gtcagattct gatattgaaa 1980
gatggtaaaa tgggtgcagaa ggggacttac actgagttcc taaaatctgg tatagatttt 2040
ggctcccttt taaagaagga taatgaggaa agtgaacaac ctccagttcc aggaactccc 2100
acactaagga atcgtacctt ctacagagct tccgttttgt ctcaacaatc ttctagacct 2160
tcttgaaag atggtgctct ggagagccaa gatacagaga atgtcccagt tacactatca 2220
gaggagaacc gttctgaagg aaaagtgtgt tttcaggcct ataagaatta cttcagagct 2280
ggtgctcact ggattgtctt cattttcctt attctcctaa acactgcagc tcaggttgcc 2340
tatgtgcttc aagattggtg gctttcatac tgggcaaaaca aacaaagtat gctaaatgtc 2400
actgtaaatg gaggaggaaa tgtaaccgag aagctagatc ttaactggta cttaggaatt 2460
tattcaggtt taactgtacg taccgttctt tttggcatag caagatctct attggtattc 2520
tacgtccttg ttaactcttc aaaaactttg cacaacaaaa tgtttgagtc aattctgaaa 2580
gctccggtat tattctttga tagaaatcca ataggaagaa ttttaaatcg tttctccaaa 2640
gacattggac acttgatgga tttgctgccg ctgacgtttt tagatttcat ccagacattg 2700
ctacaagtgg ttggtgtggt ctctgtggtc gtggccgtga ttccttggat aacaaatccc 2760
ttggttcccc ttggaatcat tttcattttt ctccggcat attttttgga aacgtcaaga 2820
gatgtgaagc gcctggaatc tacaactcgg agtcagatgt tttccactt gtcattctct 2880
ctccaggggc tctggaccat ccgggcatac aaagcagaag agaggtgtca ggaactgttt 2940
gatgcacacc aggatttaca ttcagaggct tggttcttgt ttttgacaac gtcccgctgg 3000
ttcgccgtcc gtctggatgc catctgtgcc atgtttgtca tcatcgttgc ctttgggtcc 3060
ctgattctgg caaaaactct ggatgccggg caggttgggt tggcactgtc ctatgccctc 3120
acgtcatggt ggatgtttca gtggtgtgtt cgacaaagtg ctgaagttga gaatatgatg 3180
atctcagtag aaagggtcat tgaatacaca gaccttgaaa aagaagcacc ttgggaatat 3240
cagaaacgcc caccaccagc ctggcccat gaaggagtga taatctttga caatgtgaac 3300
ttcatgtaca gtccaggtgg gcctctggtg ctgaagcatc tgacagcact cattaaatca 3360
caagaaaagg ttggcattgt gggagaagcc ggagctggaa aaagtccct catctcagcc 3420
cttttagat tgtcagaacc cgaaggtaaa atttggattg ataagatctt gacaactgaa 3480

```

```

attggacttc acgattttaag gaagaaaatg tcaatcatatc ctcaggaacc tgttttgttc 3540
actggaacaa tgaggaaaaa cctggatccc tttaatgagc acacggatga ggaactgtgg 3600
aatgccttac aagaggtaca acttaaagaa accattgaag atcttcctgg taaaatggat 3660
actgaattag cagaatcagg atccaatttt agtgttggac aaagacaact ggtgtgcctt 3720
gccagggcaa ttctcaggaa aaatcagata ttgattattg atgaagcgac ggcaaatgtg 3780
gatccaagaa ctgatgagtt aatacaaaaa aaaatccggg agaaatttgc ccactgcacc 3840
gtgctaacca ttgcacacag attgaacacc attattgaca gcgacaagat aatggtttta 3900
gattcaggaa gactgaaaga atatgatgag ccgatgtttt tgctgcaaaa taaagagagc 3960
ctattttaca agatgggtgca acaactgggc aaggcagaag ccgctgccct cactgaaaca 4020
gcaaaacaga gatgggggtt cccatgtttg gccaggctgg tctcaaaactc ctgacctcaa 4080
gtgatccacc tgccttggcc tcccaaaactg ctgagattac aggtgtgagc caccacgccc 4140
agcctgagta tacttcaaaa gaaattatcc acatattggt cacactgacc acatggttac 4200
aaacacttcc aatggacagc cctcgacctt aactattttc gagacagcac tgtgaatcca 4260
accaaaatgt caagtccgtt ccgaaggcat ttgccactag tttttggact atgtaaacca 4320
cattgtactt ttttttactt tggcaacaaa tatttataca tacaagatgc tagttcattt 4380
gaatatctct cccaacttat ccaaggatct ccagctctaa caaatgggtt tttttttatt 4440
taaagtgtcaa tagtkgkttt ttaaaatcca aatcagaggt gcaggccacc agttaaattg 4500
cgtctatcag gttttgtgcc ttaagagact acagnagtca gaagctcatt tttaaaggag 4560
taggacagag ttgtcacagg tttttgttgg tgtttktatt gcccccaaaa ttacatgtta 4620
atttccattt atatcagggg attctattta cttgaagact gtgaagttgc cattttgtct 4680
cattgttttc tttgacatam ctaggatcca ttatttcccc tgaaggcttc ttgkagaaaa 4740
tagtacagtt acaaccaata ggaactamca aaaagaaaaa gttttgtgaca ttgtagtagg 4800
gagtgtgtac cccttactcc ccatcaaaaa aaaaaatgga tacatggtta aaggatagaa 4860
gggcaatatt ttatcatatg ttctaaaaga gaaggaagag aaaatactac tttctcaaaa 4920
tggaagccct taaagggtgct ttgatactga aggacacaaa tgtgaccgtc catcctcctt 4980
tagagttgca tgacttggac acggttaactg ttgcagtttt agactcagca ttgtgacact 5040
tccaagaag gccaaacctc taaccgacat tcctgaaata cgtggcatta ttcttttttg 5100
gattttctcat ttagggaaggc taaccctctg ttgamtgtam kccttttggg ttgggctgta 5160
ttgaaatcct ttctaaattg catgaatagg ctctgctaac cgtgatgaga caaactgaaa 5220
attattgtcaa gcattgacta taattatgca gtacgttctc aggatgcatc caggggttca 5280
ttttcatgag cctgtccagg ttagtttact cctgaccact aatagcattg tcatttgggc 5340
tttctgttga atgaatcaac aaaccacaat acttcctggg accttttgta ctttatttga 5400
actatgagtc ttttaattttt cctgatgatg gtggctgtaa tatgttgagt tcagtttact 5460
aaagggttta ctattatggt ttgaaggagg tctcatgacc tctcagaaaa ggtgcacctc 5520
cctgaaattg catatatgta tatagacatg cacacgtgtg catttgtttg tatacatata 5580
tttgtccttc gtatagcaag ttttttgctc atcagcagag agcaacagat gttttattga 5640
gtgaagcctt aaaaagcaca caccacacac agctaactgc caaaatacat tgaccgtagt 5700
agctgttcaa ctctagtac ttagaaatac acgtatggtt aatgttcagt ccaacaaacc 5760
acacacagta aatgtttatt aatagtcag gtctgtattt taggtgactg aaattgcaac 5820
agtgatcata atgaggtttg ttaaaatgat agctatattc aaaatgtcta tatgtttatt 5880
tggaactttt aggttaaaga cagtcataata aacgtcctgt ttctgtttta atgttatcat 5940
agaatttttt aatgaaacta aattcaattg aaataaatga tagttttcat ctccaaaaaa 6000
aaaaaaaaag ggcggcccg cgcagtcctag agggcccggt ttaaaccgcg tgatcagcct 6060
cgactgtgcc ttctagttgc cagccatctg ttgtttggcc ctcccccggt ccttccttga 6120
ccctggaagg ggcactccc 6140

```

&lt;210&gt; 537

&lt;211&gt; 1228

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 537

Met Leu Pro Val Tyr Gln Glu Val Lys Pro Asn Pro Leu Gln Asp Ala  
5 10 15

Asn Leu Cys Ser Arg Val Phe Phe Trp Trp Leu Asn Pro Leu Phe Lys  
20 25 30

Ile Gly His Lys Arg Arg Leu Glu Glu Asp Asp Met Tyr Ser Val Leu  
 35 40 45  
 Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp  
 50 55 60  
 Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu  
 65 70 75 80  
 Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser Tyr Leu Val Leu Gly  
 85 90 95  
 Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val Ile Gln Pro Ile Phe  
 100 105 110  
 Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr Asp Pro Met Asp Ser  
 115 120 125  
 Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr Val Leu Thr Phe Cys  
 130 135 140  
 Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr Phe Tyr His Val Gln  
 145 150 155 160  
 Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys His Met Ile Tyr Arg  
 165 170 175  
 Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly Lys Thr Thr Thr Gly  
 180 185 190  
 Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn Lys Phe Asp Gln Val  
 195 200 205  
 Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro Leu Gln Ala Ile Ala  
 210 215 220  
 Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile Ser Cys Leu Ala Gly  
 225 230 235 240  
 Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln Ser Cys Phe Gly Lys  
 245 250 255  
 Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr Phe Thr Asp Ala Arg  
 260 265 270  
 Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile Arg Ile Ile Lys Met  
 275 280 285  
 Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile Thr Asn Leu Arg Lys  
 290 295 300  
 Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys Leu Arg Gly Met Asn  
 305 310 315 320  
 Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile Val Phe Val Thr Phe  
 325 330 335  
 Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr Ala Ser Arg Val Phe

340	345	350
Val Ala Val Thr Leu Tyr Gly	Ala Val Arg Leu Thr	Val Thr Leu Phe
355	360	365
Phe Pro Ser Ala Ile Glu Arg	Val Ser Glu Ala Ile	Val Ser Ile Arg
370	375	380
Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg		
385	390	395 400
Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr		
405	410	415
Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser		
420	425	430
Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly		
435	440	445
Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro		
450	455	460
Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln		
465	470	475 480
Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly		
485	490	495
Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala		
500	505	510
Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile		
515	520	525
Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln Lys Ala Arg Val Asn		
530	535	540
Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp		
545	550	555 560
Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu		
565	570	575
Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His		
580	585	590
Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp		
595	600	605
Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly		
610	615	620
Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln		
625	630	635 640
Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu		
645	650	655

Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly  
 660 665 670  
 Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu  
 675 680 685  
 Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr  
 690 695 700  
 Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu  
 705 710 715 720  
 Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser  
 725 730 735  
 Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn Gly Gly  
 740 745 750  
 Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp Tyr Leu Gly Ile Tyr  
 755 760 765  
 Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly Ile Ala Arg Ser Leu  
 770 775 780  
 Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln Thr Leu His Asn Lys  
 785 790 795 800  
 Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu Phe Phe Asp Arg Asn  
 805 810 815  
 Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys Asp Ile Gly His Leu  
 820 825 830  
 Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe Ile Gln Thr Leu Leu  
 835 840 845  
 Gln Val Val Gly Val Val Ser Val Ala Val Ala Val Ile Pro Trp Ile  
 850 855 860  
 Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe Ile Phe Leu Arg Arg  
 865 870 875 880  
 Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg Leu Glu Ser Thr Thr  
 885 890 895  
 Arg Ser Pro Val Phe Ser His Leu Ser Ser Ser Leu Gln Gly Leu Trp  
 900 905 910  
 Thr Ile Arg Ala Tyr Lys Ala Glu Glu Arg Cys Gln Glu Leu Phe Asp  
 915 920 925  
 Ala His Gln Asp Leu His Ser Glu Ala Trp Phe Leu Phe Leu Thr Thr  
 930 935 940  
 Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile Cys Ala Met Phe Val  
 945 950 955 960

Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala Lys Thr Leu Asp Ala  
 965 970 975  
 Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu Thr Leu Met Gly Met  
 980 985 990  
 Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val Glu Asn Met Met Ile  
 995 1000 1005  
 Ser Val Glu Arg Val Ile Glu Tyr Thr Asp Leu Glu Lys Glu Ala Pro  
 1010 1015 1020  
 Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp Pro His Glu Gly Val  
 1025 1030 1035 1040  
 Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser Pro Gly Gly Pro Leu  
 1045 1050 1055  
 Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser Gln Glu Lys Val Gly  
 1060 1065 1070  
 Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser Leu Ile Ser Ala Leu  
 1075 1080 1085  
 Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp Ile Asp Lys Ile Leu  
 1090 1095 1100  
 Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys Lys Met Ser Ile Ile  
 1105 1110 1115 1120  
 Pro Gln Glu Pro Val Leu Phe Thr Gly Thr Met Arg Lys Asn Leu Asp  
 1125 1130 1135  
 Pro Phe Asn Glu His Thr Asp Glu Glu Leu Trp Asn Ala Leu Gln Glu  
 1140 1145 1150  
 Val Gln Leu Lys Glu Thr Ile Glu Asp Leu Pro Gly Lys Met Asp Thr  
 1155 1160 1165  
 Glu Leu Ala Glu Ser Gly Ser Asn Phe Ser Val Gly Gln Arg Gln Leu  
 1170 1175 1180  
 Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn Gln Ile Leu Ile Ile  
 1185 1190 1195 1200  
 Asp Glu Ala Thr Ala Asn Val Asp Pro Arg Thr Asp Glu Leu Ile Gln  
 1205 1210 1215  
 Lys Lys Ser Gly Arg Asn Leu Pro Thr Ala Pro Cys  
 1220 1225  
 <210> 538  
 <211> 1261  
 <212> PRT  
 <213> Homo sapiens  
 <400> 538  
 Met Tyr Ser Val Leu Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu

5					10					15						
Leu	Gln	Gly	Phe	Trp	Asp	Lys	Glu	Val	Leu	Arg	Ala	Glu	Asn	Asp	Ala	
20					25					30						
Gln	Lys	Pro	Ser	Leu	Thr	Arg	Ala	Ile	Ile	Lys	Cys	Tyr	Trp	Lys	Ser	
35					40					45						
Tyr	Leu	Val	Leu	Gly	Ile	Phe	Thr	Leu	Ile	Glu	Glu	Ser	Ala	Lys	Val	
50					55					60						
Ile	Gln	Pro	Ile	Phe	Leu	Gly	Lys	Ile	Ile	Asn	Tyr	Phe	Glu	Asn	Tyr	
65					70					75					80	
Asp	Pro	Met	Asp	Ser	Val	Ala	Leu	Asn	Thr	Ala	Tyr	Ala	Tyr	Ala	Thr	
85					90					95						
Val	Leu	Thr	Phe	Cys	Thr	Leu	Ile	Leu	Ala	Ile	Leu	His	His	Leu	Tyr	
100					105					110						
Phe	Tyr	His	Val	Gln	Cys	Ala	Gly	Met	Arg	Leu	Arg	Val	Ala	Met	Cys	
115					120					125						
His	Met	Ile	Tyr	Arg	Lys	Ala	Leu	Arg	Leu	Ser	Asn	Met	Ala	Met	Gly	
130					135					140						
Lys	Thr	Thr	Thr	Gly	Gln	Ile	Val	Asn	Leu	Leu	Ser	Asn	Asp	Val	Asn	
145					150					155					160	
Lys	Phe	Asp	Gln	Val	Thr	Val	Phe	Leu	His	Phe	Leu	Trp	Ala	Gly	Pro	
165					170					175						
Leu	Gln	Ala	Ile	Ala	Val	Thr	Ala	Leu	Leu	Trp	Met	Glu	Ile	Gly	Ile	
180					185					190						
Ser	Cys	Leu	Ala	Gly	Met	Ala	Val	Leu	Ile	Ile	Leu	Leu	Pro	Leu	Gln	
195					200					205						
Ser	Cys	Phe	Gly	Lys	Leu	Phe	Ser	Ser	Leu	Arg	Ser	Lys	Thr	Ala	Thr	
210					215					220						
Phe	Thr	Asp	Ala	Arg	Ile	Arg	Thr	Met	Asn	Glu	Val	Ile	Thr	Gly	Ile	
225					230					235					240	
Arg	Ile	Ile	Lys	Met	Tyr	Ala	Trp	Glu	Lys	Ser	Phe	Ser	Asn	Leu	Ile	
245					250					255						
Thr	Asn	Leu	Arg	Lys	Lys	Glu	Ile	Ser	Lys	Ile	Leu	Arg	Ser	Ser	Cys	
260					265					270						
Leu	Arg	Gly	Met	Asn	Leu	Ala	Ser	Phe	Phe	Ser	Ala	Ser	Lys	Ile	Ile	
275					280					285						
Val	Phe	Val	Thr	Phe	Thr	Thr	Tyr	Val	Leu	Leu	Gly	Ser	Val	Ile	Thr	
290					295					300						
Ala	Ser	Arg	Val	Phe	Val	Ala	Val	Thr	Leu	Tyr	Gly	Ala	Val	Arg	Leu	
305					310					315					320	

Thr Val Thr Leu Phe Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala  
 325 330 335  
 Ile Val Ser Ile Arg Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile  
 340 345 350  
 Ser Gln Arg Asn Arg Gln Leu Pro Ser Asp Gly Lys Lys Met Val His  
 355 360 365  
 Val Gln Asp Phe Thr Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr  
 370 375 380  
 Leu Gln Gly Leu Ser Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val  
 385 390 395 400  
 Val Gly Pro Val Gly Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu  
 405 410 415  
 Gly Glu Leu Ala Pro Ser His Gly Leu Val Ser Val His Gly Arg Ile  
 420 425 430  
 Ala Tyr Val Ser Gln Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser  
 435 440 445  
 Asn Ile Leu Phe Gly Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val  
 450 455 460  
 Ile Lys Ala Cys Ala Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly  
 465 470 475 480  
 Asp Leu Thr Val Ile Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln  
 485 490 495  
 Lys Ala Arg Val Asn Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile  
 500 505 510  
 Tyr Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg  
 515 520 525  
 His Leu Phe Glu Leu Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr  
 530 535 540  
 Ile Leu Val Thr His Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile  
 545 550 555 560  
 Leu Ile Leu Lys Asp Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu  
 565 570 575  
 Phe Leu Lys Ser Gly Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn  
 580 585 590  
 Glu Glu Ser Glu Gln Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn  
 595 600 605  
 Arg Thr Phe Ser Glu Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro  
 610 615 620



Ser Leu Lys Asp Gly Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro  
 625 630 635 640  
 Val Thr Leu Ser Glu Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln  
 645 650 655  
 Ala Tyr Lys Asn Tyr Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile  
 660 665 670  
 Phe Leu Ile Leu Leu Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln  
 675 680 685  
 Asp Trp Trp Leu Ser Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val  
 690 695 700  
 Thr Val Asn Gly Gly Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp  
 705 710 715 720  
 Tyr Leu Gly Ile Tyr Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly  
 725 730 735  
 Ile Ala Arg Ser Leu Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln  
 740 745 750  
 Thr Leu His Asn Lys Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu  
 755 760 765  
 Phe Phe Asp Arg Asn Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys  
 770 775 780  
 Asp Ile Gly His Leu Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe  
 785 790 795 800  
 Ile Gln Thr Leu Leu Gln Val Val Gly Val Val Ser Val Ala Val Ala  
 805 810 815  
 Val Ile Pro Trp Ile Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe  
 820 825 830  
 Ile Phe Leu Arg Arg Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg  
 835 840 845  
 Leu Glu Ser Thr Thr Arg Ser Pro Val Phe Ser His Leu Ser Ser Ser  
 850 855 860  
 Leu Gln Gly Leu Trp Thr Ile Arg Ala Tyr Lys Ala Glu Glu Arg Cys  
 865 870 875 880  
 Gln Glu Leu Phe Asp Ala His Gln Asp Leu His Ser Glu Ala Trp Phe  
 885 890 895  
 Leu Phe Leu Thr Thr Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile  
 900 905 910  
 Cys Ala Met Phe Val Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala  
 915 920 925  
 Lys Thr Leu Asp Ala Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu

930	935	940
Thr Leu Met Gly Met	Phe Gln Trp Cys Val	Arg Gln Ser Ala Glu Val
945	950	955 960
Glu Asn Met Met Ile	Ser Val Glu Arg Val	Ile Glu Tyr Thr Asp Leu
965	970	975
Glu Lys Glu Ala Pro	Trp Glu Tyr Gln Lys Arg	Pro Pro Pro Ala Trp
980	985	990
Pro His Glu Gly Val	Ile Ile Phe Asp Asn Val	Asn Phe Met Tyr Ser
995	1000	1005
Pro Gly Gly Pro Leu	Val Leu Lys His Leu Thr	Ala Leu Ile Lys Ser
1010	1015	1020
Gln Glu Lys Val Gly	Ile Val Gly Arg Thr	Gly Ala Gly Lys Ser Ser
1025	1030	1035 1040
Leu Ile Ser Ala Leu	Phe Arg Leu Ser Glu	Pro Glu Gly Lys Ile Trp
1045	1050	1055
Ile Asp Lys Ile Leu	Thr Thr Glu Ile Gly	Leu His Asp Leu Arg Lys
1060	1065	1070
Lys Met Ser Ile Ile	Pro Gln Glu Pro Val	Leu Phe Thr Gly Thr Met
1075	1080	1085
Arg Lys Asn Leu Asp	Pro Phe Asn Glu His	Thr Asp Glu Glu Leu Trp
1090	1095	1100
Asn Ala Leu Gln Glu	Val Gln Leu Lys Glu	Thr Ile Glu Asp Leu Pro
1105	1110	1115 1120
Gly Lys Met Asp Thr	Glu Leu Ala Glu Ser	Gly Ser Asn Phe Ser Val
1125	1130	1135
Gly Gln Arg Gln Leu	Val Cys Leu Ala Arg	Ala Ile Leu Arg Lys Asn
1140	1145	1150
Gln Ile Leu Ile Ile	Asp Glu Ala Thr Ala	Asn Val Asp Pro Arg Thr
1155	1160	1165
Asp Glu Leu Ile Gln	Lys Lys Ile Arg Glu	Lys Phe Ala His Cys Thr
1170	1175	1180
Val Leu Thr Ile Ala	His Arg Leu Asn Thr	Ile Ile Asp Ser Asp Lys
1185	1190	1195 1200
Ile Met Val Leu Asp	Ser Gly Arg Leu Lys	Glu Tyr Asp Glu Pro Tyr
1205	1210	1215
Val Leu Leu Gln Asn	Lys Glu Ser Leu Phe	Tyr Lys Met Val Gln Gln
1220	1225	1230
Leu Gly Lys Ala Glu	Ala Ala Ala Leu Thr	Glu Thr Ala Lys Gln Arg
1235	1240	1245

Trp Gly Phe Thr Met Leu Ala Arg Leu Val Ser Asn Ser  
 1250 1255 1260

<210> 539  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 539  
 Cys Leu Ser His Ser Val Ala Val Val Thr  
 1 5 10

<210> 540  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 540  
 Ala Val Val Thr Ala Ser Ala Ala Leu  
 1 5

<210> 541  
 <211> 14  
 <212> PRT  
 <213> Homo sapiens

<400> 541  
 Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu  
 5 10

<210> 542  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 542  
 Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
 5 10 15

<210> 543  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<400> 543  
 Phe Met Gly Ser Ile Val Gln Leu Ser Gln Ser Val  
 5 10

```
<210> 544
<211> 18
<212> PRT
<213> Homo sapiens
```

<400> 544  
 Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val Glu Glu Lys Phe  
                   5                  10                  15

Met Thr

```
<210> 545
<211> 18
<212> PRT
<213> Homo sapiens
```

<400> 545  
Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala  
                  5                  10                  15

Ser Val

```
<210> 546
<211> 29
<212> PRT
<213> Homo sapiens
```

<400> 546  
Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu ·Pro Gly  
51015

Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met  
20 25

```
<210> 547
<211> 58
<212> PRT
<213> Homo sapiens
```

<400> 547  
Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu  
5 10 15

Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala Arg Leu  
20 25 30

Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln Leu Cys  
35 40 45

Cys Arg Met Pro Arg Thr Leu Arg Arg Leu  
50 55

200

<210> 548  
<211> 18  
<212> PRT  
<213> Homo sapiens

<400> 548  
Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu  
                          5                          10                          15

Glu Cys

<210> 549  
<211> 18  
<212> PRT  
<213> Homo sapiens

<400> 549  
Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg  
                          5                          10                          15

Gln Ala

<210> 550  
<211> 14  
<212> PRT  
<213> Homo sapiens

<400> 550  
Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe  
                          5                          10

<210> 551  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 551  
Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
                          5                          10

<210> 552  
<211> 2577  
<212> DNA  
<213> Homo sapiens

<400> 552  
agcatatgta acatgacctg tgettcagtg ttcttttgtg atcaaaaatt ccttactttt 60  
agtttttttat ctatggtaga accaccacaga gcaggggtcc tcaactccca ggccacagac 120  
tcataaccagt ccacggacta ttatgaacca caccacacag gaggaggtga gcactaggca 180  
agccaaggaa gcttcacctg tacttacagc cacacgccat ggctcatatt acagcctgaa 240

```

ctctgcctcc actcagatca gtgataacat tagaaactca ttggagcacg aaccctgttg 300
tgaactgcct atccgaagga tctaggttgt gtgcttcgta tgagaatcta atgccagatg 360
atctatcatt gtctcacttt gccccagat aagaccatct agttgcagaa aaataagctc 420
agagcttcca ctgattctac attatggata tgtgccgccg aagcaagcac aaagccctac 480
ttttacacat gcctagtgat gcttcatgga caaggcttgg ctctgttgag tccaactaac 540
ctacctgaga ttctgagatt tctcttcaat ggcttcctgt gagctagagt ttgaaaatat 600
cttaaaatct tgagctagag atggaagtag cttggacgat ttccattatc atgtaaatcg 660
ggctactcaa ggggcccaacc acagctggga gccactgctc aggggaaggt tcatatggga 720
ctttctactg cccaaggttc tatacaggat ataaagggtgc ctcacagtat agatctggta 780
gcaaagaaga agaaacaaac actgatctct ttctgccacc cctctgaccc tttggaactc 840
ctctgaccct ttagaacaag cctaccta atctgtctaga gaaaagacca acaacggcct 900
caaaggatct cttaccatga aggtctcagc taattcttgg ctaagatgtg ggttccacat 960
taggttctga atatgggggg aagggtcaat ttgctcattt tgtgtgtgga taaagtccag 1020
atgccagggg gccagagcag ggggctgctg ctttggggaa aatggctgag catataacca 1080
taggtatggg aacaaaaaac atcaaagtca ctgtatcaat tgccatgaag actcgaggga 1140
cctgaatcta ccgattcatc ttaaggcagc aggaccagtt tgagtggcaa caatgcagca 1200
gcagaatcaa tggaaacaac agaattgatt caatgtcctt tttttctcc tcctctgac 1260
ttgataaaa ggaccgtctt ccttggattt agtgaacccc tttggttcct gaaaaattca 1320
aggagtatct aggacatagt cccagaaga cagtacaaga ctttctgata aactggacat 1380
ttcaagrccc aaataactaa tcagaaaaat caaagatgtg atactatttt ttatcccatg 1440
cataggtgct acacttggat caaatgaaca atgttgggat ctytatggat aaaggtctta 1500
aaagtcctga gataaagaat cctgcaccca ctggtacttc taacttgtct tgtttttgt 1560
ctgwtttctg gctgatgcag gggactaact cactgccacg cgaaaactac ctgaactgaa 1620
ctatgacatc tcacctgata tgtaagatgt aactgttata attattttaa acctcaattt 1680
agcattaact agccttttaa tgtaaacact tacacattat gaygactaga aacagcatac 1740
tctctggccg tctgtccaga tagatcttga gaagatacat caatgttttg ctcaagtaga 1800
aggctgacta tacttgccga tccacaacat acagcaagta tgagagcagt tctaaaatga 1860
cagagatagg aacagtaata aagttattkt aaaagcta at ttgatatact ttaccaattt 1920
aacatcttgc ctgtccgtgc agaatcaaac atttacatgc actaaaagac ataagcatct 1980
tcagtgtctc agtgttcatc tttgtaaaat accaccaagg ttaaaaggaa gggacaaaaa 2040
aaaaaaaccc tcttatctca gtgggttatt gcatagcaga agctactaat ttgaagtcct 2100
ttgatggaca agaaacaata ttagggccac ttatctgaaa tgaacaaaga ttaagtga 2160
gatttcatca cagcttcctt agactgatat gctgtaatag aaaatcagct agggggtaaa 2220
ataaataaga gctctctgca tgcgtgaaag aagtaagatt aataataatg gtaagaatag 2280
tagtcacagg agtttcagtt aatgatgcca ataagcatgt gctaggcact gaattaaatg 2340
ccacatata ctttcttatg cgcagcaaac tttgaaggat atattctcct acttttcata 2400
tatgacaaca tatttggtgg taaataacgt tccaaggtc acacacctag caagtaagaa 2460
agttaggaat taaacccagt attgtgtgaa tctaaagcct aacttttttc tctttatcac 2520
ccacctacgg cttgtcttca ttaaaggaaa agtgtatcca cttaaaaaaa aaaaaaa 2577

```

&lt;210&gt; 553

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 553

Ser Ile Cys Asn Met Thr Cys Ala Ser Val Phe Phe Cys Asp Gln Lys  
5 10 15

Phe Leu Thr Phe Ser Phe Leu Ser Met Val Glu Pro Pro Arg Ala Gly  
20 25 30

Val Leu Asn Ser Gln Ala Thr Asp Ser Tyr Gln Ser Thr Asp Tyr Tyr  
35 40 45

Glu Pro His His Thr Gly Gly Gly Glu His  
50 55

&lt;210&gt; 554

&lt;211&gt; 59

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 554

Leu Gln Lys Asn Lys Leu Arg Ala Ser Thr Asp Ser Thr Leu Trp Ile  
                                   5                                  10                                  15

Cys Ala Ala Glu Ala Ser Thr Lys Pro Tyr Phe Tyr Thr Cys Leu Val  
                                   20                                  25                                  30

Met Leu His Gly Gln Gly Leu Ala Leu Leu Ser Pro Thr Asn Leu Pro  
                                   35                                  40                                  45

Glu Ile Leu Arg Phe Leu Phe Asn Gly Phe Leu  
                                   50                                  55

&lt;210&gt; 555

&lt;211&gt; 71

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 555

Leu Gly Arg Phe Ser Leu Ser Cys Lys Ser Gly His Ser Arg Gly Gln  
                                   5                                  10                                  15

Pro Gln Leu Gly Ala Thr Ala Gln Gly Lys Val His Met Gly Leu Ser  
                                   20                                  25                                  30

Thr Ala Gln Gly Ser Ile Gln Asp Ile Lys Val Pro His Ser Ile Asp  
                                   35                                  40                                  45

Leu Val Ala Lys Lys Lys Lys Gln Thr Leu Ile Ser Phe Cys His Pro  
                                   50                                  55                                  60

Ser Asp Pro Leu Glu Leu Leu  
                                   65                                  70

&lt;210&gt; 556

&lt;211&gt; 81

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 556

Asn His Pro Glu Gln Gly Ser Ser Thr Pro Arg Pro Gln Thr His Thr  
                                   5                                  10                                  15

Ser Pro Arg Thr Ile Met Asn His Thr Thr Gln Glu Glu Val Ser Thr  
                                   20                                  25                                  30

Arg Gln Ala Lys Glu Ala Ser Pro Val Leu Thr Ala Thr Arg His Gly  
                                   35                                  40                                  45

Ser Tyr Tyr Ser Leu Asn Ser Ala Ser Thr Gln Ile Ser Asp Asn Ile





<213> Homo sapiens

<400> 559

Thr Leu Pro Pro Leu Arg Ser Val Ile Thr Leu Glu Thr His Trp Ser  
5 10 15

Thr Asn Pro Val Val Asn Cys Leu Ser Glu Gly Ser Arg Leu Cys Ala  
20 25 30

Ser Tyr Glu Asn Leu Met Pro Asp Asp Leu Ser Leu Ser His Phe Ala  
35 40 45

Pro Arg  
50

<210> 560

<211> 56

<212> PRT

<213> Homo sapiens

<400> 560

Ile Gly Ser Leu Lys Gly Pro Thr Thr Ala Gly Ser His Cys Ser Gly  
5 10 15

Glu Gly Ser Tyr Gly Thr Phe Tyr Cys Pro Arg Phe Tyr Thr Gly Tyr  
20 25 30

Lys Gly Ala Ser Gln Tyr Arg Ser Gly Ser Lys Glu Glu Glu Thr Asn  
35 40 45

Thr Asp Leu Phe Leu Pro Pro Leu  
50 55

<210> 561

<211> 57

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(57)

<223> Xaa = Any amino acid

<400> 561

Val Leu His Leu Asp Gln Met Asn Asn Val Gly Ile Xaa Met Asp Lys  
5 10 15

Gly Leu Lys Ser Pro Glu Ile Lys Asn Pro Ala Pro Thr Gly Thr Ser  
20 25 30

Asn Leu Ser Cys Phe Leu Ser Xaa Phe Trp Leu Met Gln Gly Thr Asn  
35 40 45

Ser Leu Pro Arg Glu Asn Tyr Leu Asn  
50 55

```
<220>  
<221> VARIANT  
<222> (1)...(59)  
<223> Xaa = Any amino acid
```

```

<400> 562
Asp Leu Tyr Pro Xaa Arg Ser Gln His Cys Ser Phe Asp Pro Ser Val
          5                      10                      15
Ala Pro Met His Gly Ile Lys Asn Ser Ile Thr Ser Leu Ile Phe Leu
          20                      25                      30
Ile Ser Tyr Leu Xaa Leu Glu Met Ser Ser Leu Ser Glu Ser Leu Val
          35                      40                      45
Leu Ser Ser Gly Asp Tyr Val Leu Asp Thr Pro
          50                      55

```

```
<210> 563
<211> 79
<212> PRT
<213> Homo sapiens
```

<400> 563

Cys Phe Leu Phe Pro Tyr Leu Trp Leu Tyr Ala Gln Pro Leu Phe Pro  
                    5                        10                        15

Lys Gln Gln Pro Pro Ala Leu Ala Pro Gly His Pro Asp Phe Ile His  
                    20                        25                        30

Thr Gln Asn Glu Gln Ile Asp Pro Ser Pro His Ile Gln Asn Leu Met  
                    35                        40                        45

Trp Asn Pro His Leu Ser Gln Glu Leu Ala Glu Thr Phe Met Val Arg  
                    50                        55                        60

Asp Pro Leu Arg Pro Leu Leu Val Phe Ser Leu Ala Asp Ile Arg  
                    65                        70                        75

```
<210> 564
<211> 64
<212> PRT
<213> Homo sapiens
```

<400> 564  
Ala Cys Ser Lys Gly Ser Glu Glu Phe Gln Arg Val Arg Gly Val Ala  
5 10 15  
Glu Arg Asp Gln Cys Leu Phe Leu Leu Cys Tyr Gln Ile Tyr Thr  
20 25 30

Val Arg His Leu Tyr Ile Leu Tyr Arg Thr Leu Gly Ser Arg Lys Ser  
                   35                                  40                                  45

His Met Asn Leu Pro Leu Ser Ser Gly Ser Gln Leu Trp Leu Ala Pro  
           50                                  55                                  60

<210> 565

<211> 57

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(57)

<223> Xaa = Any amino acid

<400> 565

Leu Tyr Tyr Cys Ser Tyr Leu Cys His Phe Arg Thr Ala Leu Ile Leu  
                                   5                                  10                                  15

Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln  
                                   20                                  25                                  30

Asn Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu  
                   35                                  40                                  45

Tyr Ala Val Ser Ser Xaa His Asn Val  
           50                                  55

<210> 566

<211> 55

<212> PRT

<213> Homo sapiens

<400> 566

Ile Leu Leu Glu Phe Phe Arg Asn Gln Arg Gly Ser Leu Asn Pro Arg  
                                   5                                  10                                  15

Lys Thr Val Pro Phe Ile Lys Ser Glu Gly Gly Glu Lys Lys Gly His  
                   20                                  25                                  30

Cys Asn His Ser Val Val Ser Ile Asp Ser Ala Ala Ala Leu Leu Pro  
           35                                  40                                  45

Leu Lys Leu Val Leu Leu Pro  
           50                                  55

<210> 567

<211> 51

<212> PRT

<213> Homo sapiens

<400> 567

Tyr Ser Asp Phe Asp Val Phe Cys Ser His Thr Tyr Gly Tyr Met Leu

207

5 10 15  
 Ser His Cys Ser Gln Ser Ser Ser Pro Leu Leu Trp Pro Leu Gly Ile  
 20 25 30  
 Leu Thr Leu Ser Thr His Lys Met Ser Lys Leu Thr Leu Pro Pro Ile  
 35 40 45  
 Phe Arg Thr  
 50

<210> 568  
 <211> 75  
 <212> PRT  
 <213> Homo sapiens

<400> 568  
 Lys Val Gly Glu Tyr Ile Leu Gln Ser Leu Leu Arg Ile Arg Lys Ile  
 5 10 15  
 Tyr Val Ala Phe Asn Ser Val Pro Ser Thr Cys Leu Leu Ala Ser Leu  
 20 25 30  
 Thr Glu Thr Pro Val Thr Thr Ile Leu Thr Ile Ile Ile Asn Leu Thr  
 35 40 45  
 Cys Phe Gln His Ala Glu Ser Ser Tyr Leu Phe Tyr Pro Leu Ala Asp  
 50 55 60  
 Phe Leu Leu Gln His Ile Ser Leu Gly Lys Leu  
 65 70 75

<210> 569  
 <211> 4809  
 <212> DNA  
 <213> Homo sapiens

<400> 569  
 gcatccagag tgggtggactg gttacaggct atgaacctac actgatgcgg caccaccacc 60  
 cagagtccac rggttatggt ggttcacatt tactcttgct gtggtatggt ctatagggtt 120  
 ggacagatgt ccgataatcc tttttacatt ttggcatcct tgggtagctc gtctttagg 180  
 aatggacttg cttcaaagtg gaggcaggca gatccttcag acgggtatat ggagccctgt 240  
 tttcagttgc ttttctaatt ctctcttata gtttacctca aaatcttcct gaggtctcgc 300  
 ttctttttaa aatccttgct tactttgcag catcactctg acactcccat tgattcctca 360  
 gcacctactg actacacggg taggagtgcagggttagaat tcatgtttta ttcatctttg 420  
 ggtctgtagc acccagcaaa gtgctcagta aatgcgcagt aattgatttg acctctgaac 480  
 aaatacacac tgtactaaga atctacacac cgaaagacaa aaacaagaca aatttgagt 540  
 ctacaggtgt cacgcttggt atcacacatg tgccctgtgta ttctcttagg tggttaccag 600  
 gagctctgcc actgcatgtc cactagtgcagggttcgctc caccacccca gctgggtagc 660  
 cgctgctctc acataagggg tccaattaaa attgccagga ataaattccc ccggactttg 720  
 acttctcaag agctaagaag gtttgctgag tattctggca tgatgtttgg tgatcaaaca 780  
 actgctggcc aaaaatgatg agtatttccc cctcttgctg aagatgtgct ccatacaata 840  
 gtccatcaca ttcatcattc atcagtctgg aagtgtgcag aacaacatgt aatagataat 900  
 atgattggct gcacacttcc agactgatga atgatgaatg tgatggacta ttgtatggag 960  
 cacatcttca gcaagagggg gaaatactca tcattttatc tattacatgt tgttctgggt 1020

tttttttttt	tccaatgtcc	agcctaaact	ataaagtact	ttgagaacgc	acagtgagcc	1080
ataagcttgc	caataaagag	tcctctgtgg	tatggaactg	gcttatttca	tacacaatct	1140
gcaaacatg	agggcactat	tggaacata	ctgtgctgca	cagagcattt	acaccgctta	1200
tctttaatct	tccccagcaa	tccttgcttt	gtgcgcatth	atgatccttg	ctctcagaag	1260
tccacatact	tttccccaac	cgtaacaaat	tatttaactc	atctaattga	tgtatgtccg	1320
cgcagtctga	aaacagtaat	tgtccttggg	aagaagttag	tttaagagag	ctctagggca	1380
ctcatcacia	ctccagccct	gccctccatg	tggtagcagc	tctttggact	ggggctaaat	1440
gcttattctt	gtgcttcatt	cctggtaagc	tcaatttctt	taccttagga	taactttgct	1500
ggaaaagggc	tcagattcag	cagaccattg	tggcctctgt	ggctgtcaca	gcttgtccct	1560
gacatgctat	gatgttgggt	ccccttctca	tccccttggg	atttcttctg	ctggcccaca	1620
gccagaacaa	ctaggccctt	tactccacca	tccccttgtt	ttcttttgtt	tcgttggtaa	1680
aaatcaatcc	ttctaccatc	catgcatagc	aatttctaaa	aactgaattt	caagagcagt	1740
atctgaagaa	acaaacatga	tttggctcct	ttagtaaaaa	gaataaattt	taataaatca	1800
actttgaaat	agttgtaaga	gttaagaaaa	agcacaaaa	tgagatcatc	agagcagctt	1860
ggcctcaag	gacaggcagc	aggattctac	agggtttgag	ccttcctaag	tgaagctgtt	1920
tctgcaggc	tcctgtctcc	aagctcctag	ctaacagccc	cttctccac	gattggcaac	1980
aaagagcaaa	aataactttg	tacttgatgc	tgagtcagt	taaaaagcca	taaaaaattc	2040
cctctaaatg	tcaaaatgtt	tgcctccttt	gaggcttctc	tcctcctact	gggtctggat	2100
aaattagcac	tgggcttata	ttgagtcaca	gatctgggccc	ctgccacaga	gagcttcctc	2160
ctagtgtgtg	atgctttttc	tccaaactat	tgatacaaaa	tgacttgaa	tagaaatcaa	2220
cagaaaactgg	tcaaagggtg	ggcatacaca	ttctcatgta	gatgtaaaagc	tgtgcttaga	2280
attcctttgt	ggagtctggg	ttggctcttg	ttttcttggg	gtttgattca	tttttttacg	2340
taaattacaa	aaaccctcca	catttcttca	tggattgtat	tagtccatgt	tctccagaga	2400
agcagaacga	gttggtatga	tgttttgaa	gagattatga	ggaaccggct	catgtgatga	2460
aggaggttga	gaggtcctgt	gctctgccat	ctgcaagctg	aagacctgga	aagctgaggg	2520
tgtggctcca	gtctgagctc	gaaggcccaa	gaaccagggg	aaccaacggt	gtagattcca	2580
ggttgaaggc	aggagaagat	ggatgtccca	gctcagcagg	caggcaggaa	gcaaatgggg	2640
taaattcctc	cttctccac	cttttgttcc	attcaggcct	tcaacagatt	ggatgagcgc	2700
ccccccaccc	ccacactagg	gagggccatc	tgttttactg	agtccgctga	gtcaagtgcc	2760
agcctcatcc	caaaacactc	tccagacaca	cgcagaaatg	tttcatctgg	gcaccctgtg	2820
gccagtcattg	ctgacacaca	gaactaacca	tgacatggat	tcttctttaa	gcagtgatag	2880
gagcgaacag	aaacattttc	ataattttca	attattttta	atgaaaacta	tatctgatgg	2940
aattgtttta	acctagtctg	gccacacatt	atttctctgg	accgcccctc	cttcaatccc	3000
ttggacactg	atgactttat	gccagatta	cactggaggc	ctgtgctgat	tttctaacac	3060
atacctgcaa	ctgagctggc	aaaaagaaaa	ctaggcaagt	atgacagata	catgatgcac	3120
aggctaagt	caaaggaaag	aaaaacacca	actgcaggga	tgagggaactc	acccctttag	3180
aagtttctac	ttgagcagct	agaagactac	aatgccactc	atcaaaacag	tgactcaggg	3240
ggagtatttg	ggataaagga	ggaatctgat	gttgagggtc	aaatttgaag	tgtctttaag	3300
acctacaggt	aacgagacag	ctggacaaac	acatggaact	caggacaaag	gctctaagga	3360
cagcacagca	gctgacatcc	tgtgtgacag	ccttgaaagc	agcaggcccc	ccgctcacat	3420
tttgaagggg	aaaatgggta	caatgttgct	tgccactttg	gggccttctt	gggtcacatg	3480
cattttacat	ttatgcagtt	gatataattta	tgtttcctgg	gtcttttata	cattagacac	3540
catgattctc	aatcctttgt	tattttgtat	tacaaaaagc	tgaattatta	tttcaaatat	3600
gggcaaatta	gagccttcca	tattgccaag	gtgtatcaac	cacactgata	ycaygatctc	3660
tcttttgaat	tagttttcca	gttcacacct	accatttatt	tcatgattgg	tttcagactt	3720
gttcctcctg	gaaacactcc	ctaacaagca	cccttgagg	aatgaagaca	caccacacac	3780
atctacecca	ttactgcatg	tactcaagag	tcagctttta	tatgatctct	cccaagtgtc	3840
cctataatgg	ggatctttca	ctcaccctaa	agtgaggaca	aaatacttga	aagcatgagc	3900
ccagtgcctg	taggtgtgca	attaacctca	gaccaaggaa	gtgccgaacg	catctggctt	3960
ttagcaaggc	acctgacaaa	gtccttcagg	atgtttttgt	acatgagcta	gagaaatgta	4020
cctggagaac	agcttctact	gccagatgat	cttactcaaa	agatgcagat	taagcaaaat	4080
atcaacccaa	agggtgggtc	ctgatggccc	accagcccct	gtgcctggct	cgtttcctat	4140
gtttcctaga	tttggtttca	gacttgctcc	tcctgcagac	actccctaac	cagcatcctt	4200
gcagaaaact	ggtgaactag	aaaaggcctg	tgtgggtcac	gtggccaccc	aacaccacag	4260
cagtgtctaa	ggtatgcgtg	ggagcctgca	cagcaggagc	gggtcttctt	ggagacccgc	4320
atgagatgca	aagggcagtg	gacaaggagc	caagggaggt	ggctctagtc	acgtgggtat	4380
ggtgccagct	tgaggatgct	gggcaagtcc	cgagccgtct	gccttcctag	taccacagtt	4440
accactgtct	gttacctcgc	gagttcaagt	gcttcacgtg	agacagctac	gagacaggcc	4500

```

cctggaaact ggaaaatgcy aagtaaatgt catgcacaat tgttggtcac attttatctc 4560
aatcactttt accaaatcag gctaaaccct gggatttcat aacgtcttgg gctgtacaaa 4620
ttgttccttg aaatgactca gagacatttt ctgaattggc ttccatcagc caagcatttc 4680
ttcagaactg gaaaaatgct ttaaatttgg ctttgtcatg attattaaaa cactctgtac 4740
attttttatt attgaaatta acacattgcc tactttttta aaattggaaa aagaaaaaaa 4800
aaaaaaaaa 4809

```

&lt;210&gt; 570

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 570

```

aaaattgaat attgagatac cattcttttag tgttaccttt tttaccacaca tgtgtttctg 60
aaaatattgg aatttttattc atcttaaaaa ttggaccggg ccttatttac catctttaat 120
ccatttttagt actatgggtg agtacatgga attgaagtct ggcttaaadc ttcagaaagt 180
tatatatcta ttttatttta tttttttgag acagagtctc gctgtgtcac ccaggctgga 240
gtgcgggtgcc acaatcttgg ctactgcaa cctctgagtc ccaggttcaa gcgatactca 300
tgccctggcc tcttgagtag ctgggactac aggcgtgcac caccacatct ggctaactct 360
tttttgtatt ttttagtagag acgggggttc actgtggtct ccactctctg acctcgtgat 420
ccgcctgcct cccaaagtgc tgggattaca ggcatgagcc accgcacaca gctgggactg 480
ggtaatttat aaagaaaaga ggtttaatga ctacagttc cgcattggctg gagaggcctc 540
aggaaactta caatcatggg ggaaggcgaa ggggaagcaa ggcacgtctt acatgggtggc 600
aggagagAAC gagtgagggg ggagactgcc aaaaactttt tttttttgag acaagagtct 660
ggccctgttg ccaggctgg agtgacgtgg catgatctca gctcactgca acctctgcct 720
cacaggttca agcaattctc atgcctcagc ctccgcata gctgggacca caggtatgca 780
ccaccacacc tagctaattt ttgtagtttt agtagagatg gggctctact atgttgctca 840
ggctggtcta aaactcctgg gctccagcaa tccgcctgcc ttggcctccc aaagtgctgg 900
ggttacaggc ataagccacc acatccagcc tgccacatac ttttaaacta t 951

```

&lt;210&gt; 571

&lt;211&gt; 819

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 571

```

cagcttaaaa atgggtttctt gaaatcagtg attagcatto actcaccagt acccctacta 60
aggggtaggc actgggttctt actcctggga atacaggagt acaccagaat ttatttctgc 120
ttattgcttt tgttgcaaat gccgtggctt catctgagga attctagaat tcagagggtg 180
tagccctcca ctctgctgtc ttgctatctg ctctcattgc atccgtttaa cctgcattct 240
gaaagatggt tctcagggtt ttctttgacg attttcttct tttctgattc tgacaatggt 300
ttaaatcatt gtactgtggg tatcatttct ctgcatttat tttaccatc ttctttgta 360
actgttccta ttgtctttta atttctgcct gttctttatg gctttcaact tcataaataa 420
catgttttct caaatctctt tgtgaattcc agagagggc aggcacgggt gctcacatct 480
gtaatcccag cactttgggg aggctgagac ggggtggatca cttgagggtc ggagtttgag 540
accagcctgg ccaacatggg gaaatccgt ttactaaaa atacaaaaat taccaggga 600
tggtggcggg cgctgtaat ccaggtact cgggaggctg agggaggaga atcgcttgaa 660
cctgggaggc tgaggggagg gaatcgcttg aaccggggg gcagagggtg cagtgaaccg 720
agatcatggt gctgcactcc agcctggtca acagagcaag actctgcctc aaaaacaaac 780
aaataaacia acaaacaaac aaaacagaga gattttgct 819

```

&lt;210&gt; 572

&lt;211&gt; 203

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 572

```

tatagaatac tcaagctatg catcaagctt ggtaccgagc tcggatccac tatttacggc 60

```



211

<211> 76  
 <212> PRT  
 <213> Homo sapiens

<400> 575  
 Met Val Lys Ser Arg Phe Thr Lys Asn Thr Lys Ile Thr Gln Ala Trp  
                           5                          10                          15  
 Trp Arg Ala Pro Val Ile Pro Gly Thr Arg Glu Ala Glu Gly Gly Glu  
                           20                          25                          30  
 Ser Leu Glu Pro Gly Arg Leu Arg Glu Glu Asn Arg Leu Asn Pro Gly  
                           35                          40                          45  
 Gly Arg Gly Cys Ser Glu Pro Arg Ser Cys Cys Cys Thr Pro Ala Trp  
                           50                          55                          60  
 Ser Thr Glu Gln Asp Ser Ala Ser Lys Thr Asn Lys  
                           65                          70                          75

<210> 576  
 <211> 68  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(68)  
 <223> Xaa = Any Amino Acid

<400> 576  
 Met Leu Gly Lys Ser Arg Ala Val Cys Leu Pro Ser Thr Thr Val Thr  
                           5                          10                          15  
 Thr Val Cys Tyr Leu Ala Ser Ser Ser Ala Ser Arg Glu Thr Ala Thr  
                           20                          25                          30  
 Arg Gln Ala Pro Gly Asn Trp Lys Met Xaa Ser Lys Cys His Ala Gln  
                           35                          40                          45  
 Leu Leu Phe Thr Phe Tyr Leu Asn His Phe Tyr Gln Ile Arg Leu Asn  
                           50                          55                          60  
 Pro Gly Tyr Ser  
 65

<210> 577  
 <211> 57  
 <212> PRT  
 <213> Homo sapiens

<400> 577  
 Met Tyr Leu Glu Asn Ser Phe Tyr Cys Gln Met Ile Leu Leu Lys Arg  
                           5                          10                          15  
 Cys Arg Leu Ser Lys Ile Ser Thr Gln Arg Val Val Pro Asp Gly Pro



20 25 30  
 Pro Ala Pro Val Pro Gly Ser Phe Pro Met Phe Pro Arg Phe Gly Phe  
           35                  40                  45

Arg Leu Ala Pro Pro Ala Asp Thr Pro  
       50                  55

<210> 578  
 <211> 51  
 <212> PRT  
 <213> Homo sapiens

<400> 578  
 Met Gln Leu Ile Tyr Leu Cys Phe Leu Gly Leu Leu Tyr Ile Arg His  
                   5                  10                  15

His Asp Ser Gln Ser Phe Val Ile Leu Tyr Tyr Lys Lys Leu Asn Tyr  
           20                  25                  30

Tyr Phe Lys Tyr Gly Gln Ile Arg Ala Phe His Ile Ala Lys Val Tyr  
       35                  40                  45

Gln Pro His  
       50

<210> 579  
 <211> 56  
 <212> PRT  
 <213> Homo sapiens

<400> 579  
 Met His Phe Thr Phe Met Gln Leu Ile Tyr Leu Cys Phe Leu Gly Leu  
                   5                  10                  15

Leu Tyr Ile Arg His His Asp Ser Gln Ser Phe Val Ile Leu Tyr Tyr  
       20                  25                  30

Lys Lys Leu Asn Tyr Tyr Phe Lys Tyr Gly Gln Ile Arg Ala Phe His  
       35                  40                  45

Ile Ala Lys Val Tyr Gln Pro His  
       50                  55

<210> 580  
 <211> 67  
 <212> PRT  
 <213> Homo sapiens

<400> 580  
 Met Glu Leu Arg Thr Lys Ala Leu Arg Thr Ala Gln Gln Leu Thr Ser  
                   5                  10                  15

Cys Val Thr Ala Leu Lys Ala Ala Gly Pro Pro Leu Thr Phe Trp Lys  
       20                  25                  30

Gly Lys Trp Val Gln Cys Cys Leu Pro Leu Trp Gly Leu Leu Gly Ser  
                   35                                  40                                  45

His Ala Phe Tyr Ile Tyr Ala Val Asp Ile Phe Met Phe Pro Gly Ser  
           50                                  55                                  60

Phe Ile His  
       65

<210> 581

<211> 77

<212> PRT

<213> Homo sapiens

<400> 581

Met Leu Glu Val Lys Phe Glu Val Ser Leu Arg Pro Thr Gly Asn Glu  
                                   5                                  10                                  15

Thr Ala Gly Gln Thr His Gly Thr Gln Asp Lys Gly Ser Lys Asp Ser  
                   20                                  25                                  30

Thr Ala Ala Asp Ile Leu Cys Asp Ser Leu Glu Ser Ser Arg Pro Ala  
                   35                                  40                                  45

Ala His Ile Leu Glu Gly Lys Met Gly Thr Met Leu Ser Ala Thr Leu  
           50                                  55                                  60

Gly Pro Ser Trp Val Thr Cys Ile Leu His Leu Cys Ser  
       65                                  70                                  75

<210> 582

<211> 51

<212> PRT

<213> Homo sapiens

<400> 582

Met Leu Phe Leu Gln Thr Ile Asp Thr Lys Cys Thr Gly Ile Glu Ile  
                                   5                                  10                                  15

Asn Arg Asn Trp Ser Lys Val Trp His Thr His Ser His Val Asp Val  
                   20                                  25                                  30

Lys Leu Cys Leu Glu Phe Leu Cys Gly Val Trp Phe Gly Leu Gly Phe  
                   35                                  40                                  45

Leu Gly Val  
       50

<210> 583

<211> 60

<212> PRT

<213> Homo sapiens

<400> 583

214

Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg  
                           5                          10                          15

Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro  
                           20                          25                          30

Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly  
                   35                          40                          45

Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys  
           50                          55                          60

<210> 584  
 <211> 76  
 <212> PRT  
 <213> Homo sapiens

<400> 584  
 Met Cys Leu Cys Ile Pro Leu Gly Gly Tyr Gln Glu Leu Cys His Cys  
                           5                          10                          15

Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg  
                   20                          25                          30

Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro  
           35                          40                          45

Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly  
           50                          55                          60

Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys  
           65                          70                          75

<210> 585  
 <211> 50  
 <212> PRT  
 <213> Homo sapiens

<400> 585  
 Met Val Tyr Arg Phe Gly Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu  
                           5                          10                          15

Ala Ser Leu Gly Ser Ser Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp  
           20                          25                          30

Arg Gln Ala Asp Pro Ser Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu  
           35                          40                          45

Leu Phe  
       50

<210> 586  
 <211> 60  
 <212> PRT  
 <213> Homo sapiens



Gly Ala Cys Phe Thr Val Ala Gly Leu Pro Arg Ala Trp Thr Thr Gln  
           35                  40                  45  
 Tyr Ser Ile Ile Asp Lys Arg Ile Arg Gln Glu Ile Tyr Thr Cys Cys  
           50                  55                  60  
 Leu Ala Phe Val Val Ile Tyr Thr Asn Glu Asn Met Tyr Tyr Ser Tyr  
       65                  70                  75                  80  
 Ile

<210> 589  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 589  
 Met Thr Met Cys Leu Cys Val Ala Pro Met Gly Arg Ala Thr Arg Met  
                   5                  10                  15  
 Ser Val Thr Cys Asp Arg Leu His Ala Asn Ser Arg Val Arg Tyr Leu  
                   20                  25                  30  
 Trp Cys Gln Lys Asp His Val Pro Gln Met Gln Asp Gln Asp Leu Glu  
           35                  40                  45  
 Met Glu Ser Met Lys Ala Leu Glu Lys Leu Val Lys Arg Arg His Pro  
       50                  55                  60  
 Pro Val Ile Phe Ala Ser Leu Val Gln Asn Val Thr Lys Met Pro Arg  
       65                  70                  75                  80  
 Met Ser Gly Val Cys Val Ile Leu Thr Val Leu Lys Pro Thr Ser Ile  
                   85                  90                  95  
 Pro Ser Ala Leu Leu Met Gly Asn Leu Met Ile Met His Ala Lys Ser  
           100                  105                  110  
 Lys Lys His Arg Val Arg Asn Arg Arg Lys Leu Lys Ser Cys Leu Trp  
       115                  120                  125  
 Val Asp Val Lys Ile Thr Gln Leu Gln Leu Leu Ser Leu Lys Met Gly  
       130                  135                  140  
 Ile Met Gln Glu Gln Ile Met Gln Arg Met Leu Thr Asn  
       145                  150                  155

<210> 590  
 <211> 347  
 <212> PRT  
 <213> Homo sapiens

<400> 590  
 Met Leu Leu Ile Val Ala Arg Pro Val Lys Leu Ala Ala Phe Pro Thr  
                   5                  10                  15

Ser Leu Ser Asp Cys Gln Thr Pro Thr Gly Trp Asn Cys Ser Gly Tyr  
                   20                                  25                                  30  
 Asp Asp Arg Glu Asn Asp Leu Phe Leu Cys Asp Thr Asn Thr Cys Lys  
                   35                                  40                                  45  
 Phe Asp Gly Glu Cys Leu Arg Ile Gly Asp Thr Val Thr Cys Val Cys  
                   50                                  55                                  60  
 Gln Phe Lys Cys Asn Asn Asp Tyr Val Pro Val Cys Gly Ser Asn Gly  
                   65                                  70                                  75                                  80  
 Glu Ser Tyr Gln Asn Glu Cys Tyr Leu Arg Gln Ala Ala Cys Lys Gln  
                                   85                                  90                                  95  
 Gln Ser Glu Ile Leu Val Val Ser Glu Gly Ser Cys Ala Thr Asp Ala  
                                   100                                  105                                  110  
 Gly Ser Gly Ser Gly Asp Gly Val His Glu Gly Ser Gly Glu Thr Ser  
                   115                                  120                                  125  
 Gln Lys Glu Thr Ser Thr Cys Asp Ile Cys Gln Phe Gly Ala Glu Cys  
                   130                                  135                                  140  
 Asp Glu Asp Ala Glu Asp Val Trp Cys Val Cys Asn Ile Asp Cys Ser  
                   145                                  150                                  155                                  160  
 Gln Thr Asn Phe Asn Pro Leu Cys Ala Ser Asp Gly Lys Ser Tyr Asp  
                                   165                                  170                                  175  
 Asn Ala Cys Gln Ile Lys Glu Ala Ser Cys Gln Lys Gln Glu Lys Ile  
                                   180                                  185                                  190  
 Glu Val Met Ser Leu Gly Arg Cys Gln Asp Asn Thr Thr Thr Thr Thr  
                   195                                  200                                  205  
 Lys Ser Glu Asp Gly His Tyr Ala Arg Thr Asp Tyr Ala Glu Asn Ala  
                   210                                  215                                  220  
 Asn Lys Leu Glu Glu Ser Ala Arg Glu His His Ile Pro Cys Pro Glu  
                   225                                  230                                  235                                  240  
 His Tyr Asn Gly Phe Cys Met His Gly Lys Cys Glu His Ser Ile Asn  
                                   245                                  250                                  255  
 Met Gln Glu Pro Ser Cys Arg Cys Asp Ala Gly Tyr Thr Gly Gln His  
                   260                                  265                                  270  
 Cys Glu Lys Lys Asp Tyr Ser Val Leu Tyr Val Val Pro Gly Pro Val  
                   275                                  280                                  285  
 Arg Phe Gln Tyr Val Leu Ile Ala Ala Val Ile Gly Thr Ile Gln Ile  
                   290                                  295                                  300  
 Ala Val Ile Cys Val Val Val Leu Cys Ile Thr Arg Lys Cys Pro Arg  
                   305                                  310                                  315                                  320

Ser Asn Arg Ile His Arg Gln Lys Gln Asn Thr Gly His Tyr Ser Ser  
                   325                                  330                                  335

Asp Asn Thr Thr Arg Ala Ser Thr Arg Leu Ile  
                   340                                  345

<210> 591

<211> 565

<212> DNA

<213> Homo sapien

<400> 591

actaaagcaa	atgaacaagc	tgacttgcta	gtatcatctg	cattcattga	agcacaagaa	60
cttcatgcct	tgactcatgt	aaatgcaata	ggattaaaaa	ataaatttga	tatcacatgg	120
aaacagacaa	aaaatattgt	acaacattgc	acccagtgtc	agattctaca	cctggccact	180
caggaagcaa	gagttaatcc	cagaggtcta	tgctctaata	tgttatggca	aatggatgtc	240
atgcacgtac	cttcatttgg	aaaattgtca	tttgtccatg	tgacagttga	tacttattca	300
catttcataat	gggcaacctg	ccagacagga	gaaagtactt	cccatgttaa	aagacattta	360
ttatcttgtt	ttcctgtcat	gggagttcca	gaaaaagtta	aaacagacaa	tgggcccagg	420
tactgtagta	aagcatttca	aaaattctta	aatcagtggg	aaattacaca	tacaatagga	480
attctctata	attcccaagg	acaggccata	attgaaggaa	ctaatagaac	actcaaagct	540
caattgggta	aacaaaaaaa	aaaaaa				565

<210> 592

<211> 188

<212> PRT

<213> Homo sapien

<400> 592

Thr	Lys	Ala	Asn	Glu	Gln	Ala	Asp	Leu	Leu	Val	Ser	Ser	Ala	Phe	Ile
1			5					10						15	
Glu	Ala	Gln	Glu	Leu	His	Ala	Leu	Thr	His	Val	Asn	Ala	Ile	Gly	Leu
		20						25					30		
Lys	Asn	Lys	Phe	Asp	Ile	Thr	Trp	Lys	Gln	Thr	Lys	Asn	Ile	Val	Gln
	35						40					45			
His	Cys	Thr	Gln	Cys	Gln	Ile	Leu	His	Leu	Ala	Thr	Gln	Glu	Ala	Arg
	50				55						60				
Val	Asn	Pro	Arg	Gly	Leu	Cys	Pro	Asn	Val	Leu	Trp	Gln	Met	Asp	Val
65				70					75					80	
Met	His	Val	Pro	Ser	Phe	Gly	Lys	Leu	Ser	Phe	Val	His	Val	Thr	Val
		85						90					95		
Asp	Thr	Tyr	Ser	His	Phe	Ile	Trp	Ala	Thr	Cys	Gln	Thr	Gly	Glu	Ser
		100					105					110			
Thr	Ser	His	Val	Lys	Arg	His	Leu	Leu	Ser	Cys	Phe	Pro	Val	Met	Gly
	115					120						125			
Val	Pro	Glu	Lys	Val	Lys	Thr	Asp	Asn	Gly	Pro	Gly	Tyr	Cys	Ser	Lys
	130					135				140					
Ala	Phe	Gln	Lys	Phe	Leu	Asn	Gln	Trp	Lys	Ile	Thr	His	Thr	Ile	Gly
145				150					155					160	
Ile	Leu	Tyr	Asn	Ser	Gln	Gly	Gln	Ala	Ile	Ile	Glu	Gly	Thr	Asn	Arg
		165					170							175	
Thr	Leu	Lys	Ala	Gln	Leu	Val	Lys	Gln	Lys	Lys	Lys				
	180						185								

<210> 593

<211> 271

<212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(271)  
 <223> n = A,T,C or G

<400> 593	
actttatggt cnagtgcana aancncctg gattgccacc ntactctcag ggctgtgant	60
tgtgcnccca nagcaacctg ggcacgcggg gacagggggg ccnacaattg agggagcggg	120
gtccctagct ggggtctata catgncnggg naagggcngc tgagtnccat nagcaaagga	180
nctagnatnt gcgggggtgc ggcctgggcc taccctttna agcatccntn gatccactcc	240
angaanccng gggtagncag gtttnccaac a	271

<210> 594  
 <211> 376  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(376)  
 <223> n = A,T,C or G

<400> 594	
cctttggggg nggggggaac ctttaccatt gtncccccttt atttcatttg gttnggggttc	60
gcgccctcnn gggccaacaa agttatcgtn nttgaagaga anattttttt ggnttngncc	120
cgattaagcg ncaaatgtgt agcaaaangc cgtgccactt gtggcgtagc tncgtcgggt	180
cgattcgacg acaaggcgtn gcgcgntanc gttagtctcn aatngaccn gtggcatgag	240
cccacgangg nttcgtgtcg tcacatggnc tctagacata acgcncnccn ttttttncag	300
agggggntgc cgcccttagg gaggnagggg tggggacact agccaancca nantctnacc	360
ccattgaaga aaaggn	376

<210> 595  
 <211> 242  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(242)  
 <223> n = A,T,C or G

<400> 595	
agnctgctgn tcgtncctn tatgtggctt catnntgagg acaanagtng cactgaggct	60
tgngnatgcc aggcaaggnc aagctggctc aaaaagcatc caccacctc tgnaangggg	120
atgccangag cangtgcacc agtcccaact angagnccn ggcatgntac atcttcttcc	180
acccctnaaa ntttgngcta caangnccat ttttcttttt ctcttaaggg ncnctggct	240
tc	242

<210> 596  
 <211> 535  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature



gcatgacatc	ancgatgtnt	ttggnnacct	ganattngct	aaaactngng	natgccgggn	60
atgnagggtt	ggtantgac	tatgcactca	catctcatgg	ggacgtttca	tgtggagtgn	120
tcgacaangt	tgctgnancn	gagaagtgat	gatctcagtt	gaaaggggtca	tgtgaataca	180
cnttacactt	gaaaaagaag	cacattggga	atatcacgaa	acgnccacca	acatcctg	238

&lt;210&gt; 600

&lt;211&gt; 232

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(232)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 600

cgaactat	tt	agactaccta	gg	aaaaattat	tt	tagtatca	ga	agaatata	ag	ggggtgtag	60
tactcatcag	ag	ctaaatga	ga	gcgccttta	aa	aatgttag	tt	gtcttcc	gc	catttcta	120
cagaaagctg	ca	atttcagg	tt	tttcaacct	aa	taggtgat	att	taaaaa	aa	aaaaaagc	180
aatcgcaaat	ag	ccccactg	ct	ttttacaaa	tc	attttttc	cc	caacacaa	tg		232

&lt;210&gt; 601

&lt;211&gt; 547

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(547)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 601

cattgtgttg	gg	gaaaaaat	ga	tttgtata	ag	cagtgggg	ct	atttgcga	tt	gtttttt	60
tttttcttaa	at	atcaccta	tt	agggttgaa	aa	cctgaaat	tg	cagctttc	tg	tagaaatg	120
gcggaagaca	aa	ctaacatt	tt	taagcgc	tc	tcatttag	ct	ctgatgag	ta	ctacaccc	180
ctnatattct	tc	tgatacta	aa	ataatttt	cc	tagtgtag	tc	taaaacttt	tt	taaaaaaga	240
catgtaatcc	gc	ggagtttag	ta	actcaaaa	cg	agtgcata	tn	ggaagtat	cg	cagccgtt	300
nctggatnaa	at	cccagct	tg	ctngcttg	ct	nagccggg	gg	cggtnaa	aa	aaacatct	360
gcagcccngg	gg	naaaaacc	tt	cgattgt	tc	ttacgtgt	tt	acgttatt	tt	atttccct	420
nnagcaaggc	ng	gganttgg	gg	actcgaaa	tg	gtacagtt	gg	gctgggga	tc	gcccttgt	480
tacataaaaag	nc	gtccagaa	ga	ggggacgg	ta	caggcngg	ga	ntccaaa	gg	tcagtcct	540
tgccatt											547

&lt;210&gt; 602

&lt;211&gt; 826

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(826)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 602

cggggggg	nn	tacgtctctc	tg	gaagcttt	ta	ttgtacca	gg	cgatccc	ag	cccaactg	60
taccattoga	gt	ccctaactc	ct	gccttgc	ct	agggaaat	aa	ataacgt	aa	acacgtaa	120
gaacaatg	gc	aaagcgtttt	ct	tccttagg	ct	gcagattg	tc	ttcttcac	cg	ccccctgt	180
tagctagcta	gc	tagctggg	aa	tttaatcc	ag	aaacggct	tg	cgatacct	cc	tagatgca	240

ctcgttttga	gttacaaact	ccgcggatta	catgtctttt	taaaaaagtt	tagactacac	300
tagggaaaat	tatttttagta	tcagaagaat	atcagggggt	gtagtactca	tcagagctna	360
atgagagcgc	tttaaaaatg	ttagtttgtc	ttccgccatt	tctacagaaa	gctgcaattt	420
caggttttca	ncctaatagg	tgatatntaa	gaaaaaaaaa	acaatcgcan	atagcccact	480
gctttttacaa	atcatttttc	tcttctaggt	atagcctgtc	aggtggccta	atgtattttt	540
gacatctcta	ggaattttta	tagaccagaa	atgggtgcca	gagatatgcc	tgcactaatc	600
ttaagtgggg	atztatgtat	ttctcaanca	agtgtattaa	gcaaaactag	gcacgaatga	660
aatcaagatc	tttaggccag	aaatcatgaa	nanttttana	attattttan	gaatctgtgg	720
cttctcttct	taaaatngaa	aaaaaaattg	tttaaaccce	naaggtctga	ataccceaagc	780
nccctgaacn	anagaacaan	gccggagcac	cccctcccaa	atcccc		826

&lt;210&gt; 603

&lt;211&gt; 817

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(817)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 603

nnangacttt	tgtggtntta	tacaattntt	ttttctattt	ctatgaagag	aaagccacag	60
agtcctaaaa	taattctaaa	actcatcatg	actttcttgc	ctaaaagatc	ttgatttcaa	120
tcgtgcctag	ttttgcttta	atcacttgct	tgagaaatac	ataaatcccc	acttaagatt	180
agtgcaggca	tatctctggc	acccatttct	ggttctatta	aaattcctag	agatgtcaaa	240
aattacatta	ggccacctga	caggctatac	ctagaagaga	aaaaatgatt	tgtaaaagca	300
gtggggctat	ttgcgattgc	tttttttttt	tcttaaatat	cacctattag	gttgaaaacc	360
tgaaattgca	gctttctgta	gaaatggcgg	aagacaaact	aacattttta	aagcgctctc	420
atttagctct	gatgagtact	acacccctga	tattcttctg	atactaaaat	aattttccta	480
gtgtagtcta	aactttttta	aaaagacatg	taatccgcgg	agtttgtaac	tcaaaacgag	540
tgcacttagg	aggtatcgca	agccgtttct	ggattaaatt	cccagctagc	ttgcttgctt	600
agcaggggcg	ggnaaanaag	acatctgcag	cctaggggaag	aaaacctttc	gcattgttct	660
tacgtgttta	cgttatttta	tttcctanaa	caaggcngaa	ttgggactcg	aatggttcag	720
ttgggggtgg	ggatcccctg	gtncataaaa	ngtcanaaag	anggtacagg	cggaaaccca	780
agggtcgtcc	tgcatttana	ctcggaattt	tggtgccc			817

&lt;210&gt; 604

&lt;211&gt; 694

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(694)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 604

cttttcaa	atcattttt	cttctaggt	atancctgt	caaggtggc	ctaaatgt	taattttt	60
gacatctcta	ngaattttta	tagaaccaga	aatgggtg	ccagagata	tgcactaat		120
cttaagtggg	gatttatgta	tttctcaagc	aagtgtat	aaagcaaaa	ggcagattg		180
aatcaagat	cttttaggca	anaaagtc	atgatgatt	tttagaatt	taggactctg		240
tggcttttct	ttcatagaaa	tagaaaaaaa	aattgtata	aaaccacaaa	ggtcctgaat		300
agccaaagca	acactganca	aaaagaacan	agcaggga	agcaacacta	ccngaattca		360
aattatacta	ccagggtgta	gtaaccaaaa	cagcattcta	ttggcataaa	atagacacca		420
agaccaatgg	ancagaataa	agaacccccc	aaataaatcc	atataatntac	cgccanctga		480
ttatcaataa	cnaacaccaa	gaacatatnt	taagggaant	nctatttcaat	aantagtgtc		540
ggnaaaaa	ctgggaaat	ccatgcagaa	naatgaaact	agacccttat	ccctcaccat		600

acgcaaannt caacttcgga atgggattac aaaacttaag acattccaac ccaagaaact 660  
atnaaancta ctattaagaa aacagatcnc nccc 694

<210> 605  
<211> 678  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(678)  
<223> n = A,T,C or G

<400> 605  
taaaaatcta gactacacta ggaaattatt ttantatcag aagaatatca ggggtgtagt 60  
actcatcana gctaaatgag agcgctttaa aaatgttagt ttgtcttccg ccatttctac 120  
agaaagctgc aatttcaggt tttcaacctata atagggtgata ttttaagaaaa aaaaaaagca 180  
atcgcaata gccccactgc ttttacaat cattttttct cttctaggta tagcctgtca 240  
gggtggcctaa tgtaatTTTT gacatctcta ggaattttaa tagaaccaga aatgggtgcc 300  
agagatatgc ctgcactaat ctttaagtggg gatttatgta tttctcaagc aagtgattaa 360  
agcaaaacta ggcacgattg aaatcaanat cttttaggca agaaagtcac gatgagtttt 420  
anaattattt taggactctg tggctttctc ttcataaaaa tagaaaaaaa aaattgtata 480  
aaaaccacaa aaggtcctga atagcccaaa gcaacactga acaaaaangaa caaagcagga 540  
agcaacacac taccggaatt caattatact accaaggtgt antaaccaaa acagcattct 600  
attgggcata aaatagacca aagaccagtg ggaaacagaa taaagaancc caaaataaat 660  
cctatatatta cngcccnc 678

<210> 606  
<211> 263  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(263)  
<223> n = A,T,C or G

<400> 606  
gtgggggtcng cancagccaa ctcagcttcc tttcgggctt tgtagcaga cggatcatcc 60  
tctagtccac tgtgntcaaa ttccattgtg tggggggcnc tcgcctcggc canagatctg 120  
agtgancana cntgtcccca ctgaggtgcc ccacagcngn ttgtnttcag cangggctna 180  
caactcgacc ggcagcgan ggcgtggcaga antgngcgcc tnnctcattc ctacgngtn 240  
ngccgcagga aggangacag gcc 263

<210> 607  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 607  
ccatgtgggt cccggttgtc tt 22

<210> 608  
<211> 22  
<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 608

gataggggtg ctcaggggtt gg

22

<210> 609

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 609

gctggacagg gggcaaaagc tggggcagtg aaccatgtgc

40

<210> 610

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 610

ccttgtccag atagcccagt agctgac

27

<210> 611

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 611

gatagagaaa accgtccagg ccagtattgt gggaggctgg gagtgc

46

<210> 612

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 612

gcacatgggtt cactgccccca gcttttgccc cctgtccagc

40

<210> 613

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 613

gccgctcgag ttagaattcg gggttggcca cgatgggtg

38

<210> 614

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 614

cggcgggcat atgcatcacc atcaccatca catcataaac ggcgaggact gca

53

<210> 615

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 615

gcactcccag cctcccacaa tactggcctg gacggttttc tctatc

46

<210> 616

<211> 1350

<212> DNA

<213> Homo sapien

<400> 616

atgcatcacc	atcaccatca	catcataaac	ggcgaggact	gcagcccga	ctcgcagccc	60
tggcaggcgg	cactgggtcat	ggaaaacgaa	ttgttctgct	cgggcgctcct	ggtgcatccg	120
cagtgggtgc	tgtagccgc	acactgtttc	cagaactcct	acaccatcgg	gctgggcctg	180
cacagtcttg	aggccgacca	agagccaggg	agccagatgg	tggaggccag	cctctccgta	240
cggcaccag	agtacaacag	acccttgctc	gctaacgacc	tcatgctcat	caagttggac	300
gaatccgtgt	ccgagtctga	caccatccgg	agcatcagca	ttgcttcgca	gtgccctacc	360
gcggggaact	cttgccctcg	ttctggctgg	ggtctgctgg	cgaacggcag	aatgcctacc	420
gtgctgcagt	gcgtgaacgt	gtcgggtggtg	tctgaggagg	tctgcagtaa	gctctatgac	480
ccgctgtacc	accccagcat	gttctgcgcc	ggcgaggggc	aagaccagaa	ggactcctgc	540
aacgggtgact	ctggggggcc	cctgatctgc	aacgggtact	tgcagggcct	tgtgtctttc	600
ggaaaagccc	cgtgtggcca	agttggcgtg	ccagggtgtct	acaccaacct	ctgcaaattc	660
actgagtga	tagagaaaac	cgtccaggcc	agtattgtgg	gaggctggga	gtgcgagaag	720
cattcccaac	cctggcaggt	gcttgtggcc	tctcgtggca	gggcagtctg	cggcgggtgt	780
ctggtgcacc	cccagtgggt	cctcacagct	gccactgca	tcaggaacaa	aagcgtgatc	840
ttgctgggtc	ggcacagcct	gtttcatcct	gaagacacag	gccagggtatt	tcagggtcagc	900
cacagcttcc	cacaccgct	ctacgatatg	agcctcctga	agaatcgatt	cctcaggcca	960
ggtgatgact	ccagccacga	cctcatgctg	ctccgcctgt	cagagcctgc	cgagctcacg	1020
gatgctgtga	aggtcatgga	cctgccacc	caggagccag	cactggggac	cacctgctac	1080
gcctcaggct	ggggcagcat	tgaaccagag	gagttcttga	cccaaagaa	acttcagtgt	1140
gtggacctcc	atgttatttc	caatgacgtg	tgtgcgcaag	ttcaccctca	gaaggtgacc	1200
aagttcatgc	tgtgtgctgg	acgctggaca	gggggcaaaa	gctggggcag	tgaaccatgt	1260
gccctgcccg	aaaggccttc	cctgtacacc	aaggtggtgc	attaccggaa	gtggatcaag	1320
gacaccatcg	tggccaaccc	cgaattctaa				1350

<210> 617

<211> 449  
 <212> PRT  
 <213> Homo sapien

<400> 617

```

Met His His His His His Ile Ile Asn Gly Glu Asp Cys Ser Pro
 1          5          10          15
His Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu Phe
          20          25          30
Cys Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Ala His
          35          40          45
Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu Glu
          50          55          60
Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala Ser Leu Ser Val
          65          70          75          80
Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala Asn Asp Leu Met Leu
          85          90          95
Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp Thr Ile Arg Ser Ile
          100          105          110
Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn Ser Cys Leu Val Ser
          115          120          125
Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro Thr Val Leu Gln Cys
          130          135          140
Val Asn Val Ser Val Val Ser Glu Glu Val Cys Ser Lys Leu Tyr Asp
          145          150          155          160
Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly Gly Gly Gln Asp Gln
          165          170          175
Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro Leu Ile Cys Asn Gly
          180          185          190
Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala Pro Cys Gly Gln Val
          195          200          205
Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys Phe Thr Glu Trp Ile
          210          215          220
Glu Lys Thr Val Gln Ala Ser Ile Val Gly Gly Trp Glu Cys Glu Lys
          225          230          235          240
His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala Val
          245          250          255
Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala His
          260          265          270
Cys Ile Arg Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu Phe
          275          280          285
His Pro Glu Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe Pro
          290          295          300
His Pro Leu Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg Pro
          305          310          315          320
Gly Asp Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu Pro
          325          330          335
Ala Glu Leu Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln Glu
          340          345          350
Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu
          355          360          365
Pro Glu Glu Phe Leu Thr Pro Lys Lys Leu Gln Cys Val Asp Leu His
          370          375          380
Val Ile Ser Asn Asp Val Cys Ala Gln Val His Pro Gln Lys Val Thr
          385          390          395          400
Lys Phe Met Leu Cys Ala Gly Arg Trp Thr Gly Gly Lys Ser Trp Gly
          405          410          415
Ser Glu Pro Cys Ala Leu Pro Glu Arg Pro Ser Leu Tyr Thr Lys Val

```

420 425 430  
 Val His Tyr Arg Lys Trp Ile Lys Asp Thr Ile Val Ala Asn Pro Glu  
 435 440 445  
 Phe

<210> 618  
 <211> 3923  
 <212> DNA  
 <213> Homo sapien

<400> 618  
 acagaagaaa tagcaagtgc cgagaagctg gcatcagaaa aacagagggg agatttgtgt 60  
 ggctgcagcc gagggagacc aggaagatct gcatgggtgg aaggacctga tgatacagag 120  
 gaattacaac acatatactt agtgtttcaa tgaacaccaa gataaataag tgaagagcta 180  
 gtccgctgtg agtctcctca gtgacacagg gctggatcac catcgacggc actttctgag 240  
 tactcagtgc agcaaagaaa gactacagac atctcaatgg caggggtgag aaataagaaa 300  
 ggctgctgac ttaccatctt gaggccacac atctgctgaa atggagataa ttaacatcac 360  
 tagaaacagc aagatgacaa tataatgtct aagtagtgac atgtttttgc acatttccag 420  
 cccctttaa tatccacaca cacaggaagc acaaaaggaa gcacagagat ccctgggaga 480  
 aatgcccggc cgccatcttg ggtcatcgat gagcctcgcc ctgtgcctgg tcccgttgt 540  
 gaggaagga cattagaaaa tgaattgatg tgttccttaa aggatgggca ggaaaacaga 600  
 tctgttgtg gatatttatt tgaacgggat tacagatttg aaatgaagtc acaaagtga 660  
 cattaccaat gagaggaaaa cagacgagaa aatcttgatg gcttcacaag acatgcaaca 720  
 aacaaaatgg aatactgtga tgacatgagg cagccaagct ggggaggaga taaccacggg 780  
 gcagaggggc aggattctgg ccctgctgcc taaactgtgc gttcataacc aaatcatttc 840  
 atatttctaa cctcaaaac aaagctgttg taatatctga tctctacggc tcttctggg 900  
 cccaacattc tccatatatc cagccacact catttttaat atttagttcc cagatctgta 960  
 ctgtgacctt tctacactgt agaataacat tactcatttt gttcaaagac cttctgtgtt 1020  
 gctgcctaata atgtagctga ctgtttttcc taaggagtgt tctggcccag gggatctgtg 1080  
 aacaggctgg gaagcatctc aagatctttc cagggttata cttactagca cacagcatga 1140  
 tcattacgga gtgaattatc taatcaacat catcctcagt gtctttgccc atactgaaat 1200  
 tcatttccca cttttgtgcc cattctcaag acctcaaaat gtcattccat taatatcaca 1260  
 ggattaactt ttttttttaa cctggaagaa ttcaatgtta catgcagcta tgggaattta 1320  
 attacatatt ttgttttcca gtgcaaagat gactaagtcc tttatccctc ccctttgttt 1380  
 gatttttttt ccagtataaa gttaaaatgc ttagccttgt actgaggctg tatacagcac 1440  
 agcctctccc catccctcca gccttatctg tcatcaccat caaccctcc cataccacct 1500  
 aaacaaaatc taacttgtaa ttccttgaac atgtcaggac atacattatt ccttctgcct 1560  
 gagaagctct tccttgtctc ttaaactctag aatgatgtaa agttttgaat aagttgacta 1620  
 tcttacttca tgcaaagaag ggacacatat gagattcatc atcacatgag acagcaata 1680  
 ctaaaagtgt aatttgatta taagagtta gataaatata tgaaatgcaa gagccacaga 1740  
 gggaatgttt atggggcacg tttgtaagcc tgggatgtga agcaaaggca gggaaacctca 1800  
 tagtatctta tataatatac ttcatttctc tatctctatc acaatatcca acaagctttt 1860  
 cacagaattc atgcagtgca aatcccaaaa ggtaaccttt atccatttca tggtagagtgc 1920  
 gctttagaat tttggcaaat catactggtc acttatctca actttgagat gtgtttgtcc 1980  
 ttgtagttaa ttgaaagaaa tagggcactc ttgtgagcca ctttaggggt cactcctggc 2040  
 aataaagaat ttacaaagag ctactcagga ccagttgtta agagctctgt gtgtgtgtgt 2100  
 gtgtgtgtgt gagtgtacat gccaaagtgt gcctctctct cttgacccat tatttcagac 2160  
 ttaaaacaag catgttttca aatggcacta tgagctgcca atgatgtatc accaccatat 2220  
 ctcatatttc tccagtaaat gtgataataa tgtcatctgt taacataaaa aaagtttgac 2280  
 ttcacaaaag cagctggaaa tggacaacca caatatgcat aaatctaact cctaccatca 2340  
 gctacacact gcttgacata tattgttaga agcacctcgc atttgtgggt tctcttaagc 2400  
 aaaatacttg cattaggtct cagctggggc tgtgcatcag gcggtttgag aaatattcaa 2460  
 ttctcagcag aagccagaat ttgaattccc tcatctttta ggaatcattt accagggtttg 2520  
 gagaggattc agacagctca ggtgctttca ctaatgtctc tgaacttctg tccctctttg 2580  
 tgttcatgga tagtccaata aataatgtta tctttgaact gatgctcata ggagagaata 2640  
 taagaactct gagtgatatc aacattaggg attcaaagaa atattagatt taagctcaca 2700

ctggtcaaaa	ggaaccaaga	tacaaagaac	tctgagctgt	catcgcccc	atctctgtga	2760
gccacaacca	acagcaggac	ccaacgcatg	tctgagatcc	ttaaatcaag	gaaaccagt	2820
tcagtgattg	aattctccta	ttatggatgc	tagcttctgg	ccatctctgg	ctctcctctt	2880
gacacatatt	agcttctagc	ctttgcttcc	acgactttta	tcttttctcc	aacacatcgc	2940
ttaccaatcc	tctctctgct	ctgttgcttt	ggacttcccc	acaagaattt	caacgactct	3000
caagtctttt	cttccatccc	caccactaac	ctgaatgcct	agacccttat	ttttattaat	3060
ttccaataga	tgctgcctat	gggctatatt	gcttttagatg	aacattagat	atttaaagct	3120
caagagggtc	aaaatccaac	tcattatctt	ctctttcttt	cacctccctg	ctcctctccc	3180
tatattactg	attgcactga	acagcatggg	ccccaatgta	gccatgcaaa	tgagaaaccc	3240
agtggctcct	tggtgtacat	gcatgcaaga	ctgctgaagc	cagaaggatg	actgattacg	3300
cctcatgggt	ggaggggacc	actcctgggc	cttcgtgatt	gtcaggagca	agacctgaga	3360
tgctccctgc	cttcagtgtc	ctctgcatct	cccccttcta	atgaagatcc	atagaatttg	3420
ctacatttga	gaattccaat	taggaactca	catgttttat	ctgccctatc	aattttttaa	3480
acttgctgaa	aattaagttt	tttcaaaatc	tgctcctgta	aattactttt	tcttacagt	3540
tcttggcata	ctatatcaac	tttgattctt	tgttacaact	tttcttactc	ttttatcacc	3600
aaagtggctt	ttattctctt	tattattatt	attttctttt	actactatat	tacgttggtta	3660
ttattttgtt	ctctatagta	tcaattttatt	tgatttaggtt	tcaattttatt	ttttgtctg	3720
acttttaaaa	taagtgatcc	gggggggtgg	agaacagggg	agggagagca	ttaggacaaa	3780
tacctaatgc	atgtgggact	taaaacctag	atgatgggtt	gatagggtgca	gcaaaccact	3840
atggcacacg	tatacctgtg	taacaaacct	acacattctg	cacatgtatc	ccagaacgta	3900
aagtaaaatt	taaaaaaaag	tga				3923

&lt;210&gt; 619

&lt;211&gt; 3674

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 619

agaaagtttc	cttttttttt	tttaatgggtg	aaaagatata	cacatattta	gaattagcca	60
gctggggtca	gttttagatta	ttccaatttt	gttggcaaca	tccagagcat	cgtaatcagg	120
agccagtga	acatattcct	tcttctctcc	atcaggccaa	atcacgggtg	tgacctgggc	180
cacatcaatg	tcttagaact	tcttcacagc	ctgtttgatc	tggtgcttgt	tggtcttaac	240
atccacaatg	aacacaagt	tggtgtgtgc	ttctatcttc	ttcgtgggtga	ctcagtggc	300
agcggaaact	tgatgatagc	gtagtgggtca	agcttgatc	tcctgggagc	gctcttccaa	360
agatatattg	gctgcctcgg	gagttgcagc	gtcttgggcc	gccggaagg	gggtgacgta	420
cggatcttct	ttttttgtgt	ggctgtggac	acctttcaac	actgtcttct	tggtctttaa	480
atccttcgct	ttgggttcgg	ctataggagg	ggcaggagct	tccttcttca	ctttcggggc	540
catcttgtga	aaagggaag	tttcccttct	aataccattt	tcacttctcc	cgaattttgt	600
ggatcgtttc	ttggtatcta	cccagattt	caggagtgtt	ggctggatct	tagggattgt	660
gaagtcttca	tttccctgtg	gtgagatctg	aggcatgatt	ttaaacagt	tgagggaagg	720
agatctccag	gcactttaat	agaatggaga	agcaggatgg	gatttgagag	gaaatctgat	780
tttgaaaaaa	ggagaactag	agttgagttc	gtaatttaact	agcaccttaa	aggtcattca	840
gcatgcccac	ctgcacagtg	ggtgtaatca	ccctacagaa	caaaaacaaa	aaggcaatgg	900
agaggaagct	gtaaagcact	gtacatgttt	aactcattgt	tatgtaagct	agccgaaggc	960
ttcacagact	tgaattcatc	tcccaagttc	tcttccctgta	ctggaaactc	tgcccttaggt	1020
tgcttaaaaac	ttgagaaaca	gaatattgct	tccctgcct	gccttcttga	gtacacttgc	1080
ctacacaaaag	atgcacatcc	ttgtttgtgt	gtgtgtgtcc	atttgctgtg	acattcttgt	1140
gaaagtcaaaa	gtttcccagc	tggtgacata	cacaagtttg	tttggtgcaa	cctgtcagat	1200
gcatccctta	gacaggccct	ttgatactct	gggaaagaca	ttggacttac	agtcggaacg	1260
aaaagaaaaga	aatgtgatat	gtatagcgtg	cagtgaagttg	gagttttacc	tgtattgttt	1320
taatttcaac	aagcctgagg	actagccaca	aatgtaccca	gtttacaaat	gaggaaacag	1380
gtgcaaaaag	gttgttacct	gtcaaagggt	gtatgtggca	gagccaagat	ttgagcccag	1440
ttatgtctga	tgaacttagc	ctatgctctt	ttaacttctg	aatgctgacc	attgaggata	1500
tctaaactta	gatcaattgc	attttccctc	caagactatt	tacttatcaa	tacaataata	1560
ccacctttac	caatctattg	ttttgatacg	agactcaaat	atgccagata	tatgtaaaaag	1620
caacctacaa	gctctcta	catgctcacc	taaaagattc	ccgggatcta	ataggctcaa	1680
agaaacttct	tctagaaata	taaaagagaa	aattggatta	tgcaaaaatt	cattattaat	1740



ttttttcatc	catcctttaa	ttcagcaaac	atttatctgt	tggtgacttt	atgcagtatg	1800
gccttttaag	gattggggga	caggtgaaga	acgggggtgcc	agaatgcatc	ctcctactaa	1860
tgaggtcagt	acacatttgc	atttttaaat	gccctgtcca	gctgggcatg	gtggatcatg	1920
cctgtaatct	caacattgga	aggccaaggc	aggaggattg	cttcagccca	ggagttcaag	1980
accagcctgg	gcaacataga	aagaccccat	ctctcaatca	atcaatcaat	gccctgtctt	2040
tgaaaataaa	actctttaag	aaaggtttaa	tgggcagggg	gtggtagctc	atgcctataa	2100
tacagcactt	tgggaggctg	aggcaggagg	atcactttag	cccagaagtt	caagaccagc	2160
ctgggcaaca	agtgcacact	catctcaatt	ttttaataaa	atgaatacat	acataaggaa	2220
agataaaaaa	aaaagtttaa	tgaaagaata	cagtataaaa	caaactctct	ggacctaaaa	2280
gtatttttgt	tcaagccaaa	tattgtgaat	cacctctctg	tggtgaggat	acagaatatc	2340
taagcccagg	aaactgagca	gaaagtccat	gtactaacta	atcaaccoga	ggcaaggcaa	2400
aaatgagact	aactaatcaa	tccgaggcaa	ggggcaaat	agacgggaac	tgactctggg	2460
ctattaagcg	acaactttcc	ctctgttgta	tttttctttt	attcaatgta	aaaggataaa	2520
aactctctaa	aactaaaaac	aatgtttgtc	aggagttaca	aaccatgacc	aactaattat	2580
ggggaatcat	aaaatatgac	tgtatgagat	cttgatgggt	tacaaagtgt	acccactggt	2640
aatcacttta	aacattaatg	aacttaaaaa	tgaatttacg	gagattggaa	tgtttctttc	2700
ctgttgattt	agttggctca	ggctgccata	acaaaatacc	acagactggg	aggcttaagt	2760
aacagaaatt	cattttctcac	agttctgggg	gctggaagtc	cacgatcaag	gtgcaggaaa	2820
ggcaggcttc	attctgaggc	ccctctcttg	gctcacatgt	ggccaccctc	ccactgcgtg	2880
ctcacatgac	ctctttgtgc	tccctggaaa	agggtgtggg	ggacagaggg	aaagagaagg	2940
agagggaact	ctctggtgtc	togtctttca	aggaccctaa	cctggggccac	tttggcccag	3000
gcaactgtgg	gtgggggggt	gtggctgctc	tgctctgagt	ggccaagata	aagcaacaga	3060
aaaatgtcca	aagctgtgca	gcaaagacaa	gccaccgaac	agggatctgc	tcatcagtgt	3120
ggggacctcc	aagtcggcca	ccctggaggc	aagcccccam	agagcccatg	caagggtggca	3180
gcagcagaag	aagggaattg	tccctgtcct	tggcacattc	ctcaccgacc	tggtgatgct	3240
ggacactgcg	atgaatggta	atgtggatga	gaatatgatg	gactcccaga	aaaggagacc	3300
cagctgctca	ggtggctgca	aatcattaca	gccttcatcc	tggggaggaa	ctgggggcct	3360
ggttctgggt	cagagagcag	cccagtggag	gtgagagcta	cagcctgtcc	tgccagctgg	3420
atccccagtc	ccggtcaacc	agtaatcaag	gctgagcaga	tcaggcttcc	cggagctggg	3480
cttggggaagc	cagccctggg	gtgagttggc	tccctgctgtg	gtactgagac	aatattgtca	3540
taaattcaat	gcgcccttgt	atcccttttt	cttttttatc	tgtctacatc	tataatcact	3600
atgcatacta	gtctttgtta	gtgtttctat	tcmacttaat	agagatatgt	tatacttaaa	3660
aaaaaaaaaa	aaaa					3674

&lt;210&gt; 620

&lt;211&gt; 2051

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(2051)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 620

ggaccagggg	ctgaagtga	ccccagcac	agcacagctg	ctctataaaa	acgtggccag	60
actttttttt	ttgaagcaag	tccctgttct	tggttgcctc	gactagtccc	atcagggccc	120
tggatcccaa	gactcagcat	ccaaggtccc	ctccaggaat	cctggcagct	cagcatactt	180
tatcctgttt	catctgagag	caaaaatgta	aaattggatg	cacagaaaag	tgactcaaag	240
tgcttaatga	ctagaagaaa	tctaggagca	gcaagaagag	caggacaaac	aggccaggcg	300
gtgtcaggag	cccaggtctc	cagctggang	gaacgtcaac	cctgcagtgg	gagcaggggc	360
cctttgcaca	tccatggcac	agatggtaat	gtagacacca	caggtaagct	gggcttggtta	420
cctacccttc	cccgatttca	gaaagaaacc	aaacaaggag	ctttgtgtgg	aatgaaacct	480
cctttcctcc	cagaagcact	gctgaactgt	tggtggttgc	catttgtggc	agtgaacctt	540
tggttgttct	gaggttgggc	tggtttctcc	tcttggccct	gccctacaga	tcataaagga	600
gaacagcaag	acgtccccag	caaacatcca	cagatggcct	tggaaataag	tcaccttctt	660
cacctgcag	gaatgccagt	gaacatattg	ctgacatctt	ggagctcagt	acctcatagt	720
gtaacggcgt	cagtagatct	gcctgtgctg	ggacttccctg	tactacctat	tccatgagggg	780

cgatgcttct	gcagggcctg	tgacttgggtg	cacaacttca	gacaccatca	tcttgcagca	840
gcaccgcacc	ctcactagcc	aggggtgttg	tgacttcttc	aaggccaagg	ccacattcaa	900
ggcttcggac	ttcattgatg	cgcttgtgct	gagcaagggtg	gcttctccgg	gatcttaatt	960
caggaggtag	aatggagctt	gagatcaagt	gtctgatcaa	gcctcagtgt	atgggcgtg	1020
ttcatcctct	ggtgctgaag	cagccaagag	acccaagtct	gcctggctgc	ctcttaggat	1080
atgacagcag	agccagtggc	ctctactaga	tctgtacaa	cctcacaaaa	caccagaca	1140
tcgggagtgc	tgccagcctg	tgatgcaaga	gtcctaattcc	tgaagacatt	gaatgacctg	1200
tcgttgtgct	gtttttacca	aaaaggatca	tgaggatcag	agaggaaaag	tcacttgccc	1260
aaagtacacac	agctgaacag	tggtggagtt	caactttgac	cgtgggctgt	ctggcccca	1320
aggtgtatgc	ttgcttctct	cccaagagac	tcctttctta	tcaggctcaa	atgaatgaaa	1380
ggaggatgtt	aaagacaacg	ccattattga	cgagatcact	cccaagcggg	ttggagattg	1440
tcccaatatt	tagacctata	gcaaggcctt	gggagaaatg	gtggtgcagc	aggagagcag	1500
gaacctaac	attgccatcc	taaggccctc	cattgtgtgg	agcaacgtgg	caccagcttt	1560
tcctgggttg	ggttgataat	ctaaatggat	gtagccgact	cattattgcg	gtatgtatag	1620
ggatgaagaa	gtaactgtaa	tgtagtggag	gaatagtaag	aaaattctta	gtgctggctt	1680
agcttaattg	atccaaaaac	ataaatgcta	ctttactatc	aattgaagca	tattatttca	1740
attattctgg	ttataatatg	gaggcaggat	gaaattgttt	ttattctttt	agaatttttt	1800
tttatcagga	aaacagaggt	aaagtgtctat	caattactat	ttaagagttc	tattttgaaa	1860
agtgagaatt	aaggattttt	cttttctttt	taaaaaaaac	ttttttaaaa	attaaaaata	1920
aaagaagcaa	aagtcttagg	aaaatgaagc	aagtagccct	gccactctat	gtacagtaat	1980
aacaatatct	gtcccagtta	ttatgtacaa	tattataaaa	aatgtcgag	acagtaaaaa	2040
aaaaaaaaaa	a					2051

&lt;210&gt; 621

&lt;211&gt; 2841

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(2841)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 621

gcagagcaca	gcatagctgc	tttaccaaat	catggccaga	ctgcttctgt	aagcaggccc	60
ctgatcctgt	tccacctcac	tggacaggac	ctcccaactg	gggcctccag	ctacccccac	120
cagcatccct	tggccaatgg	aaatttgaaa	tgttcctggg	acagagctcc	tggagagagg	180
ggcaggccac	cacctttgct	gtttgggtga	ctagccgttc	tggcctgcag	gctttggaga	240
gcccagctg	acaaggggta	gaagagggtg	ctcagcacag	cacagccacg	ctacgaaaac	300
atggccagac	tcttgtttaa	gtcagtcctc	gaacacattt	ctagtcagtg	ggtgaagtct	360
ttcaaccagg	gtctctggct	accttgactg	ctgttctctg	gccgacagag	gtctcaggcc	420
tccctgagtc	agagctcccg	gggggaggac	cagattgtca	tctttgctgt	ttgggtgacc	480
cagccatttc	agccttaggg	cttcagagtg	tctgaggtag	ccaggggctg	aagtgaaccc	540
ccagcacagc	acagctgctg	tataaaaacg	tggccagact	ttttctttta	gcaagtccct	600
gttcttattc	ctcctgacta	ggtaagactt	ctcaacttgc	ctccagccac	atcttattgg	660
tgtgttcaga	ttggcaacag	gtttgtacct	cagtggtaga	gagctcccag	aggaaggggt	720
aggctatcat	cttccctgga	aaatacagag	caattagggg	cttgagggga	ccccagcat	780
tccacagcag	cccttcagaa	aagtggccag	actctgtact	tgatgggcag	atcctcctgg	840
cctgtgtctc	tagccagccc	accactggag	ctatcaagcc	agtagcaact	cagcagttcc	900
ttggacagag	cttcaggag	caaatagaat	cctttctgcc	actgcctttg	cagtgaactg	960
cccttgctat	cctcagaaga	tatatcacgg	gagcaaagac	cctaagtgcc	atatcaacac	1020
ctccaataag	ctgcagttga	cccaaagaac	aagccaatcc	atctcccaca	ggttccacac	1080
acactccact	actcatcacc	agacagggaa	ccctggcttg	ggcccacagc	acagaccctc	1140
catcctgggc	cgattacact	gagtgattgc	taactcacat	gtctctggga	tggagcacc	1200
aggagacaag	caaagtgggtg	gagcagcaag	tcagggtgatg	tggagcccag	agggcaggga	1260
gagctatctc	tctgggctcc	acttgccctt	gtgagacact	ttgtccagc	actccttagt	1320
ctgcttgctc	ctcccagggc	cccagcctgg	ccacacctgc	ttacagggca	ctctcagatg	1380
cccataccat	agtttctgtg	ctagtggacc	gtaccatata	agtggagagc	tgcagcaagg	1440

tggcccntac	ggccacgcac	cagcctgcac	attacctctc	catactgcag	ccctttatat	1500
ggaaacttcc	tacatcactt	tgtgtgtgt	gtttacacag	gtggattttg	ctttacttgc	1560
actgacagca	cacaggaggg	cagcacacac	cccaaccac	atcaactgcc	attaaagaaa	1620
agaaatttca	gcccataaatt	tcatgtccag	caaaattagg	catcataagt	gaaggagaaa	1680
taagatcctt	ttcagacaag	caaagtctga	gggaattcaa	tatcaccaga	tctaccttac	1740
aagagctcct	gaaggaagca	ctaaatatgg	aaagaaaaaa	ccatcaccag	ccactacaaa	1800
aatgcagtga	agaacgcagt	gaattacgca	gtccagtgat	gctaaaaacc	aaccacatac	1860
gttaagtctg	caaaataaacc	agctgacagc	atgacgacag	gataaatcca	cacataccat	1920
tactaacctt	aaatgaaaat	gggctaaatg	ctccattga	aagacatggg	gcaagctgga	1980
taaagaacca	agaccactg	gagtatgctg	tcttcaagaa	acccatctca	catgcggtgg	2040
catacatagg	ctcaaaataa	aggaatggag	aaaaatattt	caagcaaattg	gaaaacagaa	2100
aaaagcaggt	gttgcactcc	tactttctga	caaaacagac	tatgccaata	aagataaaaa	2160
agagaaggac	attacaaagg	tggtcctgac	ctttgatata	tctcattgct	tgataccaac	2220
ctgggctgtt	ttaattgccc	aaanccaata	ggataatttg	ctgaggttgt	ggagcttctc	2280
ccctgcagag	agtccctgat	ctcccaaaat	ttggttgaga	tgtaaggttg	attttgctgt	2340
acaactcctt	ttctgaagtt	ttactcattt	ccaaaaagga	aggcaagttt	tcctgcttcc	2400
atgacgatgg	agagcaggca	tctcctttcc	tgagtttcag	cttgcttctg	acagggaagg	2460
tgagtgttaag	ttttttccag	cttctaagat	ggcagagaac	gatcaccagc	ctgagcctta	2520
tttccaggta	agtagctgaa	ttagagtttt	gtcttaaaat	tttcccttaa	tgattaaaat	2580
gtaagattac	ccaccagctg	cttttaattt	ctcccttagc	attagaacac	tcagtaatca	2640
tatgaattgt	gcatttgttt	gttttgctta	actctttctg	tttggttatg	tttggggttt	2700
tattgttggt	gtttcacttt	tctcccatct	cttcctgact	tgggtcaaata	caaaggaatg	2760
ttcgaaattg	tggggagcaa	ggcatctgaa	atggctaaaa	ctcctgtggc	tgcaaaaaat	2820
agaaataaaa	aaaaaaaaaa	a				2841

&lt;210&gt; 622

&lt;211&gt; 3228

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(3228)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 622

tccgccccat	tgacgcaaat	ggcggtaggc	gtgtacggtg	ggaggtctat	ataagcagag	60
ctctcnggct	aactagagaa	cccactgctt	actggcttat	cgaaattaat	acgactcact	120
ataggagagc	ccaagctggc	tagcgtttaa	acttaagctt	ggtaccgagc	tcggatccac	180
tagtcagtg	tgggtggaatt	ccattgtgtt	gggcaggaaa	caagcaaagt	ggtggagcag	240
caagtcaggt	gatgtggagc	ccagaggtca	gggatggctg	tctctctagg	gtccacttgc	300
ccttgtgaga	cactttatcc	cagcacttta	ggaatactga	ggtcatacca	gccacatctt	360
atatgcaaga	ttgccagca	gagatcaggt	ccgagagttc	cctttttaaa	aaaaggagac	420
ttgcttaata	aaagaagtct	agccacgttt	gtgtagagcg	gctgtgctgt	gctgggggtt	480
cacttttgag	agagttctcc	tctgagacct	gatctctgga	ggctgggcaa	tcttgcaactt	540
gagatggggc	tgggtctgatc	tcagcactcc	ttagtctgct	cgcctctccc	atggccccag	600
cctggccaca	cctgcttacg	gggcactctt	agatgcccac	accataactt	ccatgctagt	660
ggactgtacc	atatcagtgg	agagctgcag	caaggtggcc	cctagagcca	cgcaccagcc	720
tgcacattgc	ctctccatac	ggcagccctt	tatttggaat	cttcctaaat	cactttgctg	780
tgtgtgttta	caagggtgtg	ttttgcttta	cttgccctga	gagcacacgg	gagtgcagca	840
cacaccccaa	cccacatcaa	ctgccattaa	agaaaagaaa	tttcagccca	gaatttcagt	900
tccagcaaaa	ttaagcatca	taagtgaagg	agaaataaga	tccttttcag	acaagcaagt	960
gctgagggaa	tttgggtatca	ccagatctac	cttacgagag	ctcctgaagg	aagcactaaa	1020
tatggaaaga	aaagatcatc	acctgctact	acaaaaacac	actgaagtac	acagtccaat	1080
gatgctaaaa	agcaagcaca	tatgtaagtc	tgcaaaataa	ccagctgaca	gcatgcagac	1140
aggataaaat	ccacacatac	cattactaac	cttaaatgta	aatgggctaa	atgctcccat	1200
tgaaagacac	ggggcaagct	gggtaaagaa	ccaagaccca	ctggagtatg	ccgtcttcaa	1260
gcaacccatc	tcacgtgcag	tgccatacat	aggctcaaaa	ttaaggaatg	gagaaaaata	1320

tttcaagcaa	atggaaaaca	gaaaaaaggt	gttgcactcc	cagtttctga	caaaacagac	1380
tctaccaata	aagataaaaa	aagagaagga	cattacaaag	gtggctctga	cctttgataa	1440
atctcattat	tgcttgatac	caacctgggc	tatttgattt	gccccaaag	ataggataat	1500
ttgctgaggt	tgtggagctt	ctccccttca	cagagtcctt	gatctccgaa	aatttggttg	1560
agatgtaagg	ttgattttgc	tgtacaactc	cttttttgaa	gttttactca	tttccaacaa	1620
ggaaggcaag	ttttcctgct	tccattgaca	aaggagagca	ggcacctcct	ttcctgagtt	1680
tcagcttgct	tctgacaggg	aaggagcttt	gagatttgaa	tactggcctg	ctgggttttg	1740
gacgtgcatt	gggcctgtgg	tcccatttgt	gttatttttc	tgggaaattt	cttccctttg	1800
gagtgaagaa	gcttacccaa	tgctgttacc	atcatcgtag	cttaaaagaa	ctccatttta	1860
agttcagggg	ctccttgcca	gaagagaccg	tagccttgta	tcagatcata	aaggagaaga	1920
gcaagaggtc	cccggaacac	atccacagat	ggccttgga	ataagtcacc	ttgctcacc	1980
tgcaggaatg	ccagtgaact	tattgctgac	atcttggagc	tcagtaccct	catagtgtaa	2040
cggcgctcagc	agatctgcct	gtgctgggac	ttcctgtact	acccattcct	gaggggagat	2100
gcttctgcag	ggcctgtgac	ttggtgcaca	acttcagaca	ccatcatctt	gcagcagcac	2160
cgcaccctca	ctagccaggg	tggtgatgac	ttcctcaagg	ccaaggccac	attcaaggct	2220
tcggacttca	ttgatgcgct	tgtgctgagc	aagggtgctt	ctccgggagc	tttaattcagg	2280
aggtagaatg	gagcttgaga	tcaagtgtct	gatcaagcct	cagtgtatgg	gcgctgttca	2340
tcntctggtg	ctgaagcagc	caagagaccc	aagtctgcct	ggctgcntct	taggatatga	2400
cagcagagcc	agtggcctct	actagatcct	gtacaacctc	acaaaacacc	cagacatcgg	2460
gagtgtctgc	agcctgtgat	gcaagagtc	taatcctgaa	gacattgaat	gacctgtcat	2520
tctgctgttt	ttacccaaaa	ggatcatgag	gatcagagag	gaaaagtcac	ttgccccaaag	2580
tcacacagct	gaacagtggg	ggagttcaac	tttgaccgtg	ggctgtctga	ccccaaagtg	2640
tatgcttgct	tctctcccaa	gagacaactt	tcttatcagg	ctcaaatgaa	tgaaaggagg	2700
atgttaaagg	taggatctct	gaagcctgtg	ccagtggaa	cgcagctcat	ggctggcacc	2760
tgtgttctca	ttcttacctc	attaagagta	aagtttattg	agtttattga	atttaagtat	2820
ctttagttag	atcatatatt	attagtaaga	actgggacca	aacagatttt	ctgactctaa	2880
aagagagatt	ttcacagaaa	cagatatata	cctgtaagta	tacagacacg	catacacaca	2940
tttctttact	gctcataaaa	attagtcctt	attagaatgt	gggatgtata	aatgtaagag	3000
aattttcatg	ttaaaattga	cagatacatt	tttaaattgt	cctaaaataa	atttaattat	3060
ttttntttta	gaattttcca	ttattaatgt	tatttttatg	agaaactata	taactttatt	3120
gataatacat	acaataaccc	tttgtttttc	aaattgaaaa	tacagtgtat	tttgcaaata	3180
actaagtcct	aattttgtat	taaaatttta	aattttcaaa	aaaaaaaa		3228

&lt;210&gt; 623

&lt;211&gt; 4894

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 623

ctgcacgcgc	tggtctccggg	tgacagccgc	gcgccctcggc	caggatctga	gtgatgagac	60
gtgtccccac	tgaggtgccc	cacagcagca	ggtgttgagc	atgggctgag	aagctggacc	120
ggcaccaaaag	ggctggcaga	aatgggcgcc	tggtgatctc	ctaggcagtt	ggcggcagca	180
aggaggagag	gccgcagctt	ctggagcaga	gccgagacga	agcagttctg	gagtgcctga	240
acggccccct	gagccctacc	cgcctggccc	actatggtcc	agaggctgtg	ggtgagccgc	300
ctgctgcggc	accggaaagc	ccagctcttg	ctggtcaacc	tgctaacctt	tgccctggag	360
gtgtgttttg	ccgcaggcat	cacctatgtg	ccgcctctgc	tgttggaagt	gggggtagag	420
gagaagttca	tgaccatggt	gctgggtgag	tcactacatc	ctccttcctt	cctgttccag	480
atacatgcc	cctggcatgt	gggacaggag	tacctctgcc	ctgggagctg	cttggaggga	540
gaggtggtct	gctgggaagg	cattgctggg	caggaggggtg	accctgggct	gagggggcac	600
accaagagaa	agaagagaat	accaaggaca	tacccagctc	acctctggat	ccctggctct	660
gcacagagcc	tggtcatatg	gagacactgg	agaaatgctc	ctaacctttg	gctagccctt	720
ttataattta	tagcgattat	ctcatttaat	gcttacaacc	accatttgag	gtgatccatt	780
ttacagagaa	ggaagcagag	gcttttaaga	ggttaggtaa	gtcttagcca	aagccaaata	840
gcagctgaac	agtagagctg	ggactccatc	aaggtctccc	agccggagct	tgctccctac	900
cctaggacaa	ggggtggact	cctgactctg	cagataaatt	ctacaaaagc	cacagaaggc	960
aagtagtaac	cattgtgtga	caaccctca	ccccaggaa	gagggggccc	tgtagaggatt	1020
gcaggctctg	gagtcacact	gcttgttgaa	acgctgcctc	ttaccctccc	taggtctgag	1080

```

cctttgaata agtatcactt cttagttgct ccatgcctca gtttgtccat ctgaaaatgg 1140
gggcatctgt aatgcctgtg ttatgaggag taaattacag catccctgtg aagacgtagc 1200
acagtgtcga gtaocggaatg ttatttccat ccttctcagc gagcttggtt ccccttcccc 1260
ttgcccttta cttgtcccag ccattgactc atactacttc ccttcttgca ggcattggtc 1320
cagtgtcggg cctgggtctgt gtcccgtccc taggctcagc cagtgaccac tggcgtggac 1380
gctatggccg ccgcccggccc ttcactctggg cactgtcctt gggcatcctg ctgagcctct 1440
ttctcatccc aaggggccggc tggctagcag ggctgctgtg cccggatccc agggccctgg 1500
agctggcact gctcatcctg ggcgtggggc tgcgtggactt ctgtggccag gtgtgcttca 1560
ctccactgga ggccctgctc tctgacctct tccgggaccc ggaccactgt cgccaggcct 1620
actctgtcta tgccttcatg atcagtcttg ggggctgcct gggctacctc ctgcctgcca 1680
ttgactggga caccagtgcc ctggcccccct acctgggcac ccaggaggag tgcctctttg 1740
gcctgctcac cctcatcttc ctacacctgc tagcagccac actgctgggtg gctgaggagg 1800
cagcgtcggg ccccaccgag ccagcagaag ggctgtcggc cccctccttg tcgccccact 1860
gctgtccatg ccggggccgc ttggctttcc ggaacctggg cgccctgctt ccccggtgc 1920
accagctgtg ctgccgcatg ccccgccccc tgcgcccgtt cttcgtggct gagctgtgca 1980
gctggatggc actcatgacc ttacgctgt tttacacgga tttcgtggg gaggggctgt 2040
accagggcgt gccagagct gagccgggca ccgaggcccg gagacactat gatgaagta 2100
aggccttggc agccagcaga ggctgggtgt ggagccgccc accagagacg acactcgggg 2160
ctgtgtcttg gctgggtgct ctccatcctg gccccgactt ctctgtcagg aaagtgggga 2220
tggaccccat ctgcatacac ggcttctcat ggggtgtgga catctctgct tgcggtttca 2280
ggaaggcctc tggctgctct aggagtctga tcagagtcgt tgcctcagtt tgacagaagg 2340
aaaggcggag cttattcaaa gtctagagg agtggaggag ttaaggctgg atttcagatc 2400
tgcttggttc cagccgcagt gtgcctctg ctcccccac gactttccaa ataatctcac 2460
cagcgccttc cagctcaggc gtccctagaag cgtcttgaag cctatggcca gctgtctttg 2520
tgctccctct caccgcctg tccctacagc tgagactccc aggaaacctt cagactacct 2580
tcctctgcct tcagcaagg gcgttgccca cattctctga gggtcagtgg aagaacctag 2640
actcccattg ctagaggtag aaaggggaag ggtgctgggg agcagggtgt gtccacagca 2700
ggctctcgtg agcaggtacc tgtggttccg ccttctcatc tccctgagac tgctccgacc 2760
cttccctccc aggtctgtct tgatggcccc tctccctctg caggcgttcg gatgggcagc 2820
ctggggctgt tcctgcagtg cgccatctcc ctggtcttct ctctggtcat ggaccggctg 2880
gtgcagcgat tcggcactcg agcagtctat ttggccagtg tggcagcttt ccctgtggct 2940
gccggtgcca catgcctgtc ccacagtgtg gccgtggtga cagcttcagc cgccctcacc 3000
gggttcacct tctcagccct gcagatcctg ccctacacac tggcctccct ctaccaccgg 3060
gagaagcagg tgttcctgcc caaataccga ggggacactg gaggtgctag cagtaggagc 3120
agcctgatga ccagcttctt gccaggccct cctcctggag ctcccttccc taatggacac 3180
gtgggtgyt gaggcagtgg cctgctccca cctccacccg cgctctgcgg ggcctctgcc 3240
tgtgatgtct ccgtacgtgt ggtgggtggg gagccaccg aggccagggt ggttccgggc 3300
cggggcatct gccctggacct cgccatcctg gatagtgcct tcctgctgtc ccagggtggc 3360
ccatccctgt ttatgggctc cattgtccag ctccagcagt ctgtcactgc ctatatggtg 3420
tctgcgcag gcctgggtct ggtcgccatt tactttgcta cacaggtagt atttgacaag 3480
agcgacttg ccaaatactc agcgtagaaa acttccagca cattgggggt gagggcctgc 3540
ctcactgggt ccagctccc tgctcctgtt agcccatgg ggctgccggg ctggccgcca 3600
gtttctgttg ctgccaaagt aatgtggctc tctgctgcca ccctgtgctg ctgagggtgcg 3660
tagctgcaca gctgggggct ggggcgtccc tctcctctct cccagctctc tagggctgcc 3720
tgactggagg ccttccaagg ggggttcagt ctggacttat acagggaggc cagaagggtc 3780
ccatgcactg gaatgcgggg actctgcagg tggattacco aggtcagggt ttaacagcta 3840
gcctcctagt tgagacacac ctagagaagg gtttttgga gctgaataaa ctcagtcacc 3900
tgggttccca tctctaagcc ccttaacctg cagcttcgtt taatgtagct cttgcatggg 3960
agtttctagg atgaaacact ccaccatggg atttgaacat atgaaagtta tttgtagggg 4020
aagagtccct aggggcaaca cacaagaacc aggtccctc agcccacagc actgtctttt 4080
tgctgatcca cccctctctt accttttctc aggatgtggc ctggttggtc ttctggtgac 4140
atcacagaga cacaggcatt taaatattta acttatttat ttaacaaagt agaagggaat 4200
ccattgctag cttttctgtg ttggtgtcta atatttgggt aggggtgggg atcccaaca 4260
atcagggtccc ctgagatagc tggtcatttg gctgatcatt gccagaatct tcttctcctg 4320
gggtctggcc ccccaaatg cctaaccagg gaccttgaa atttactca tcccaaatga 4380
taattccaaa tgtgttacc caaggttagg gtgttgagg aaggtagagg gtggggcttc 4440
aggtctcaac ggcttcccta accacccctc ttctcttggc ccagcctggg tcccccaact 4500
tccactcccc tctactctct ctaggactgg gctgatgaag gcactgcca aaatttcccc 4560

```

```

tacccecaac tttccctac ccccaacttt ccccaccagc tccacaaccc tgtttggagc 4620
tactgcagga ccagaagcac aaagtgcggt ttcccaagcc tttgtccatc tcagcccca 4680
gagtatatct gtgcttgggg aatctcacac agaaactcag gagcaccccc tgcctgagct 4740
aagggagggtc ttatctctca ggggggggtt aagtgcggt tgcaataatg tcgtcttatt 4800
tatttagcgg ggtgaatatt ttatactgta agtgagcaat cagagtataa tgtttatggt 4860
gacaaaatta aaggctttct tatatgttta aaaa 4894

```

&lt;210&gt; 624

&lt;211&gt; 2904

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 624

```

gtctatgcct tcatgatcag tcttgggggc tgcctgggct acctcctgcc tgcattgac 60
tgggacacca gtgcctggc cccctacctg ggcacccagg aggagtgcct ctttggcctg 120
ctcaccctca tcttctcac ctgcgtagca gccacactgc tgggtggctga ggaggcagcg 180
ctgggccccca ccgagccagc agaagggctg tcggccccct ccttgtcgcc cactgctgt 240
ccatgccggg cccgcttggc tttccggaac ctgggcgccc tgcctccccg gctgcaccag 300
ctgtgctgcc gcatgccccg caccctgcgc cggtcttctg tggctgagct gtgcagctgg 360
atggcactca tgacctcac gctgttttac acggatttctg tgggcgaggg gctgtaccag 420
ggcgtgcccc gagctgagcc gggcaccgag gcccgagac actatgatga aggaaggcct 480
ctggctgctc taggagtctg atcagagtctg ttgccccagt ttgacagaag gaaaggcgga 540
gcttattcaa agtctagagg gagtggagga gttaaaggctg gatttcagat ctgcctggtt 600
ccagcccgag tgtgccctct gctcccccaa cgactttcca aataatctca ccagcgctt 660
ccagctcagg cgtcctagaa gctcttgaa gcctatggcc agctgtcttt gtgttccctc 720
tcaccgcctc gtcctcacag ctgagactcc caggaaacct tcagactacc ttctctgcc 780
ttcagcaagg ggcgttgccc acattctctg agggcgcttg gatggcagc ctggggctgt 840
tctgacgtg cgccatctcc ctggtcttct ctctggctat ggaccggctg gtgcagcgat 900
tcggcactcg agcagtctat ttggccagtg tggcagcttt cctgtggct gccggtgcca 960
catgcctgtc ccacagtgtg gccgtggtga cagcttcagc cgccctcacc ggggtcacct 1020
tctcagccct gcagatcctg ccctacacac tggcctccct ctaccaccgg gagaagcagg 1080
tgttctgcc caaataaccga ggggacactg gaggtgctag cagtgaggac agcctgatga 1140
ccagcttccct gccaggccct aagcctggag ctcccttccc taatggacac gtgggtgctg 1200
gaggcagtgg cctgctccca cctccaccgg cgctctgcgg gcctctgcc tgtgatgtct 1260
ccgtacgtgt ggtggtgggt gagcccaccg aggcagggt ggttccgggc cggggcatct 1320
gcctggacct cgccatcctg gatagtgcct tctgtctgtc ccaggtggcc ccatccctgt 1380
ttatgggtc cattgtccag ctccagcagt ctgtcactgc ctatatggtg tctgcccgag 1440
gcctgggtct ggtcgccatt tactttgcta cacaggtagt atttgacaag agcagacttg 1500
ccaaatactc agcgtagaaa acttccagca cattggggtg gagggcctgc ctcaactggg 1560
cccagctccc cgctcctgtt agccccatgg ggctgcggg ctggccgcca gtttctgttg 1620
ctgcccgaagt aatgtggctc tctgctgcca ccctgtgctg ctgaggtgcg tagctgcaca 1680
gctgggggct ggggcgtccc tctcctctct cccagctctc tagggctgcc tgactggagg 1740
ccttccaagg ggttttcagt ctggacttat acagggaggc cagaagggt ccatgcaactg 1800
gaatgcggg actctgcagg tggattacc aggtcagggt ttaacageta gcctcctagt 1860
tgagacacac ctagagaagg gtttttggga gctgaataaa ctcagtcacc tggtttccca 1920
tctctaagcc ccttaacctg cagcttctgt taatgtagct cttgcatggg agtttctagg 1980
atgaaacact cctccatggg atttgaacat atgaaagtta tttgtagggg aagagtccctg 2040
aggggcaaca cacaagaacc aggtccctc agcccacagc actgtctttt tgctgatcca 2100
ccccctctt accttttatc aggatgtggc ctgttgggtc ttctgttgcc atcacagaga 2160
cacaggcatt taaatattta acttatttat ttaacaaagt agaagggaat ccattgctag 2220
cttttctgtg ttggtgtcta atatttgggt aggggtgggg atccccaca atcaggtccc 2280
ctgagatagc tggtcattgg gctgatcatt gccagaatct tcttctcctg gggctcggcc 2340
cccaaatg cctaaccag gacottggaa attctactca tcccaaatga taattccaaa 2400
tgctgttacc caaggtagg gtgttgaagg aaggtagagg gtggggcttc aggtctcaac 2460
ggcttcccta accaccctc ttctcttggc ccagcctggt tccccact tccactcccc 2520
tctactctct ctaggactgg gctgatgaag gcactgccc aaatttccc tacccecaac 2580
tttccctac ccccaacttt ccccaccagc tccacaaccc tgtttggagc tactgcagga 2640

```

```

ccagaagcac aaagtgcggt ttcccaagcc tttgtccatc tcagccccca gagtatatct 2700
gtgcttgggg aatctcacac agaaactcag gagcaccccc tgccctgagct aaggagggtc 2760
ttatctctca gggggggttt aagtgccgtt tgcaataatg tcgtcttatt tatttagcgg 2820
gggtaatat ttatactgta agtgagcaat cagagtataa tgtttatggt gacaaaatta 2880
aaggctttct tatatgttta aaaa 2904

```

&lt;210&gt; 625

&lt;211&gt; 4034

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 625

```

aaccagcctg cagcgctggt ctccgggtga cagccgcgcg cctcggccag gatctgagtg 60
atgagacgtg tccccactga ggtgccccac agcagcaggt gttgagcatg ggctgagaag 120
ctggaccggc accaaagggc tggcagaaat gggcgccctg ctgattccta ggcagttggc 180
ggcagcaagg aggagaggcc gcagcttctg gagcagagcc gagacgaagc agttctggag 240
tgccctgaacg gccccctgag cctaccgcgc ctggcccact atggtccaga ggctgtgggt 300
gagccgcctg ctgcggcacc ggaaagccca gctcttgctg gtcaacctgc taacctttgg 360
cctggagggtg tgtttggccg caggcatcac ctatgtgccg cctctgctgc tggaaagtggg 420
ggtagaggag aagttcatga ccatgggtgct gggcattggt ccagtgtctg gcctggtctg 480
tgtcccgctc ctaggctcag ccagtgaaca ctggcgtgga cgtctatggc gccgcccggc 540
cttcatctgg gcaactgtct tgggcatact gctgagcctc tttctcatcc caagggcccg 600
ctggctagca gggctgctgt gcccgatcc caggcccctg gagctggcac tgctcatcct 660
gggctggtgg ctgctggact tctgtggcca ggtgtgcttc actccactgg aggccctgct 720
ctctgacctc ttccgggacc cggaccactg tcgccaggcc tactctgtct atgccttcat 780
gatcagttct gggggctgcc tgggctacct cctgcctgcc attgactggg acaccagtgc 840
cctggccccc tacctgggca cccaggagga gtgcctcttt ggccctgctc ccctcatctt 900
cctcacctgc gtagcagcca cactgctggt ggctgaggag gcagcgtggt gccccaccga 960
gccagcagaa gggctgtcgg cccctcctt gtgcgccac tgctgtccat gccgggcccg 1020
cttggtcttc cggaacctgg ggcctctgct tccccggctg caccagctgt gctgccgcct 1080
gccccgcacc ctgcgcgggc tottctgtgg tgagctgtgc agctggatgg cactcatgac 1140
cttcacgctg ttttacacgg atttctgtgg cgaggggctg taccaggcg tgcccagagc 1200
tgagccgggc accgaggccc ggagacacta tgatgaaggt aaggccttgg cagccagcag 1260
aggctggtgt gggagccgcc caccagagac gacactggg gctgtgtctg ggctgtgccc 1320
tctccatcct ggccccgact tctctgtcag gaaagtggg atggaccca tctgcataca 1380
cggcttctca tgggtgtgga acatctctgc ttgcggtttc aggaaggcct ctggctgctc 1440
taggagtctg atcagagtgc ttgccccagt ttgacagaag gaaaggcgga gcttattcaa 1500
agtctagagc gagtggagga gttaaggctg gatttcagat ctgcctggtt ccagccgcag 1560
tgtgccctct gctcccccaa cgactttcca aataatctca ccagcgctt ccagctcagg 1620
cgtcctagaa gcgtcttgaa gcctatggcc agctgtcttt gtgttccctc tcaccgcct 1680
gtcctcacag ctgagactcc caggaaacct tcagactacc ttcctctgcc ttcagcaagg 1740
ggcgttgccc acattctctg agggtcagtg gaagaaccta gactccatt gctagaggta 1800
gaaaggggaa ggggtgctgg gagcagggct ggtccacagc aggtctctgt cagcaggtac 1860
ctgtggttcc gccttctcat ctccctgaga ctgctccgac ccttccctcc caggctctgt 1920
ctgatggccc ctctccctct gcaggcgttc ggatgggag cctggggctg ttcctgcagt 1980
gcgccatctc cctggtcttc tctctggtca tggaccggct ggtgcagcga ttcggcactc 2040
gagcagtcta tttggccagt gtggcagctt tccctgtggc tgccggtgcc acatgcctgt 2100
cccacagtgt ggccgtggtg acagcttcag ccgccctcac cgggttcacc ttctcagccc 2160
tgagatcct gccctacaca ctggcctccc tctaccaccg ggagaagcag gtgttctctg 2220
ccaaataccg aggggacact ggaggtgcta gcagtgagga cagcctgatg accagcttcc 2280
tgccaggccc taagcctgga gctcccttcc ctaatggaca cgtgggtgct ggaggcagt 2340
gcctgtctcc acctccacc gcgctctgct gggcctctgc ctgtgatgtc tccgtacgtg 2400
tgggtgtggg tgagcccacc gaggccaggg tggttccggg ccggggccatc tgccctggacc 2460
tcgccatcct ggatagtgcc ttcctgctgt cccaggtggc cccatccctg tttatgggct 2520
ccattgtcca gctcagccag tctgtcactg cctatatggt gtctgccgca ggcctgggtc 2580
tggctgccat ttaacttctg acacaggtag tatttgacaa gagcgacttg gccaaatact 2640
cagcgtagaa aacttccagc acattggggt ggagggcctg cctcactggg tcccagctcc 2700

```

```

ccgctcctgt tagcccatg gggctgccgg gctggccgcc agtttctgtt gctgccaaag 2760
taatgtggct ctctgctgcc accctgtgct gctgaggtgc gtagctgcac agctgggggc 2820
tggggcgtcc ctctcctctc tccccagtcct ctagggctgc ctgactggag gccttccaag 2880
ggggtttcag tctggactta tacagggagg ccagaagggc tccatgcact ggaatgcggg 2940
gactctgcag gtggattacc caggctcagg gttaacagct agcctcctag ttgagacaca 3000
cctagagaag ggtttttggg agctgaataa actcagtcac ctggtttccc atctctaagc 3060
cccttaacct gcagcttcgt ttaatgtagc tcttgcatgg gagtttctag gatgaaacac 3120
tcctccatgg gatttgaaca tatgaaagtt atttgtaggg gaagagtcct gaggggcaac 3180
acacaagaac caggccccct cagcccacag cactgtcttt ttgctgatcc acccccctct 3240
taccttttat caggatgtgc ctgttggtcc ttctgttgcc atcacagaga cacaggcatt 3300
taaataattta acttatttat ttaacaaagt agaagggaat ccattgctag cttttctgtg 3360
ttgggtgcta atatttgggt aggggtgggg atccccaaca atcagggtccc ctgagatagc 3420
tggtcattgg gctgatcatt gccagaatct tcttctcctg ggggtctggcc ccccaaaatg 3480
cctaaccag gaccttgga attctactca tcccaaata taattocaaa tgcgtgttacc 3540
caaggtagg gtgttgaagg aaggtagagg gtggggcttc aggtctcaac ggcttcccta 3600
accacccctc ttctcttggc ccagcctggg tcccccaact tccactcccc tctactctct 3660
ctaggactgg gctgatgaag gcactgccca aaatttcccc taccoccaa tttccctac 3720
ccccacttt cccaccagc tccacaacct tgtttgagc tactgcagga ccagaagcac 3780
aaagtgcggg ttcccaagcc tttgtccatc tcagcccca gagtatatct gtgcttgggg 3840
aatctcacac agaaactcag gagcaccccc tgctgagct aaggagggtc ttatctctca 3900
ggggggggtt aagtgccgtt tgcaataatg tcgtcttatt tatttagcgg ggtgaatatt 3960
ttatactgta agtgagcaat cagagtataa tgtttatggt gacaaaatta aaggctttct 4020
tatatgttta aaaa 4034

```

&lt;210&gt; 626

&lt;211&gt; 6976

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 626

```

gaagctggac cggcaccaaa gggctggcag aaatgggcgc ctggctgatt cctaggcagt 60
tgggcgagc aaggaggaga ggccgcagct tctggagcag agccgagacg aagcagttct 120
ggagtgcctg aacggccccc tgagccctac ccgcctggcc cactatggtc cagaggctgt 180
gggtgagccg cctgctgcgg caccgaaaag ccagctctt gctggtcaac ctgctaacct 240
ttggcctgga ggtgtgtttg gccgcaggca tcacctatgt gccgcctctg ctgctggaag 300
tgggggtaga ggagaagttc atgacctgg tgctgggtga gtcactacat cctccttctc 360
tcctgttcca gatacatgcc acctggcatg tgggacagga gtacctctgc cctgggagct 420
gcttgagggg agaggtggtc tgctgggaag gcattgctgg gcaggagggt gaccctgggc 480
tgagggggca caccaagaga aagaagagaa taccaaggac ataccacagt cacctctgga 540
tccttggctc tgcacagagc ctggctcata ggagacactg gagaaatgct cctaaccttt 600
ggctaggcct tttataattt atagcgatta tctcatthaa tgcttacaac caccatttga 660
ggtgatccat tttacagaga aggaagcaga ggcttttaag aggttaggta agtcttagcc 720
aaagccaaat agcagctgaa cagtagagct gggactccat caaggtctcc cagccggagc 780
ttgctoctac ccctaggaca aggggtggac tcctgactct gcagataaat tctacaaaag 840
ccacagaagg caagtagtaa ccattgtgtg acaaccctc acccccagga agagggggcc 900
ctgtgaggat tgcaggctct ggagtcacac tgcttgttga aacgctgcct cttaccctcc 960
ctaggctctg gcctttgaat aagtatcact tmtttagttg tccatgcctc agtttgtcca 1020
tctgaaaatg ggggcatctg taatgcctgt gttatgagga gtaaattaca gcatccctgt 1080
gaagacgtag cacagtgtcg agtacggaat gttatttcca tccttctcac ggagcttggg 1140
tccccttccc cttgcccttt acttgtccca gccattgact catactactt cccttcttgc 1200
aggcattggg ccagtgtctg gcctggtctg tgtcccgctc ctaggctcag ccagtacca 1260
ctggcggtga cgctatggcc gccgcgggcc ctctcatctg gcaactgtct tgggcatcct 1320
gctgagcctc tttctcatcc caaggcgccg ctggctagca gggctgctgt gcccgatcc 1380
caggccctg gagctggcac tgetcatcct gggcgtgggg ctgctggact tctgtggcca 1440
ggtgtgcttc actccactgg aggccctgct ctctgacctc ttccgggacc cggaccactg 1500
tcgccaggcc tactctgtct atgccttcat gatcagtcct gggggctgcc tgggctacct 1560
cctgcctgcc attgactggg acaccagtgc cctggccccc tacctgggca cccaggagga 1620

```



gtgcctctttt	ggcctgctca	ccctcatctt	cctcacctgc	gtagcagcca	cactgctggt	1680
ggctgaggag	gcagcgctgg	gccccaccga	gccagcagaa	gggctgtcgg	ccccctcctt	1740
gtcgccccac	tgctgtccat	gccgggccccg	cttggtcttc	cggaacctgg	gcgccctgct	1800
tccccggctg	caccagctgt	gctgccgcat	gccccgcacc	ctgcgccggc	tcttcgtggc	1860
tgagctgtgc	agctggatgg	cactcatgac	cttcacgctg	ttttacacgg	atttcgtggg	1920
cgaggggctg	taccagggcg	tgcccagagc	tgagccgggc	accgaggccc	ggagacacta	1980
tgatgaagg	aaggccttgg	cagccagcag	aggctggtgt	gggagccgcc	caccagagac	2040
gacactcggg	gctgtgtctg	ggctggtgcc	tctccatcct	ggccccgact	tctctgtcag	2100
gaaagtgggg	atggacccca	tctgcataca	cggcttctca	tgggtgtgga	acatctctgc	2160
ttgcggtttc	aggaaggcct	ctggctgctc	taggagtctg	atcagagtcg	ttgccccagt	2220
ttgacagaag	gaaaggcgga	gcttattcaa	agtctagagg	gagtggagga	gttaaggctg	2280
gatttcagat	ctgcctggtt	ccagccgcag	tgtgccctct	gctcccccaa	cgactttcca	2340
aataatctca	ccagcgctt	ccagctcagg	cgctcctaga	gcgtcttgaa	gcctatggcc	2400
agctgtcttt	gtgttccctc	tcacccgcct	gtcctcacag	ctgagactcc	caggaaacct	2460
tcagactacc	ttcctctgcc	ttcagcaagg	ggcgttgccc	acattctctg	agggtcagt	2520
gaagaacct	gactcccatt	gctagaggta	gaaaggggaa	gggtgctggg	gagcagggct	2580
ggtccacagc	aggtctcgtg	cagcaggtac	ctgtggttcc	gccttctcat	ctccctgaga	2640
ctgctccgac	ccttccctcc	caggctctgt	ctgatggccc	ctctccctct	gcaggcgctc	2700
ggatgggagc	cctggggctg	ttcctgcagt	gcgccatctc	cctggtcttc	tctctggtca	2760
tggaccggct	ggtgcagcga	ttcggcactc	gagcagctca	tttggccagt	gtggcagctt	2820
tcctgtggc	tgccggtgcc	acatgcctgt	cccacagtgt	ggccgtgggtg	acagcttcag	2880
cgcctctcac	cgggttcacc	ttctcagccc	tgcagatcct	gccctacaca	ctggcctccc	2940
tctaccaccg	ggagaagcag	gtactcattg	gccagtgggt	ggagtccagg	tgggaggggt	3000
ggtctgggtt	tttgggaggc	caactagctc	agaacctggt	atctggcaag	caactttgga	3060
gaatgcttct	ttgaatcaga	gaagaagctt	atcctagccc	cagggccaga	ggcttgggct	3120
gcagaacagt	gtagattaga	ttctgggaat	gacttctctg	ggtcaggact	gtgtagcact	3180
tgaatggatg	attgcaggaa	atgcaaaata	cgatagtggg	aatcccgaag	ggtcaggcca	3240
gcaggagccc	taggcttcta	ggctggttgt	tctatggaga	ggcagggcgc	tgaatcagat	3300
gacccttggg	ccattcagcc	tcagcagacg	ggagtgggaa	tgggtccagcc	ttagcaacac	3360
ctttcttcag	ggagcagcaa	cctgacttag	cctgtatcct	actctggtct	ctgagatggg	3420
gcaggctcct	tcctaccccc	tttctttctg	gcttattttt	cttttctgtc	taattccctt	3480
ttcttttct	gcattccctc	tttgctcct	tccttttctc	cttccccctc	cccttcccc	3540
gtggcagata	tctgagcttg	acacctgacc	cactcacttg	ggcactgtgt	aagtgtgtgg	3600
gacctccttc	ttggttggcc	ctacactaac	cagccccctc	aggggcccc	ttccttgga	3660
agccacctaa	cccaggtagt	gtggtcatcc	ttgtccccct	cactgacctc	actgagctac	3720
aaacctgggt	gctggactct	gccttgaggg	gcatgaagtt	ggggtgtccc	aaggaggag	3780
gagatgcagg	actgctctca	tagagctctc	agactgtagg	gaagacctgc	ccctgcgtct	3840
cgtagcactt	gaggagagga	gtaggtaagt	tcgtagctga	gaggctgggt	aactgagtag	3900
gtagctgcag	gggtgagagg	tatggagggg	aggggctaag	gttttggttg	ggggagcctg	3960
gtccctgaga	cccctgttag	cccactgata	accttcttca	gccttcactc	ttctgcttgc	4020
ctgggctggg	ggcagggggc	tggcatcagc	ggccaggcct	gagtatgtgc	tgtcgtgcca	4080
gggaacgttc	tggggctagc	catcttctcc	agatggagga	gcatgtctgt	cctcggacca	4140
ctccagactc	caacctcagc	ggacattcct	ggggtggcag	gcagggagga	gaagtccctg	4200
gaggccccct	cctaacagca	gctgatggca	gacttggcac	tgcacgctgt	ctgcctgttc	4260
ctttgcccac	ttgttgagct	gcatggtgag	ccgtgggctt	ccctggtgtc	aggtttgagc	4320
tctgccatgg	ctcccacctc	gcaaattgcag	ccaactcaac	tcttctggca	tggggacaat	4380
gttgataaag	acctggcctt	gtccttaaatt	aggaggctct	gggccatcaa	gggcaggggt	4440
tggggggatg	gtggctgacc	agtcaactctg	atctaagtca	gacagcagga	aggaagttag	4500
aagccttcaa	cattagcaca	gctggggctg	ggggagggtg	gaagaggggac	attcctcctg	4560
cttggggctt	actggattct	ccctgcccc	aggctgggga	caaggagct	catggcaggg	4620
cagctaccct	agtggcatct	gggaccccag	agaggcagag	cttctctgca	ccgggcaatg	4680
aggatttcca	gatgtcggag	tggagggcag	gcaggaagga	aggttaggag	agcctgcgtg	4740
gggtttgggc	catcaggggc	cctgccttgg	cttttgttcc	tctgttctgt	gcattctctta	4800
ccaccgtctt	cattccccct	gtgtcttttc	cttaccttgg	agctctgttc	tctctgatct	4860
gtgatattga	gtttgtctgc	ctcttacctg	ttctaagagg	ctagaggaga	cctagacttc	4920
tgggttcaca	tttgtccccg	ccctaaccgg	ttacccttct	cccactcctg	aggaaggggtc	4980
ctgggttagac	ttggaccaag	tagggctctcc	atcttctctc	ctgctcctga	ttctcatgaa	5040
gtcccattgc	ccctgggatg	gaggcaaggg	tctgttctca	cagctgggggt	ggtgccagtg	5100

```

ctgggtacac acctgtcctc ttcccccttt cttcaccct ctgccttagg tgttctgcc 5160
caaataccga ggggacactg gaggtgctag cagtgaggac agcctgatga ccagcttct 5220
gccaggccct aagcctggag ctcccttccc taatggacac gtgggtgctg gaggcagtgg 5280
cctgtcccca cctccaccgg cgctctgcgg ggctctgcc tgtgatgtct ccgtacgtgt 5340
ggtggtgggt gagcccacgg agggcagggt ggttccgggc cggggcatct gcctggacct 5400
cgccatcctg gatagtgcct tcctgctgtc ccagggtggc ccatccctgt ttatgggctc 5460
cattgtccag ctccagccagt ctgtcactgc ctatatggtg tctgccgcag gcctgggtct 5520
ggtcgccatt tactttgcta cacaggtagt atttgacaag agcgacttgg ccaaatactc 5580
agcgtagaaa acttccagca cattgggggtg gagggcctgc ctactgggt cccagctccc 5640
cgctcctggt agcccatgg ggctgccggg ctggccgcca gtttctgttg ctgcaaagt 5700
aatgtggctc tctgtgcca ccctgtgctg ctgagggtgc tagctgcaca gctgggggct 5760
ggggcgctcc tctcctctct cccagctctc tagggctgcc tgactggagg ccttccaagg 5820
gggtttcagt ctggacttat acaggggagg cagaagggt ccatgcactg gaatgctggg 5880
actctgcagg tggattaccc aggtcagggt ttaacagcta gcctcctagt tgagacacac 5940
ctagagaagg gtttttggga gctgaataaa ctcatgcacc tggtttccca tctctaagcc 6000
ccttaacctg cagcttcgtt taatgtagct ctgcatggg agtttctagg atgaaacact 6060
cctccatggg atttgaacat atgaaagtta tttgtagggg aagagtcctg aggggcaaca 6120
cacaagaacc aggtccctc agcccacagc actgtctttt tgctgatcca cccccctct 6180
accttttatc aggatgtggc ctgttgggtc ttctgttgcc atcacagaga cacaggcatt 6240
taaataattt acttatttat ttaacaaagt agaagggaat ccattgctag cttttctgtg 6300
ttggtgtcta atatttgggt aggggtgggg atccccaaca atcagggtccc ctgagatagc 6360
tggtcattgg gctgatcatt gccagaatct tcttctcctg gggctctggc ccccaaatg 6420
cctaaccag gaccttgaa attctactca tcccaaatga taattccaa tgctgttacc 6480
caagggttag gtgttgaagg aaggtagagg gtggggcttc aggtctcaac ggcttcccta 6540
accaccctc ttctcttggc ccagcctggt tccccccact tccactccc tctactctct 6600
ctaggactgg gctgatgaag gcactgcca aaatttcccc taccaccaac tttccctac 6660
ccccaacttt ccccaccagc tccacaaccc tgtttggagc tactgcagga ccagaagcac 6720
aaagtgcggt ttccaagcc tttgtccatc tcagcccca gagtatatct gtgcttgggg 6780
aatctcacac agaaactcag gagcaccccc tgctgagct aaggagggtc ttatctctca 6840
ggggggggtt aagtgccgtt tgcaataatg tcgtcttatt tatttagcgg ggtgaatatt 6900
ttatactgta agtgagcaat cagagtataa tgtttatggt gacaaaatta aaggctttct 6960
tatatgttta aaaaaa

```

&lt;210&gt; 627

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 627

Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe  
5 10 15

Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val  
20 25 30

Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys  
35 40 45

Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly  
50 55 60

Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu  
65 70 75 80

Tyr His Arg Glu Lys Gln Val Leu Ile Gly Gln Trp Val Glu Ser Gly  
85 90 95

Val Ser Gly Lys Gln Leu Trp Arg Met Leu Leu  
115 120

```
<210> 628  
<211> 150  
<212> PRT  
<213> Homo sapiens
```

<400> 628  
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala  
                  5                  10                  15

Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu  
20 25 30

Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val  
35 40 45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Glu Ser Leu His Pro Pro  
50 55 60

Ser Phe Leu Phe Gln Ile His Ala Thr Trp His Val Gly Gln Glu Tyr  
65 70 75 80

Leu Cys Pro Gly Ser Cys Leu Glu Gly Glu Val Val Cys Trp Glu Gly  
85 90 95

Ile Ala Gly Gln Glu Gly Asp Pro Gly Leu Arg Gly His Thr Lys Arg  
100 105 110

Lys Lys Arg Ile Pro Arg Thr Tyr Pro Ser His Leu Trp Ile Pro Gly  
115 120 125

Pro Ala Gln Ser Leu Ala His Arg Arg His Trp Arg Asn Ala Pro Asn  
130 135 140

Leu Trp Leu Ala Leu Leu  
145 150

```
<210> 629
<211> 371
<212> PRT
<213> Homo sapiens
```

<400> 629  
Met Leu Phe Pro Ser Phe Ser Arg Ser Leu Val Pro Leu Pro Leu Ala  
                  5                       10                       15

Leu Tyr Leu Ser Gln Pro Leu Thr His Thr Thr Ser Leu Leu Ala Gly  
20 25 30

Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro Leu Leu Gly Ser Ala  
35 40 45

Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp  
 50 55 60  
 Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala  
 65 70 75 80  
 Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu  
 85 90 95  
 Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp Phe Cys Gly Gln Val  
 100 105 110  
 Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro  
 115 120 125  
 Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu  
 130 135 140  
 Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser  
 145 150 155 160  
 Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu  
 165 170 175  
 Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala Thr Leu Leu Val Ala  
 180 185 190  
 Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala  
 195 200 205  
 Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe  
 210 215 220  
 Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln Leu Cys Cys Arg  
 225 230 235 240  
 Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala Glu Leu Cys Ser Trp  
 245 250 255  
 Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu  
 260 265 270  
 Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg  
 275 280 285  
 Arg His Tyr Asp Glu Gly Lys Ala Leu Ala Ala Ser Arg Gly Trp Cys  
 290 295 300  
 Gly Ser Arg Pro Pro Glu Thr Thr Leu Gly Ala Val Ser Gly Leu Val  
 305 310 315 320  
 Pro Leu His Pro Gly Pro Asp Phe Ser Val Arg Lys Val Gly Met Asp  
 325 330 335  
 Pro Ile Cys Ile His Gly Phe Ser Trp Val Trp Asn Ile Ser Ala Cys  
 340 345 350

Gly Phe Arg Lys Ala Ser Gly Cys Ser Arg Ser Leu Ile Arg Val Val  
 355 360 365

Ala Pro Val  
 370

<210> 630  
 <211> 2983  
 <212> DNA  
 <213> Homo sapiens

<400> 630  
 agagatagag tcttccctgg cattgcagga gagaatctga agggatgatg gatgcatcaa 60  
 aagagctgca agttctccac attgacttct tgaatcagga caacgccgtt tctcaccaca 120  
 catgggagtt ccaaacgagc agtcctgtgt tccggcgagg acaggtgttt cacctgcggc 180  
 tgggtgctgaa ccagccccta caatcctacc accaactgaa actggaattc agcacagggc 240  
 cgaatcctag catcgccaaa cacaccctgg tgggtgctcga cccgaggacg cctcagacc 300  
 actacaactg gcaggcaacc cttcaaaatg agtctggcaa agaggtcaca gtggctgtca 360  
 ccagttcccc caatgccatc ctgggcaagt accaactaaa cgtgaaaact ggaaaccaca 420  
 tccttaagtc tgaagaaaac atcctatacc ttctcttcaa cccatgggtg aaagaggaca 480  
 tggttttcat gcctgatgag gacgagcgca aagagtacat cctcaatgac acgggctgcc 540  
 attacgtggg ggctgccaga agtatcaaat gcaaaccctg gaactttggg cagtttgaga 600  
 aaaatgtcct ggactgctgc atttccctgc tgactgagag ctccctcaag cccacagata 660  
 ggagggaccc cgtgctgggtg tgcagggcca tgtgtgctat gatgagcttt gagaaaggcc 720  
 agggcggtgct cattgggaat tggactgggg actatgaagg tggcacagcc ccatacaagt 780  
 ggacaggcag tgccccgatc ctgcagcagt actacaacac gaagcaggct gtgtgctttg 840  
 gccagtgtct ggtgtttgct gggatcctga ctacagtgtg gagagcgttg ggcattccag 900  
 cacgcagtgt gacaggcttc gattcagctc acgacacaga aaggaacctc acgggtggaca 960  
 cctatgtgaa tgagaatggc aagaaaatca ccagtatgac ccacgactct gtctggaatt 1020  
 tccatgtgtg gacggatgcc tggatgaagc gaccggatct gcccaagggc tacgacggct 1080  
 ggcaggctgt ggacgcaacg ccgcaggagc gaagccaggg tgtcttctgc tgtgggcat 1140  
 caccactgac cgccatccgc aaaggtgaca tctttattgt ctatgacacc agattcgtct 1200  
 tctcagaagt gaatggtgac aggtcatctt ggttgggtgaa gatggtgaat gggcaggagg 1260  
 agttacacgt aatttcaatg gagaccacaa gcatcgggaa aaacatcagc accaagagg 1320  
 tgggccaaga caggcggaga gatatacct atgagtaaca gtatccagaa ggctcctctg 1380  
 aggagaggca ggtcatggat catgccttcc tccttctcag ttctgagagg gagcacagac 1440  
 gacctgtaaa agagaacttt cttcacatgt cggtaacaatc agatgatgtg ctgctgggaa 1500  
 actctgttaa tttcacctgt attcttaaaa ggaagaccgc tgcctacag aatgtcaaca 1560  
 tcttgggctc ctttgaacta cagttgtaca ctggcaagaa gatggcaaaa ctgtgtgacc 1620  
 tcaataagac ctgcagatc caaggtcaag tatcagaagt gactctgacc ttggactcca 1680  
 agacctacat caacagcctg gctatattag atgatgagcc agttatcaga ggtttcatca 1740  
 ttgcggaaat tgtggagtct aaggaaatca tggcctctga agtattcacg tctttccagt 1800  
 accctgagtt ctctatagag ttgcctaaca caggcagaat tggccagcta cttgtctgca 1860  
 attgtatctt caagaatacc ctggccatcc ctttgactga cgtcaagttc tctttggaaa 1920  
 gcctgggcat ctctcacta cagacctctg accatgggac ggtgcagcct ggtgagacca 1980  
 tccaatccca aataaaatgc accccaataa aaactggacc caagaaattt atcgtcaagt 2040  
 taagttccaa acaagtgaaa gagattaatg ctcagaagat tgttctcatc accaagtagc 2100  
 cttgtctgat gctgtggagc cttagttgag atttcagcat ttctacctt gtgcttagct 2160  
 ttcagattat ggatgattaa atttgatgac ttatatgagg gcagattcaa gagccagcag 2220  
 gtcaaaaagg ccaacacaa cataagcagc cagaccacaa aggccaggtc ctgtgctatc 2280  
 acagggtcac ctcttttaca gttagaaaca ccagccgagg ccacagaatc ccatcccttt 2340  
 cctgagtcac ggcctcaaaa atcagggcca ccattgtctc aattcaaata catagatttc 2400  
 gaagccacag agtctctccc tggagcagca gactatgggc agcccagtgct tggccactgc 2460  
 tgacgaccct tgagaagctg ccatactctt agggcatggg ttcaccagcc ctgaaggcac 2520  
 ctgtcaactg gagtgtctct tcagcactgg gatgggcctg atagaagtgc attctcctcc 2580

tattgcctcc	attctcctct	ctctatccct	gaaatccagg	aagtcctct	cctggtgctc	2640
caagcagttt	gaagcccaat	ctgcaaggac	atttctcaag	ggccatgtgg	ttttgcagac	2700
aaccctgtcc	tcaggcctga	actcaccata	gagacccatg	tcagcaaacg	gtgaccagca	2760
aatcctcttc	ccttattcta	aagctgcccc	ttgggagact	ccaggagaa	ggcattgctt	2820
cctccctggg	gtgaactctt	tctttgggat	tccatccact	atcctggcaa	ctcaaggctg	2880
cttctgttaa	ctgaagcctg	ctccttcttg	ttctgccctc	cagagatttg	ctcaaagat	2940
caataagctt	taaattaaac	tctacttcaa	gaaaaaaaaa	ccg		2983

&lt;210&gt; 631

&lt;211&gt; 3064

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 631

aattctaaaa	atgcttttgc	aagcttgcac	gcctgcaggt	gcagcggccg	ccagtgtgat	60
ggatatctgc	agaattcggc	ttgcgctcag	ctggaattcc	gcagagatag	agtcttccct	120
ggcattgcag	gagagaatct	gaagggatga	tggatgcac	aaaagagctg	caagttctcc	180
acattgactt	cttgaatcag	gacaacgccg	ttctcacca	cacatgggag	ttccaaacga	240
gcagtccctg	gttccggcga	ggacaggtgt	ttcacctgcg	gctggtgctg	aaccagcccc	300
tacaatccta	ccaccaactg	aaactggaat	tcagcacagg	gccgaatcct	agcatcgcca	360
aacacacccct	ggtggtgctc	gacccgagga	cgccctcaga	ccactacaac	tggcaggcaa	420
cccttcaaaa	tgagtctggc	aaagaggtca	cagtggctgt	caccagttcc	cccaatgcca	480
tctggggcaa	gtaccaacta	aacgtgaaaa	ctggaaacca	catccttaag	tctgaagaaa	540
acatcctata	ccttctcttc	aacccatggt	gtaaagagga	catggttttc	atgcctgatg	600
aggacgagcg	caaagagtac	atcctcaatg	acacgggctg	ccattacgtg	ggggctgcca	660
gaagtatcaa	atgcaaacc	tggaactttg	gtcagtttga	gaaaaatgtc	ctggactgct	720
gcatttccct	gctgactgag	agctccctca	agccacaga	taggaggac	cccgtgctgg	780
tgtgcagggc	catgtgtgct	atgatgagct	ttgagaaagg	ccaggggcgtg	ctcattggga	840
attggactgg	ggactacgaa	ggtggcacag	ccccatacaa	gtggacaggc	agtgcctcca	900
tcctgcagca	gtactacaac	acgaagcagg	ctgtgtgctt	tggccagtgc	tgggtgtttg	960
ctgggatcct	gactacagtg	ctgagagcgt	tgggcatccc	agcacgcagt	gtgacaggct	1020
tcgattcagc	tcacgacaca	gaaaggaacc	tcacggtgga	cacctatgtg	aatgagaatg	1080
gcgagaaaat	caccagtatg	accacgact	ctgtctggaa	tttccatgtg	tggacggatg	1140
cctggatgaa	gcgaccctac	gacggctggc	aggctgtgga	cgcaacgccg	caggagcgaa	1200
gccagggtgt	cttctgctgt	gggccatcac	cactgaccgc	catccgcaaa	ggtgacatct	1260
ttattgtcta	tgacaccaga	ttcgtcttct	cagaagtga	tgggtgacagg	ctcatctggt	1320
tggatgaagt	ggtgaatggg	caggaggagt	tacacgtaat	ttcaatggag	accacaagca	1380
tcgggaaaaa	catcagcacc	aaggcagttg	gccaagacag	gcggagagat	atcacctatg	1440
agtacaagta	tcagaaggc	tcctctgagg	agaggcaggt	catggatcat	gccttccctc	1500
ttctcagttc	tgagaggag	cacagacagc	ctgtaaaaga	gaactttctt	cacatgtcgg	1560
tacaatcaga	tgatgtgctg	ctgggaaact	ctgttaattt	caccgtgatt	cttaaaagga	1620
agaccgctgc	cctacagaat	gtcaacatct	tgggtcctt	tgaactacag	ttgtacactg	1680
gcaagaagat	ggcaaaactg	tgtgacctca	ataagacctc	gcagatccaa	ggtcaagtat	1740
cagaagtgc	tctgaccttg	gactccaaga	cctacatcaa	cagcctggct	atattagatg	1800
atgagccagt	tatcagaggt	ttcatcattg	cggaaattgt	ggagtctaag	gaaatcatgg	1860
cctctgaagt	attcacgtca	aaccagtacc	ctgagttctc	tatagagttg	cctaacacag	1920
gcagaattgg	ccagctactt	gtctgcaatt	gtatcttcaa	gaataccctg	gccatccctt	1980
tgactgacgt	caagttctct	ttggaaagcc	tgggcatctc	ctcactacag	acctctgacc	2040
atgggacggt	gcagcctggg	gagaccatcc	aatcccaaat	aaaatgcacc	ccaataaaaa	2100
ctggacccaa	gaaatttatc	gtcaagttaa	gttccaaaca	agtgaagag	attaatgctc	2160
agaagattgt	tctcatcacc	aagtagcctt	gtctgatgct	gtggagcctt	agttgagatt	2220
tcagcatttc	ctaccttctg	cttagctttc	agattatgga	tgattaaatt	tgatgactta	2280
tatgagggca	gattcaagag	ccagcaggct	aaaaaggcca	acacaacccat	aagcagccag	2340
accacaagg	ccaggtcctg	tgtatcacca	gggtcacctc	ttttacagtt	agaaacacca	2400
gccgaggcca	cagaatccca	tccttttctc	gagtcattgg	ctcaaaaatc	agggccacca	2460
ttgtctcaat	tcaaatccat	agatttcgaa	gccacagagc	tcttccctgg	agcagcagac	2520
tatgggcagc	ccagtgtctg	cacctgctga	cgacccttga	gaagctgcca	tatcttcagg	2580
ccatgggttc	accagccctg	aaggcacctg	tcaactggag	tgctctctca	gcactgggat	2640

```

gggcctgata gaagtgcatt ctctctctat tgcctccatt ctctctctctc tatccctgaa 2700
atccaggaag tccctctctt ggtgctccaa gcagtttgaa gcccaatctg caaggacatt 2760
tctcaagggc catgtgggtt tgcagacaac cctgtctctc ggcctgaact caccatagag 2820
accatgtca gcaaacgggt accagcaaat cctcttccct tattctaaag ctgccccttg 2880
ggagactcca gggagaaggc attgcttctt ccctgggtgtg aactctttct ttggtattcc 2940
atccactatc ctggcaactc aaggctgctt ctgttaactg aagcctgtct cttcttgttc 3000
tgcctccag agatttgctc aaatgatcaa taagctttaa attaaaccgg aatccgcgga 3060
attc 3064

```

&lt;210&gt; 632

&lt;211&gt; 684

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 632

```

Met Met Asp Ala Ser Lys Glu Leu Gln Val Leu His Ile Asp Phe Leu
      5                      10                      15

Asn Gln Asp Asn Ala Val Ser His His Thr Trp Glu Phe Gln Thr Ser
      20                      25                      30

Ser Pro Val Phe Arg Arg Gly Gln Val Phe His Leu Arg Leu Val Leu
      35                      40                      45

Asn Gln Pro Leu Gln Ser Tyr His Gln Leu Lys Leu Glu Phe Ser Thr
      50                      55                      60

Gly Pro Asn Pro Ser Ile Ala Lys His Thr Leu Val Val Leu Asp Pro
      65                      70                      75                      80

Arg Thr Pro Ser Asp His Tyr Asn Trp Gln Ala Thr Leu Gln Asn Glu
      85                      90                      95

Ser Gly Lys Glu Val Thr Val Ala Val Thr Ser Ser Pro Asn Ala Ile
      100                     105                     110

Leu Gly Lys Tyr Gln Leu Asn Val Lys Thr Gly Asn His Ile Leu Lys
      115                     120                     125

Ser Glu Glu Asn Ile Leu Tyr Leu Leu Phe Asn Pro Trp Cys Lys Glu
      130                     135                     140

Asp Met Val Phe Met Pro Asp Glu Asp Glu Arg Lys Glu Tyr Ile Leu
      145                     150                     155                     160

Asn Asp Thr Gly Cys His Tyr Val Gly Ala Ala Arg Ser Ile Lys Cys
      165                     170                     175

Lys Pro Trp Asn Phe Gly Gln Phe Glu Lys Asn Val Leu Asp Cys Cys
      180                     185                     190

Ile Ser Leu Leu Thr Glu Ser Ser Leu Lys Pro Thr Asp Arg Arg Asp
      195                     200                     205

Pro Val Leu Val Cys Arg Ala Met Cys Ala Met Met Ser Phe Glu Lys
      210                     215                     220

Gly Gln Gly Val Leu Ile Gly Asn Trp Thr Gly Asp Tyr Glu Gly Gly

```

225		230		235		240
Thr Ala Pro Tyr Lys Trp Thr Gly Ser Ala Pro Ile Leu Gln Gln Tyr						
	245			250		255
Tyr Asn Thr Lys Gln Ala Val Cys Phe Gly Gln Cys Trp Val Phe Ala						
	260			265		270
Gly Ile Leu Thr Thr Val Leu Arg Ala Leu Gly Ile Pro Ala Arg Ser						
	275			280		285
Val Thr Gly Phe Asp Ser Ala His Asp Thr Glu Arg Asn Leu Thr Val						
	290			295		300
Asp Thr Tyr Val Asn Glu Asn Gly Lys Lys Ile Thr Ser Met Thr His						
	305			310		315
Asp Ser Val Trp Asn Phe His Val Trp Thr Asp Ala Trp Met Lys Arg						
	325			330		335
Pro Asp Leu Pro Lys Gly Tyr Asp Gly Trp Gln Ala Val Asp Ala Thr						
	340			345		350
Pro Gln Glu Arg Ser Gln Gly Val Phe Cys Cys Gly Pro Ser Pro Leu						
	355			360		365
Thr Ala Ile Arg Lys Gly Asp Ile Phe Ile Val Tyr Asp Thr Arg Phe						
	370			375		380
Val Phe Ser Glu Val Asn Gly Asp Arg Leu Ile Trp Leu Val Lys Met						
	385			390		395
Val Asn Gly Gln Glu Glu Leu His Val Ile Ser Met Glu Thr Thr Ser						
	405			410		415
Ile Gly Lys Asn Ile Ser Thr Lys Ala Val Gly Gln Asp Arg Arg Arg						
	420			425		430
Asp Ile Thr Tyr Glu Tyr Lys Tyr Pro Glu Gly Ser Ser Glu Glu Arg						
	435			440		445
Gln Val Met Asp His Ala Phe Leu Leu Leu Ser Ser Glu Arg Glu His						
	450			455		460
Arg Arg Pro Val Lys Glu Asn Phe Leu His Met Ser Val Gln Ser Asp						
	465			470		475
Asp Val Leu Leu Gly Asn Ser Val Asn Phe Thr Val Ile Leu Lys Arg						
	485			490		495
Lys Thr Ala Ala Leu Gln Asn Val Asn Ile Leu Gly Ser Phe Glu Leu						
	500			505		510
Gln Leu Tyr Thr Gly Lys Lys Met Ala Lys Leu Cys Asp Leu Asn Lys						
	515			520		525
Thr Ser Gln Ile Gln Gly Gln Val Ser Glu Val Thr Leu Thr Leu Asp						
	530			535		540



Ser Lys Thr Tyr Ile Asn Ser Leu Ala Ile Leu Asp Asp Glu Pro Val  
 545 550 555 560  
 Ile Arg Gly Phe Ile Ile Ala Glu Ile Val Glu Ser Lys Glu Ile Met  
 565 570 575

Ala Ser Glu Val Phe Thr Ser Phe Gln Tyr Pro Glu Phe Ser Ile Glu  
 580 585 590

Leu Pro Asn Thr Gly Arg Ile Gly Gln Leu Leu Val Cys Asn Cys Ile  
 595 600 605

Phe Lys Asn Thr Leu Ala Ile Pro Leu Thr Asp Val Lys Phe Ser Leu  
 610 615 620

Glu Ser Leu Gly Ile Ser Ser Leu Gln Thr Ser Asp His Gly Thr Val  
 625 630 635 640

Gln Pro Gly Glu Thr Ile Gln Ser Gln Ile Lys Cys Thr Pro Ile Lys  
 645 650 655

Thr Gly Pro Lys Lys Phe Ile Val Lys Leu Ser Ser Lys Gln Val Lys  
 660 665 670

Glu Ile Asn Ala Gln Lys Ile Val Leu Ile Thr Lys  
 675 680

<210> 633

<211> 679

<212> PRT

<213> Homo sapiens

<400> 633

Met Met Asp Ala Ser Lys Glu Leu Gln Val Leu His Ile Asp Phe Leu  
 5 10 15

Asn Gln Asp Asn Ala Val Ser His His Thr Trp Glu Phe Gln Thr Ser  
 20 25 30

Ser Pro Val Phe Arg Arg Gly Gln Val Phe His Leu Arg Leu Val Leu  
 35 40 45

Asn Gln Pro Leu Gln Ser Tyr His Gln Leu Lys Leu Glu Phe Ser Thr  
 50 55 60

Gly Pro Asn Pro Ser Ile Ala Lys His Thr Leu Val Val Leu Asp Pro  
 65 70 75 80

Arg Thr Pro Ser Asp His Tyr Asn Trp Gln Ala Thr Leu Gln Asn Glu  
 85 90 95

Ser Gly Lys Glu Val Thr Val Ala Val Thr Ser Ser Pro Asn Ala Ile  
 100 105 110

Leu Gly Lys Tyr Gln Leu Asn Val Lys Thr Gly Asn His Ile Leu Lys  
 115 120 125

Ser Glu Glu Asn Ile Leu Tyr Leu Leu Phe Asn Pro Trp Cys Lys Glu  
 130 135 140  
 Asp Met Val Phe Met Pro Asp Glu Asp Glu Arg Lys Glu Tyr Ile Leu  
 145 150 155 160  
 Asn Asp Thr Gly Cys His Tyr Val Gly Ala Ala Arg Ser Ile Lys Cys  
 165 170 175  
 Lys Pro Trp Asn Phe Gly Gln Phe Glu Lys Asn Val Leu Asp Cys Cys  
 180 185 190  
 Ile Ser Leu Leu Thr Glu Ser Ser Leu Lys Pro Thr Asp Arg Arg Asp  
 195 200 205  
 Pro Val Leu Val Cys Arg Ala Met Cys Ala Met Met Ser Phe Glu Lys  
 210 215 220  
 Gly Gln Gly Val Leu Ile Gly Asn Trp Thr Gly Asp Tyr Glu Gly Gly  
 225 230 235 240  
 Thr Ala Pro Tyr Lys Trp Thr Gly Ser Ala Pro Ile Leu Gln Gln Tyr  
 245 250 255  
 Tyr Asn Thr Lys Gln Ala Val Cys Phe Gly Gln Cys Trp Val Phe Ala  
 260 265 270  
 Gly Ile Leu Thr Thr Val Leu Arg Ala Leu Gly Ile Pro Ala Arg Ser  
 275 280 285  
 Val Thr Gly Phe Asp Ser Ala His Asp Thr Glu Arg Asn Leu Thr Val  
 290 295 300  
 Asp Thr Tyr Val Asn Glu Asn Gly Glu Lys Ile Thr Ser Met Thr His  
 305 310 315 320  
 Asp Ser Val Trp Asn Phe His Val Trp Thr Asp Ala Trp Met Lys Arg  
 325 330 335  
 Pro Tyr Asp Gly Trp Gln Ala Val Asp Ala Thr Pro Gln Glu Arg Ser  
 340 345 350  
 Gln Gly Val Phe Cys Cys Gly Pro Ser Pro Leu Thr Ala Ile Arg Lys  
 355 360 365  
 Gly Asp Ile Phe Ile Val Tyr Asp Thr Arg Phe Val Phe Ser Glu Val  
 370 375 380  
 Asn Gly Asp Arg Leu Ile Trp Leu Val Lys Met Val Asn Gly Gln Glu  
 385 390 395 400  
 Glu Leu His Val Ile Ser Met Glu Thr Thr Ser Ile Gly Lys Asn Ile  
 405 410 415  
 Ser Thr Lys Ala Val Gly Gln Asp Arg Arg Arg Asp Ile Thr Tyr Glu  
 420 425 430  
 Tyr Lys Tyr Pro Glu Gly Ser Ser Glu Glu Arg Gln Val Met Asp His

435	440	445
Ala Phe Leu Leu Leu Ser Ser Glu Arg Glu His Arg Gln Pro Val Lys 450 455 460		
Glu Asn Phe Leu His Met Ser Val Gln Ser Asp Asp Val Leu Leu Gly 465 470 475 480		
Asn Ser Val Asn Phe Thr Val Ile Leu Lys Arg Lys Thr Ala Ala Leu 485 490 495		
Gln Asn Val Asn Ile Leu Gly Ser Phe Glu Leu Gln Leu Tyr Thr Gly 500 505 510		
Lys Lys Met Ala Lys Leu Cys Asp Leu Asn Lys Thr Ser Gln Ile Gln 515 520 525		
Gly Gln Val Ser Glu Val Thr Leu Thr Leu Asp Ser Lys Thr Tyr Ile 530 535 540		
Asn Ser Leu Ala Ile Leu Asp Asp Glu Pro Val Ile Arg Gly Phe Ile 545 550 555 560		
Ile Ala Glu Ile Val Glu Ser Lys Glu Ile Met Ala Ser Glu Val Phe 565 570 575		
Thr Ser Asn Gln Tyr Pro Glu Phe Ser Ile Glu Leu Pro Asn Thr Gly 580 585 590		
Arg Ile Gly Gln Leu Leu Val Cys Asn Cys Ile Phe Lys Asn Thr Leu 595 600 605		
Ala Ile Pro Leu Thr Asp Val Lys Phe Ser Leu Glu Ser Leu Gly Ile 610 615 620		
Ser Ser Leu Gln Thr Ser Asp His Gly Thr Val Gln Pro Gly Glu Thr 625 630 635 640		
Ile Gln Ser Gln Ile Lys Cys Thr Pro Ile Lys Thr Gly Pro Lys Lys 645 650 655		
Phe Ile Val Lys Leu Ser Ser Lys Gln Val Lys Glu Ile Asn Ala Gln 660 665 670		
Lys Ile Val Leu Ile Thr Lys 675		

&lt;210&gt; 634

&lt;211&gt; 5668

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 634

```

gtcacttagg aaaaggtgtc ctttcgggca gccgggctca gcatgaggaa cagaaggaat 60
gacactctgg acagaccg gaccctgtac tccagcggt ctcggagcac agacttgtct 120
tacagtgaag gcgacttggt gaattttatt caagcaaatt ttaagaaacg agaattgtgc 180

```

ttctttacca	aagattccaa	ggccacggag	aatgtgtgca	agtgtggcta	tgcccagagc	240
cagcacatgg	aaggcaccca	gatcaaccaa	agtgagaaat	ggaactacaa	gaaacacacc	300
aaggaatttc	ctaccgacgc	ctttggggat	attcagtttg	agacactggg	gaagaaaggg	360
aagtatatac	gtctgtcctg	cgacacggac	gcggaaatcc	tttacgagct	gctgacccag	420
cactggcacc	tgaaaacacc	caacctggtc	atttctgtga	ccggggggcgc	caagaacttc	480
gccctgaagc	cgcgcatgcg	caagatcttc	agccggctca	tctacatcgc	gcagtccaaa	540
ggtgcttgga	ttctcacggg	aggcaccat	tatggcctga	cgaagtacat	cggggagggtg	600
gtgagagata	acaccatcag	caggagtcca	gaggagaata	ttgtggccat	tggcatagca	660
gcttggggca	tggtctccaa	ccgggacacc	ctcatcagga	attgcgatgc	tgagggctat	720
tttttagccc	agtaccttat	ggatgacttc	acaagggatc	cactgtatat	cctggacaac	780
aaccacacac	atttgctgct	cgtggacaat	ggctgtcatg	gacatcccac	tgtcgaagca	840
aagctccgga	atcagctaga	gaagcatatc	tctgagcgca	ctattcaaga	ttccaactat	900
ggtggcaaga	tccccattgt	gtgttttgcc	caaggagggtg	gaaaagagac	tttgaaagcc	960
atcaatacct	ccatcaaaaa	taaaattcct	tgtgtgggtg	tggaaggctc	gggccggatc	1020
gctgatgtga	tcgctagcct	ggtggagggtg	gaggatgccc	cgacatcttc	tgccgtcaag	1080
gagaagctgg	tgcgcttttt	accccgcacg	gtgtcccggc	tgtctgagga	ggagactgag	1140
agttggatca	aatggctcaa	agaaattctc	gaatgttctc	acctattaac	agttattaaa	1200
atggaagaag	ctggggatga	aattgtgagc	aatgccatct	cctacgctct	atacaaagcc	1260
ttcagcacca	gtgagcaaga	caaggataac	tggaatgggc	agctgaagct	tctgctggag	1320
tggaaccagc	tggaacttagc	caatgatgag	attttcacca	atgaccgccg	atgggagtct	1380
gctgaccttc	aagaagtcat	gtttacggct	ctcataaagg	acagacccaa	gtttgtccgc	1440
ctctttctgg	agaatggctt	gaacctacgg	aagtttctca	cccattgatg	cctcactgaa	1500
ctctttctca	accacttcag	cacgcttggtg	taccggaatc	tgcagatcgc	caagaattcc	1560
tataatgatg	ccctcctcac	gtttgtctgg	aaactgggtg	cgaacttccg	aagaggcttc	1620
cggaagggaag	acagaaatgg	cogggacgag	atggacatag	aactccacga	cgtgtctcct	1680
attactcggc	accccttgca	agctctcttc	atctgggcca	ttcttcagaa	taagaaggaa	1740
ctctccaaag	tcatttgggga	gcagaccagg	ggctgcactc	tggcagccct	gggagccagc	1800
aagcttctga	agactctggc	caaagtgaag	aacgacatca	atgctgctgg	ggagtccgag	1860
gagctggcta	atgagtacga	gacccggtct	gttgagctgt	tactgagtg	ttacagcagc	1920
gatgaagact	tggcagaaca	gctgctggtc	tattcctgtg	aagcttgggg	tggaagcaac	1980
tgtctggagc	tggcgggtgga	ggccacagac	cagcatttca	ccgcccagcc	tggggtccag	2040
aattttcttt	ctaagcaatg	gtatggagag	atttcccag	acaccaagaa	ctggaagatt	2100
atcctgtgtc	tgtttattat	acccttggtg	ggctgtggct	ttgtatcatt	taggaagaaa	2160
cctgtcgaca	agcacaagaa	gctgctttgg	tactatgtgg	cgttcttcac	ctcccccttc	2220
gtggtcttct	cctggaatgt	ggtctttctac	atcgcttcc	tcctgctgtt	tgccctacgtg	2280
ctgctcatgg	atttccattc	ggtgccacac	ccccccgagc	tggtcctgta	ctcgctggtc	2340
tttgcctct	tctgtgatga	agtgagacag	tggtacgtaa	atggggtgaa	ttattttact	2400
gacctgtgga	atgtgatgga	cacgctgggg	cttttttact	tcatagcagg	aattgtattt	2460
cggctccact	cttctaataa	aagctctttg	tattctggac	gagtcatttt	ctgtctggac	2520
tacattatth	tcactctaag	attgatccac	atttttactg	taagcagaaa	cttaggacc	2580
aagattataa	tgctgcagag	gatgctgac	gatgtgtct	tcttctgtt	cctctttgcg	2640
gtgtggatgg	tgccctttgg	cgtggccaag	caagggatcc	ttaggcagaa	tgagcagcgc	2700
tgagggtgga	tattccgttc	ggtcatctac	gagccctacc	tgccatgtt	cggccagggtg	2760
cccagtgacg	tggtatggtac	cacgtatgac	tttgcccact	gcaccttcac	tggaatgag	2820
tccaagccac	tgtgtgtgga	gctggatgag	cacaacctgc	cccggttccc	cgagtggatc	2880
accatcccc	tggtgtgcat	ctacatgtta	tccaccaaca	tcctgctggt	caacctgctg	2940
gtcgccatgt	ttggctacac	ggtgggcacc	gtccaggaga	acaatgacca	ggtctggaag	3000
ttccagaggt	acttcttggt	gcaggagtac	tgacgccgc	tcaatatccc	cttccccctc	3060
atcgtcttcg	cttacttcta	catggtgggtg	aagaagtgt	tcaagtgttg	ctgcaaggag	3120
aaaaacatgg	agtcttctgt	ctgctgtttc	aaaaatgaag	acaatgagac	tctggcatgg	3180
gagggtgtca	tgaaggaaaa	ctaccttgct	aagatcaaca	caaaaagccaa	cgacacctca	3240
gaggaaatga	ggcatcgatt	tagacaactg	gatacaaagc	ttaatgatct	caagggtctt	3300
ctgaaagaga	ttgctaataa	aatcaaataa	aactgtatga	aactctaata	gagaaaaatc	3360
taattatagc	aagatcatat	taaggaatgc	tgatgaacaa	ttttgctatc	gactactaaa	3420
tgagagattt	tcagaccctt	gggtacatgg	tggtatgattt	taaatcaccc	tagtgtgctg	3480
agaccttgag	aataaagtgt	gtgattgggt	tcatacttga	agacggatat	aaaggaagaa	3540
tatttccttt	atgtgtttct	ccagaatggt	gcctgtttct	ctctgtgtct	caatgcctgg	3600
gactggaggt	tgatagttta	agtgtgttct	taccgcctcc	tttttcttt	aatcttattt	3660

```

ttgatgaaca catatatagg agaacatcta tcctatgaat aagaacctgg tcatgcttta 3720
ctcctgtatt gttatattgt tcattttccaa ttgattctct acttttccct tttttgtatt 3780
atgtgactaa ttagttggca tattgttaaa agtctctcaa attaggccag attctaaaac 3840
atgctgcagc aagaggagccc cgctctcttc aggaaaagtg ttttcatttc tcaggatgct 3900
tcttacctgt cagaggaggt gacaaggcag tctcttgctc tcttggaactc accaggctcc 3960
tattgaagga accacccccca ttccataaata tgtgaaaagt cgcccaaaat gcaaccttga 4020
aaggcactac tgactttgtt cttattggat actcctctta tttattattt ttccattaaa 4080
aataatagct ggctattata gaaaatttag accatacaga gatgtagaaa gaacataaat 4140
tgtccccatt accttaaggt aatcactgct aacaatttct ggatggtttt tcaagtctat 4200
tttttttcta tgtatgtctc aattctcttt caaaatttta cagaatgtta tcatactaca 4260
tatatacttt ttatgtaagc tttttcactt agtattttat caaatatgtt tttattatat 4320
tcatagcctt cttaaacatt atatcaataa ttgcataata ggcaacctct agcgattacc 4380
ataattttgc tcattgaagg ctatctccag ttgatcattg ggatgagcat ctttgtgcat 4440
gaatcctatt gctgtatttg ggaaaatttt ccaagggttag attccaataa atatctattt 4500
attattaaat attaaaatat cgatttatta ttaaaacat ttataaggct ttttcataaa 4560
tgtatagcaa ataggaatta ttaacttgag cataagatat gagatacatg aacctgaact 4620
attaaaataa aatattatat ttaaccctag tttagaaga agtcaatatg cttattttaa 4680
tattatggat ggtgggcaga tcacttgagg tcaggagttc gagaccagcc tggccaacat 4740
ggcaaaacca catctctact aaaaataaaa aaattagctg ggtgtggtgg tgcactcctg 4800
taatcccagc tactcagaag gctgaggtac aagaattgct ggaacctggg aggcggaggt 4860
tgcatgtaac caagattgca ccactgcact ccagccgggg tgacagagtg agactccgac 4920
tgaaaataaa taaataaata aataaataaa taaataaata aatattatgg atggtgaagg 4980
gaatgggtata gaattggaga gattatctta ctgaacacct gtagtccag ctttctctgg 5040
aagtgggtgt atttgagcag gatgtgcaca aggcaattga aatgccata attagtttct 5100
cagctttgaa tacactataa actcagtggc tgaaggagga aatttttagaa ggaagctact 5160
aaaagatcta atttgaaaaa ctacaaaagc attaactaaa aaagtttatt ttcttttgt 5220
ctgggcagta gtgaaaataa ctactcacia cattcactat gtttgcaagg aattaacaca 5280
aataaaaagat gcctttttac ttaaacgcca agacagaaaa cttgcccatt actgagaagc 5340
aacttgcatt agagagggaa ctgttaaagt ttttcaaccc agttcatctg gtggatgttt 5400
ttgcaggtta ctctgagaat tttgcttatg aaaaatcatt atttttagtg tagttcacia 5460
taatgtattg aacatacttc taatcaaagg tgctatgtcc ttgtgtatgg tactaaatgt 5520
gtcctgtgta cttttgcaca actgagaatc ctgcggcttg gtttaatgag tgtgttcatt 5580
aaataaataa tggaggaatt gtcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 5640
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa

```

&lt;210&gt; 635

&lt;211&gt; 1095

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 635

```

Met Arg Asn Arg Arg Asn Asp Thr Leu Asp Ser Thr Arg Thr Leu Tyr
      5                      10                      15

```

```

Ser Ser Ala Ser Arg Ser Thr Asp Leu Ser Tyr Ser Glu Ser Asp Leu
      20                      25                      30

```

```

Val Asn Phe Ile Gln Ala Asn Phe Lys Lys Arg Glu Cys Val Phe Phe
      35                      40                      45

```

```

Thr Lys Asp Ser Lys Ala Thr Glu Asn Val Cys Lys Cys Gly Tyr Ala
      50                      55                      60

```

```

Gln Ser Gln His Met Glu Gly Thr Gln Ile Asn Gln Ser Glu Lys Trp
      65                      70                      75                      80

```

```

Asn Tyr Lys Lys His Thr Lys Glu Phe Pro Thr Asp Ala Phe Gly Asp
      85                      90                      95

```

Ile Gln Phe Glu Thr Leu Gly Lys Lys Gly Lys Tyr Ile Arg Leu Ser  
 100 105 110  
 Cys Asp Thr Asp Ala Glu Ile Leu Tyr Glu Leu Leu Thr Gln His Trp  
 115 120 125  
 His Leu Lys Thr Pro Asn Leu Val Ile Ser Val Thr Gly Gly Ala Lys  
 130 135 140  
 Asn Phe Ala Leu Lys Pro Arg Met Arg Lys Ile Phe Ser Arg Leu Ile  
 145 150 155 160  
 Tyr Ile Ala Gln Ser Lys Gly Ala Trp Ile Leu Thr Gly Gly Thr His  
 165 170 175  
 Tyr Gly Leu Thr Lys Tyr Ile Gly Glu Val Val Arg Asp Asn Thr Ile  
 180 185 190  
 Ser Arg Ser Ser Glu Glu Asn Ile Val Ala Ile Gly Ile Ala Ala Trp  
 195 200 205  
 Gly Met Val Ser Asn Arg Asp Thr Leu Ile Arg Asn Cys Asp Ala Glu  
 210 215 220  
 Gly Tyr Phe Leu Ala Gln Tyr Leu Met Asp Asp Phe Thr Arg Asp Pro  
 225 230 235 240  
 Leu Tyr Ile Leu Asp Asn Asn His Thr His Leu Leu Leu Val Asp Asn  
 245 250 255  
 Gly Cys His Gly His Pro Thr Val Glu Ala Lys Leu Arg Asn Gln Leu  
 260 265 270  
 Glu Lys His Ile Ser Glu Arg Thr Ile Gln Asp Ser Asn Tyr Gly Gly  
 275 280 285  
 Lys Ile Pro Ile Val Cys Phe Ala Gln Gly Gly Gly Lys Glu Thr Leu  
 290 295 300  
 Lys Ala Ile Asn Thr Ser Ile Lys Asn Lys Ile Pro Cys Val Val Val  
 305 310 315 320  
 Glu Gly Ser Gly Arg Ile Ala Asp Val Ile Ala Ser Leu Val Glu Val  
 325 330 335  
 Glu Asp Ala Pro Thr Ser Ser Ala Val Lys Glu Lys Leu Val Arg Phe  
 340 345 350  
 Leu Pro Arg Thr Val Ser Arg Leu Ser Glu Glu Glu Thr Glu Ser Trp  
 355 360 365  
 Ile Lys Trp Leu Lys Glu Ile Leu Glu Cys Ser His Leu Leu Thr Val  
 370 375 380  
 Ile Lys Met Glu Glu Ala Gly Asp Glu Ile Val Ser Asn Ala Ile Ser  
 385 390 395 400

Tyr Ala Leu Tyr Lys Ala Phe Ser Thr Ser Glu Gln Asp Lys Asp Asn  
 405 410 415  
 Trp Asn Gly Gln Leu Lys Leu Leu Leu Glu Trp Asn Gln Leu Asp Leu  
 420 425 430  
 Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg Trp Glu Ser Ala Asp  
 435 440 445  
 Leu Gln Glu Val Met Phe Thr Ala Leu Ile Lys Asp Arg Pro Lys Phe  
 450 455 460  
 Val Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr  
 465 470 475 480  
 His Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val  
 485 490 495  
 Tyr Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu  
 500 505 510  
 Thr Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys  
 515 520 525  
 Glu Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val  
 530 535 540  
 Ser Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile  
 545 550 555 560  
 Leu Gln Asn Lys Lys Glu Leu Ser Lys Val Ile Trp Glu Gln Thr Arg  
 565 570 575  
 Gly Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu  
 580 585 590  
 Ala Lys Val Lys Asn Asp Ile Asn Ala Ala Gly Glu Ser Glu Glu Leu  
 595 600 605  
 Ala Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys Tyr  
 610 615 620  
 Ser Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys Glu  
 625 630 635 640  
 Ala Trp Gly Gly Ser Asn Cys Leu Glu Leu Ala Val Glu Ala Thr Asp  
 645 650 655  
 Gln His Phe Thr Ala Gln Pro Gly Val Gln Asn Phe Leu Ser Lys Gln  
 660 665 670  
 Trp Tyr Gly Glu Ile Ser Arg Asp Thr Lys Asn Trp Lys Ile Ile Leu  
 675 680 685  
 Cys Leu Phe Ile Ile Pro Leu Val Gly Cys Gly Phe Val Ser Phe Arg  
 690 695 700  
 Lys Lys Pro Val Asp Lys His Lys Lys Leu Leu Trp Tyr Tyr Val Ala

705		710		715		720
Phe Phe Thr Ser Pro	Phe Val Val Phe Ser Trp Asn Val Val	Phe Tyr				
725		730				735
Ile Ala Phe Leu Leu Leu Phe Ala Tyr Val Leu Leu Met Asp Phe His						
740		745				750
Ser Val Pro His Pro Pro Glu Leu Val Leu Tyr Ser Leu Val Phe Val						
755		760				765
Leu Phe Cys Asp Glu Val Arg Gln Trp Tyr Val Asn Gly Val Asn Tyr						
770		775				780
Phe Thr Asp Leu Trp Asn Val Met Asp Thr Leu Gly Leu Phe Tyr Phe						
785		790				800
Ile Ala Gly Ile Val Phe Arg Leu His Ser Ser Asn Lys Ser Ser Leu						
805		810				815
Tyr Ser Gly Arg Val Ile Phe Cys Leu Asp Tyr Ile Ile Phe Thr Leu						
820		825				830
Arg Leu Ile His Ile Phe Thr Val Ser Arg Asn Leu Gly Pro Lys Ile						
835		840				845
Ile Met Leu Gln Arg Met Leu Ile Asp Val Phe Phe Phe Leu Phe Leu						
850		855				860
Phe Ala Val Trp Met Val Ala Phe Gly Val Ala Arg Gln Gly Ile Leu						
865		870				880
Arg Gln Asn Glu Gln Arg Trp Arg Trp Ile Phe Arg Ser Val Ile Tyr						
885		890				895
Glu Pro Tyr Leu Ala Met Phe Gly Gln Val Pro Ser Asp Val Asp Gly						
900		905				910
Thr Thr Tyr Asp Phe Ala His Cys Thr Phe Thr Gly Asn Glu Ser Lys						
915		920				925
Pro Leu Cys Val Glu Leu Asp Glu His Asn Leu Pro Arg Phe Pro Glu						
930		935				940
Trp Ile Thr Ile Pro Leu Val Cys Ile Tyr Met Leu Ser Thr Asn Ile						
945		950				955
Leu Leu Val Asn Leu Leu Val Ala Met Phe Gly Tyr Thr Val Gly Thr						
965		970				975
Val Gln Glu Asn Asn Asp Gln Val Trp Lys Phe Gln Arg Tyr Phe Leu						
980		985				990
Val Gln Glu Tyr Cys Ser Arg Leu Asn Ile Pro Phe Pro Phe Ile Val						
995		1000				1005
Phe Ala Tyr Phe Tyr Met Val Val Lys Lys Cys Phe Lys Cys Cys Cys						
1010		1015				1020



Lys Glu Lys Asn Met Glu Ser Ser Val Cys Cys Phe Lys Asn Glu Asp  
 1025 1030 1035 1040

Asn Glu Thr Leu Ala Trp Glu Gly Val Met Lys Glu Asn Tyr Leu Val  
 1045 1050 1055

Lys Ile Asn Thr Lys Ala Asn Asp Thr Ser Glu Glu Met Arg His Arg  
 1060 1065 1070

Phe Arg Gln Leu Asp Thr Lys Leu Asn Asp Leu Lys Gly Leu Leu Lys  
 1075 1080 1085

Glu Ile Ala Asn Lys Ile Lys  
 1090 1095

<210> 636

<211> 3639

<212> DNA

<213> Homo sapiens

<400> 636

```

gattacgcaa gctatttagg tgacactata gaatwctcag cttgcatcaa gcttggtacc 60
gagctcggat ccctagtaac ggccgccagt gtgctggaat tcgcccttgc agccgggctc 120
agcatgagga acagaaggaa tgacactctg gacagcaccg ggaccctgta ctccagcgcg 180
tctcggagca cagacttgct ttacagtgaag agcgacttgg tgaattttat tcaagcaa 240
ttaaagaac gagaatgtgt cttctttacc aaagattcca aggccacgga gaatgtgtgc 300
aagtgtggct atgccagag ccagcacatg gaaggcaccg agatcaacca aagtga 360
tggaactaca agaaacacac caaggaattt cctaccgacg cctttgggga tattcagttt 420
gagacactgg ggaagaaagg gaagtatata cgtctgtcct gcgacacgga cgcgga 480
ctttacgagc tgctgaccca gcactggcac ctgaaaaacac ccaacctggt catttctgtg 540
accgggggag ccaagaactt cgccctgaag ccgcgcacgc gcaagatctt cagccggctc 600
atctacatcg cgcagtcaca aggtgcttgg attctcacgg gaggcaccca ttatggcctg 660
atgaagtaca tcggggagggt ggtgagagat aacaccatca gcaggagttc agaggaga 720
attgtggcca ttggcatagc agcttggggc atggtctcca accgggacac cctcatcagg 780
aattgcgatg ctgagggcta ttttttagcc cagtacctta tggatgactt cacaagag 840
ccactgtata tcctggacaa caaccacaca catttgctgc tcgtggacaa tggctgtcat 900
ggacatccca ctgtcgaagc aaagctccgg aatcagctag agaagtatat ctctgagcgc 960
actattcaag attccaacta tgggtggcaag atccccattg tgtgttttgc ccaaggagg 1020
ggaaaagaga ctttgaaagc catcaatacc tccatcaaaa ataaaattcc ttgtgtggtg 1080
gtggaagggt cggggccagat cgctgatgtg atcgctagcc tgggtggagggt ggaggatgcc 1140
ctgacatctt ctgccgtcaa ggagaagctg gtgcgctttt taccocgcac ggtgtcccgg 1200
ctgcctgagg aggagactga gagttggatc aaatggctca aagaaattct cgaatgttct 1260
cacctattaa cagttattaa aatggaagaa gctggggatg aaattgtgag caatgccatc 1320
tcctacgctc tatacaaaagc cttcagcacc agtgagcaag acaaggataa ctggaatggg 1380
cagctgaagc ttctgctgga gtggaaccag ctggacttag ccaatgatga gattttcacc 1440
aatgaccgcc gatgggagtc tgctgacctt caagaagtca tgtttacggc tctcataaag 1500
gacagacca agtttgtccg cctctttctg gagaatggct tgaacctacg gaagtttctc 1560
acctatgatg tcctcactga actcttctcc aaccacttca gcacgcttgt gtaccggaat 1620
ctgcagatcg ccaagaattc ctataatgat gccctctcca cgtttgtctg gaaactgggt 1680
gcgaacttcc gaagaggctt ccggaaggaa gacagaaatg gccgggacga gatggacata 1740
gaactccacg acgtgtctcc tattactcgg caccctctgc aagctctctt catctgggcc 1800
attcttcaga ataagaaggaa actctccaaa gtcatttggg agcagaccag gggctgca 1860
ctggcagccc tgggagccag caagcttctg aagactctgg ccaaagtga gaacgacatc 1920
aatgctgctg gggagtccga ggagctggct aatgagtacg agaccggggc tgttgagctg 1980
ttcactgagt gttacagcag cgatgaagac ttggcagaac agctgctggt ctattcctgt 2040

```

```

gaagcttggg gtggaagcaa ctgtctggag ctggcggtgg aggccacaga ccagcatttc 2100
atcgcccagc ctgggggtcca gaattttctt tctaagcaat ggtatggaga gatttcccga 2160
gacaccaaga actggaagat tatcctgtgt ctgtttatta tacccttggg gggctgtggc 2220
tttgtatcat ttaggaagaa acctgtcgac aagcacaaga agctgctttg gtactatgtg 2280
gcgttcttca cctccccctt cgtgggtctt tccctggaatg tggctcttca catcgccctc 2340
ctcctgctgt ttgcctacgt gctgctcatg gatttccatt cgggtgccaca ccccccgag 2400
ctggctcctgt actcgtcgtt ctttgtcctc ttctgtgatg aagttagaca gtggtagcgt 2460
aatgggggtga attattttac tgacctgtgg aatgtgatgg acacgctggg gcttttttac 2520
ttcatagcag gaattgtatt tcggctccac tcttctaata aaagctcttt gtattctgga 2580
cgagtcattt tctgtctgga ctacattatt ttactctaa gattgatcca catttttact 2640
gtaagcagaa acttaggacc caagattata atgctgcaga ggatgctgat cgatgtgttc 2700
ttcttctgt tctcctttgc ggwtgggatg gtggcctttg gcgtggccag gcaagggatc 2760
cttaggcaga atgagcagcg ctggagggtg atattccgtt cggatcatcta cgagccctac 2820
ctggccatgt tcggccaggt gccagtgac gtggatggta ccacgtatga ctttgccac 2880
tgacacctca ctgggaatga gtccaagcca ctgtgtgtgg agctggatga gcacaacctg 2940
ccccggttcc ccgagtggat caccatcccc ctggtgtgca tctacatgtt atccaccaac 3000
atcctgctgg tcaacctgct ggtcgccatg tttggctaca cggtagggcac cgtccaggag 3060
aacaatgacc aggtctggaa gttccagagg tacttctctg tgcaggagta ctgcagccgc 3120
ctcaatatcc ccttccccct catcgtcttc gcttacttct acatggtggt gaagaagtgc 3180
ttcaagtgtt gctgcaagga gaaaaacatg gagtcttctg tctgctgttt caaaaatgaa 3240
gacaatgaga ctctggcatg ggagggtgtc atgaaggaaa actaccttgt caagatcaac 3300
acaaaagcca acgacacctc agaggaaatg aggcacgat ttagacaact ggatacaaag 3360
cttaatgac tcaagggtct tctgaaagag attgctaata aaatcaaata aaactgtatg 3420
aactctaata gagaaaaatc taattatagc aagatcatat taaggaatgc tgatgaacaa 3480
ttttgctatc gactactaaa tgagagattt tcagaccctt gggtagatgg tggatgattt 3540
taaatacccc tagtgtgctg agaccttgag aataaagtgt gaagggcgaa ttctgcagat 3600
atccatcaca ctggcggccg ctcgagcatg catctagag 3639

```

&lt;210&gt; 637

&lt;211&gt; 1095

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(1095)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 637

```

Met Arg Asn Arg Arg Asn Asp Thr Leu Asp Ser Thr Arg Thr Leu Tyr
          5                      10                      15

```

```

Ser Ser Ala Ser Arg Ser Thr Asp Leu Ser Tyr Ser Glu Ser Asp Leu
          20                      25                      30

```

```

Val Asn Phe Ile Gln Ala Asn Phe Lys Lys Arg Glu Cys Val Phe Phe
          35                      40                      45

```

```

Thr Lys Asp Ser Lys Ala Thr Glu Asn Val Cys Lys Cys Gly Tyr Ala
          50                      55                      60

```

```

Gln Ser Gln His Met Glu Gly Thr Gln Ile Asn Gln Ser Glu Lys Trp
          65                      70                      75                      80

```

```

Asn Tyr Lys Lys His Thr Lys Glu Phe Pro Thr Asp Ala Phe Gly Asp
          85                      90                      95

```

```

Ile Gln Phe Glu Thr Leu Gly Lys Lys Gly Lys Tyr Ile Arg Leu Ser

```

255

100	105	110
Cys Asp Thr Asp Ala Glu Ile Leu Tyr Glu Leu Leu Thr Gln His Trp		
115	120	125
His Leu Lys Thr Pro Asn Leu Val Ile Ser Val Thr Gly Gly Ala Lys		
130	135	140
Asn Phe Ala Leu Lys Pro Arg Met Arg Lys Ile Phe Ser Arg Leu Ile		
145	150	155
Tyr Ile Ala Gln Ser Lys Gly Ala Trp Ile Leu Thr Gly Gly Thr His		
165	170	175
Tyr Gly Leu Met Lys Tyr Ile Gly Glu Val Val Arg Asp Asn Thr Ile		
180	185	190
Ser Arg Ser Ser Glu Glu Asn Ile Val Ala Ile Gly Ile Ala Ala Trp		
195	200	205
Gly Met Val Ser Asn Arg Asp Thr Leu Ile Arg Asn Cys Asp Ala Glu		
210	215	220
Gly Tyr Phe Leu Ala Gln Tyr Leu Met Asp Asp Phe Thr Arg Asp Pro		
225	230	235
Leu Tyr Ile Leu Asp Asn Asn His Thr His Leu Leu Leu Val Asp Asn		
245	250	255
Gly Cys His Gly His Pro Thr Val Glu Ala Lys Leu Arg Asn Gln Leu		
260	265	270
Glu Lys Tyr Ile Ser Glu Arg Thr Ile Gln Asp Ser Asn Tyr Gly Gly		
275	280	285
Lys Ile Pro Ile Val Cys Phe Ala Gln Gly Gly Gly Lys Glu Thr Leu		
290	295	300
Lys Ala Ile Asn Thr Ser Ile Lys Asn Lys Ile Pro Cys Val Val Val		
305	310	315
Glu Gly Ser Gly Gln Ile Ala Asp Val Ile Ala Ser Leu Val Glu Val		
325	330	335
Glu Asp Ala Leu Thr Ser Ser Ala Val Lys Glu Lys Leu Val Arg Phe		
340	345	350
Leu Pro Arg Thr Val Ser Arg Leu Pro Glu Glu Glu Thr Glu Ser Trp		
355	360	365
Ile Lys Trp Leu Lys Glu Ile Leu Glu Cys Ser His Leu Leu Thr Val		
370	375	380
Ile Lys Met Glu Glu Ala Gly Asp Glu Ile Val Ser Asn Ala Ile Ser		
385	390	395
Tyr Ala Leu Tyr Lys Ala Phe Ser Thr Ser Glu Gln Asp Lys Asp Asn		
405	410	415

Trp Asn Gly Gln Leu Lys Leu Leu Leu Glu Trp Asn Gln Leu Asp Leu  
 420 425 430  
 Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg Trp Glu Ser Ala Asp  
 435 440 445  
 Leu Gln Glu Val Met Phe Thr Ala Leu Ile Lys Asp Arg Pro Lys Phe  
 450 455 460  
 Val Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr  
 465 470 475 480  
 His Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val  
 485 490 495  
 Tyr Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu  
 500 505 510  
 Thr Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys  
 515 520 525  
 Glu Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val  
 530 535 540  
 Ser Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile  
 545 550 555 560  
 Leu Gln Asn Lys Lys Glu Leu Ser Lys Val Ile Trp Glu Gln Thr Arg  
 565 570 575  
 Gly Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu  
 580 585 590  
 Ala Lys Val Lys Asn Asp Ile Asn Ala Ala Gly Glu Ser Glu Glu Leu  
 595 600 605  
 Ala Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys Tyr  
 610 615 620  
 Ser Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys Glu  
 625 630 635 640  
 Ala Trp Gly Gly Ser Asn Cys Leu Glu Leu Ala Val Glu Ala Thr Asp  
 645 650 655  
 Gln His Phe Ile Ala Gln Pro Gly Val Gln Asn Phe Leu Ser Lys Gln  
 660 665 670  
 Trp Tyr Gly Glu Ile Ser Arg Asp Thr Lys Asn Trp Lys Ile Ile Leu  
 675 680 685  
 Cys Leu Phe Ile Ile Pro Leu Val Gly Cys Gly Phe Val Ser Phe Arg  
 690 695 700  
 Lys Lys Pro Val Asp Lys His Lys Lys Leu Leu Trp Tyr Tyr Val Ala  
 705 710 715 720

Phe Phe Thr Ser Pro Phe Val Val Phe Ser Trp Asn Val Val Phe Tyr  
 725 730 735  
 Ile Ala Phe Leu Leu Leu Phe Ala Tyr Val Leu Leu Met Asp Phe His  
 740 745 750  
 Ser Val Pro His Pro Pro Glu Leu Val Leu Tyr Ser Leu Val Phe Val  
 755 760 765  
 Leu Phe Cys Asp Glu Val Arg Gln Trp Tyr Val Asn Gly Val Asn Tyr  
 770 775 780  
 Phe Thr Asp Leu Trp Asn Val Met Asp Thr Leu Gly Leu Phe Tyr Phe  
 785 790 795 800  
 Ile Ala Gly Ile Val Phe Arg Leu His Ser Ser Asn Lys Ser Ser Leu  
 805 810 815  
 Tyr Ser Gly Arg Val Ile Phe Cys Leu Asp Tyr Ile Ile Phe Thr Leu  
 820 825 830  
 Arg Leu Ile His Ile Phe Thr Val Ser Arg Asn Leu Gly Pro Lys Ile  
 835 840 845  
 Ile Met Leu Gln Arg Met Leu Ile Asp Val Phe Phe Phe Leu Phe Leu  
 850 855 860  
 Phe Ala Xaa Trp Met Val Ala Phe Gly Val Ala Arg Gln Gly Ile Leu  
 865 870 875 880  
 Arg Gln Asn Glu Gln Arg Trp Arg Trp Ile Phe Arg Ser Val Ile Tyr  
 885 890 895  
 Glu Pro Tyr Leu Ala Met Phe Gly Gln Val Pro Ser Asp Val Asp Gly  
 900 905 910  
 Thr Thr Tyr Asp Phe Ala His Cys Thr Phe Thr Gly Asn Glu Ser Lys  
 915 920 925  
 Pro Leu Cys Val Glu Leu Asp Glu His Asn Leu Pro Arg Phe Pro Glu  
 930 935 940  
 Trp Ile Thr Ile Pro Leu Val Cys Ile Tyr Met Leu Ser Thr Asn Ile  
 945 950 955 960  
 Leu Leu Val Asn Leu Leu Val Ala Met Phe Gly Tyr Thr Val Gly Thr  
 965 970 975  
 Val Gln Glu Asn Asn Asp Gln Val Trp Lys Phe Gln Arg Tyr Phe Leu  
 980 985 990  
 Val Gln Glu Tyr Cys Ser Arg Leu Asn Ile Pro Phe Pro Phe Ile Val  
 995 1000 1005  
 Phe Ala Tyr Phe Tyr Met Val Val Lys Lys Cys Phe Lys Cys Cys Cys  
 1010 1015 1020  
 Lys Glu Lys Asn Met Glu Ser Ser Val Cys Cys Phe Lys Asn Glu Asp

1025	1030	1035	1040
Asn Glu Thr Leu Ala Trp Glu Gly Val Met Lys Glu Asn Tyr Leu Val			
1045	1050	1055	
Lys Ile Asn Thr Lys Ala Asn Asp Thr Ser Glu Glu Met Arg His Arg			
1060	1065	1070	
Phe Arg Gln Leu Asp Thr Lys Leu Asn Asp Leu Lys Gly Leu Leu Lys			
1075	1080	1085	
Glu Ile Ala Asn Lys Ile Lys			
1090	1095		

<210> 638  
 <211> 15  
 <212> PRT  
 <213> Homo sapiens

<400> 638  
 Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser  
                   5                  10                  15

<210> 639  
 <211> 45  
 <212> DNA  
 <213> Homo sapiens

<400> 639  
 agaatgccta ccgtgctgca gtgctgaac gtgtcgggtgg tgtct 45

<210> 640  
 <211> 45  
 <212> DNA  
 <213> Homo sapiens

<400> 640  
 gagccagggga gccagatggt ggaggccagc ctctccgtac ggcac 45

<210> 641  
 <211> 45  
 <212> DNA  
 <213> Homo sapiens

<400> 641  
 gaggccgacc aagagccagg gagccagatg gtggaggcca gcctc 45

<210> 642  
 <211> 45  
 <212> DNA  
 <213> Homo sapiens

<400> 642  
 ggctgcaca gtcttgaggc cgaccaagag ccaggggagcc agatg 45

<210> 643

<211> 45

<212> DNA

<213> Homo sapiens

<400> 643

tacaccatcg ggctgggcct gcacagtctt gaggccgacc aagag

45

<210> 644

<211> 42

<212> DNA

<213> Homo sapiens

<400> 644

ttccagaact cctacacat cgggctgggc ctgcacagtc tt

42

<210> 645

<211> 45

<212> DNA

<213> Homo sapiens

<400> 645

ctgtcagccg cacactgttt ccagaactcc tacaccatcg ggctg

45

<210> 646

<211> 45

<212> DNA

<213> Homo sapiens

<400> 646

catccgcagt ggggtgctgtc agccgcacac tgtttccaga actcc

45

<210> 647

<211> 45

<212> DNA

<213> Homo sapiens

<400> 647

tcgggcgtcc tgggtgcatcc gcagtgggtg ctgtcagccg cacac

45

<210> 648

<211> 45

<212> DNA

<213> Homo sapiens

<400> 648

aacgaattgt tctgctcggg cgtcctggtg catccgcagt ggggtg

45

<210> 649

<211> 45

<212> DNA

<213> Homo sapiens

<400> 649

gcactggtca tggaaaacga attgttctgc tcgggcgtcc tgggtg

45

<210> 650

<211> 51

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 650

tcgcagccct ggcaggcggc actgggtcatg gaaaacgaat tgttctgctc g 51

&lt;210&gt; 651

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 651

atcagcattg ctctgcagtg ccctaccgag gggaaactctt gcctc 45

&lt;210&gt; 652

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 652

tccgtgtccg agtctgacac catccggagc atcagcattg ctctg 45

&lt;210&gt; 653

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 653

atcaagttgg acgaatccgt gtccgagtct gacaccatcc ggagc 45

&lt;210&gt; 654

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 654

aacgacctca tgctcatcaa gttggacgaa tccgtgtccg agtct 45

&lt;210&gt; 655

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 655

agacccttgc tcgctaacga cctcatgctc atcaagttgg acgaa 45

&lt;210&gt; 656

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 656

Glu	Pro	Gly	Ser	Gln	Met	Val	Glu	Ala	Ser	Leu	Ser	Val	Arg	His

5

10

15

&lt;210&gt; 657

&lt;211&gt; 15



<212> PRT

<213> Homo sapiens

<400> 657

Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu Ala Ser Leu  
5 10 15

<210> 658

<211> 15

<212> PRT

<213> Homo sapiens

<400> 658

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met  
5 10 15

<210> 659

<211> 15

<212> PRT

<213> Homo sapiens

<400> 659

Tyr Thr Ile Gly Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu  
5 10 15

<210> 660

<211> 14

<212> PRT

<213> Homo sapiens

<400> 660

Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly Leu His Ser Leu  
5 10

<210> 661

<211> 15

<212> PRT

<213> Homo sapiens

<400> 661

Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu  
5 10 15

<210> 662

<211> 15

<212> PRT

<213> Homo sapiens

<400> 662

His Pro Gln Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser  
5 10 15

<210> 663  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 663  
Ser Gly Val Leu Val His Pro Gln Trp Val Leu Ser Ala Ala His  
5 10 15

<210> 664  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 664  
Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val  
5 10 15

<210> 665  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 665  
Ala Leu Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val  
5 10 15

<210> 666  
<211> 17  
<212> PRT  
<213> Homo sapiens

<400> 666  
Ser Gln Pro Trp Gln Ala Ala Leu Val Met Glu Asn Glu Leu Phe Cys  
5 10 15

Ser

<210> 667  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 667  
Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn Ser Cys Leu  
5 10 15

<210> 668  
<211> 15  
<212> PRT  
<213> Homo sapiens

263

&lt;400&gt; 668

Ser Val Ser Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser  
5 10 15

&lt;210&gt; 669

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 669

Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp Thr Ile Arg Ser  
5 10 15

&lt;210&gt; 670

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 670

Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser  
5 10 15

&lt;210&gt; 671

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 671

Arg Pro Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu  
5 10 15

&lt;210&gt; 672

&lt;211&gt; 35

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 672

ggaccagcat atgaggaaca gaaggaatga cactc

35

&lt;210&gt; 673

&lt;211&gt; 29

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 673

ccgctcgagt ccacccaag cttcacagg

29

```
<210> 675
<211> 652
<212> PRT
<213> Homo sapiens
```

<400> 675																
Met	Arg	Asn	Arg	Arg	Asn	Asp	Thr	Leu	Asp	Ser	Thr	Arg	Thr	Leu	Tyr	
				5					10					15		
Ser	Ser	Ala	Ser	Arg	Ser	Thr	Asp	Leu	Ser	Tyr	Ser	Glu	Ser	Asp	Leu	
			20					25					30			
Val	Asn	Phe	Ile	Gln	Ala	Asn	Phe	Lys	Lys	Arg	Glu	Cys	Val	Phe	Phe	
		35					40					45				
Thr	Lys	Asp	Ser	Lys	Ala	Thr	Glu	Asn	Val	Cys	Lys	Cys	Gly	Tyr	Ala	
	50					55					60					

Gln Ser Gln His Met Glu Gly Thr Gln Ile Asn Gln Ser Glu Lys Trp  
 65 70 75 80  
 Asn Tyr Lys Lys His Thr Lys Glu Phe Pro Thr Asp Ala Phe Gly Asp  
 85 90 95  
 Ile Gln Phe Glu Thr Leu Gly Lys Lys Gly Lys Tyr Ile Arg Leu Ser  
 100 105 110  
 Cys Asp Thr Asp Ala Glu Ile Leu Tyr Glu Leu Leu Thr Gln His Trp  
 115 120 125  
 His Leu Lys Thr Pro Asn Leu Val Ile Ser Val Thr Gly Gly Ala Lys  
 130 135 140  
 Asn Phe Ala Leu Lys Pro Arg Met Arg Lys Ile Phe Ser Arg Leu Ile  
 145 150 155 160  
 Tyr Ile Ala Gln Ser Lys Gly Ala Trp Ile Leu Thr Gly Gly Thr His  
 165 170 175  
 Tyr Gly Leu Met Lys Tyr Ile Gly Glu Val Val Arg Asp Asn Thr Ile  
 180 185 190  
 Ser Arg Ser Ser Glu Glu Asn Ile Val Ala Ile Gly Ile Ala Ala Trp  
 195 200 205  
 Gly Met Val Ser Asn Arg Asp Thr Leu Ile Arg Asn Cys Asp Ala Glu  
 210 215 220  
 Gly Tyr Phe Leu Ala Gln Tyr Leu Met Asp Asp Phe Thr Arg Asp Pro  
 225 230 235 240  
 Leu Tyr Ile Leu Asp Asn Asn His Thr His Leu Leu Leu Val Asp Asn  
 245 250 255  
 Gly Cys His Gly His Pro Thr Val Glu Ala Lys Leu Arg Asn Gln Leu  
 260 265 270  
 Glu Lys Tyr Ile Ser Glu Arg Thr Ile Gln Asp Ser Asn Tyr Gly Gly  
 275 280 285  
 Lys Ile Pro Ile Val Cys Phe Ala Gln Gly Gly Gly Lys Glu Thr Leu  
 290 295 300  
 Lys Ala Ile Asn Thr Ser Ile Lys Asn Lys Ile Pro Cys Val Val Val  
 305 310 315 320  
 Glu Gly Ser Gly Gln Ile Ala Asp Val Ile Ala Ser Leu Val Glu Val  
 325 330 335  
 Glu Asp Ala Leu Thr Ser Ser Ala Val Lys Glu Lys Leu Val Arg Phe  
 340 345 350  
 Leu Pro Arg Thr Val Ser Arg Leu Pro Glu Glu Glu Thr Glu Ser Trp  
 355 360 365  
 Ile Lys Trp Leu Lys Glu Ile Leu Glu Cys Ser His Leu Leu Thr Val

370					375					380					
Ile 385	Lys	Met	Glu	Glu	Ala 390	Gly	Asp	Glu	Ile	Val 395	Ser	Asn	Ala	Ile	Ser 400
Tyr	Ala	Leu	Tyr	Lys 405	Ala	Phe	Ser	Thr	Ser 410	Glu	Gln	Asp	Lys	Asp	Asn 415
Trp	Asn	Gly	Gln 420	Leu	Lys	Leu	Leu	Leu	Glu 425	Trp	Asn	Gln	Leu	Asp	Leu 430
Ala	Asn	Asp 435	Glu	Ile	Phe	Thr	Asn 440	Asp	Arg	Arg	Trp	Glu 445	Ser	Ala	Asp
Leu	Gln 450	Glu	Val	Met	Phe	Thr 455	Ala	Leu	Ile	Lys	Asp 460	Arg	Pro	Lys	Phe
Val 465	Arg	Leu	Phe	Leu	Glu 470	Asn	Gly	Leu	Asn 475	Leu	Arg	Lys	Phe	Leu	Thr 480
His	Asp	Val	Leu	Thr 485	Glu	Leu	Phe	Ser	Asn 490	His	Phe	Ser	Thr	Leu	Val 495
Tyr	Arg	Asn 500	Leu	Gln	Ile	Ala	Lys	Asn 505	Ser	Tyr	Asn	Asp	Ala	Leu	Leu 510
Thr	Phe	Val 515	Trp	Lys	Leu	Val	Ala 520	Asn	Phe	Arg	Arg	Gly 525	Phe	Arg	Lys
Glu 530	Asp	Arg	Asn	Gly	Arg	Asp 535	Glu	Met	Asp	Ile	Glu 540	Leu	His	Asp	Val
Ser 545	Pro	Ile	Thr	Arg	His 550	Pro	Leu	Gln	Ala	Leu 555	Phe	Ile	Trp	Ala	Ile 560
Leu	Gln	Asn	Lys	Lys 565	Glu	Leu	Ser	Lys	Val 570	Ile	Trp	Glu	Gln	Thr	Arg 575
Gly	Cys	Thr	Leu 580	Ala	Ala	Leu	Gly	Ala 585	Ser	Lys	Leu	Leu	Lys	Thr	Leu 590
Ala	Lys	Val 595	Lys	Asn	Asp	Ile	Asn 600	Ala	Ala	Gly	Glu	Ser 605	Glu	Glu	Leu
Ala	Asn	Glu	Tyr	Glu	Thr	Arg 615	Ala	Val	Glu	Leu	Phe 620	Thr	Glu	Cys	Tyr
Ser 625	Ser	Asp	Glu	Asp	Leu	Ala	Glu	Gln	Leu	Leu 635	Val	Tyr	Ser	Cys	Glu 640
Ala	Trp	Gly	Gly	Leu 645	Glu	His	His	His	His 650	His	His	His			

<210> 676

<211> 132

&lt;212&gt; PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 676

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1          5          10          15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20          25          30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35          40          45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50          55          60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65          70          75          80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85          90          95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100         105         110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115         120         125
Gly Pro Pro Ala
130

```

&lt;210&gt; 677

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 677

ggggaattca tgatccggga gaaatttgcc cactgc

36

&lt;210&gt; 678

&lt;211&gt; 33

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 678

gggctcgagt caggagtttg agaccagcct ggc

33

&lt;210&gt; 679

&lt;211&gt; 675

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 679

```

atgcatacc atcaccatca cacggcgcgcg tccgataact tccagctgtc ccagggtggg 60
cagggtatcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120

```

```

accgttcata  tggggcctac  cgccttcctc  ggcttgggtg  ttgtcgacaa  caacggcaac  180
ggcgacagag  tocaacgcgt  ggtcgggagc  gctccggcgg  caagtctcgg  catctccacc  240
ggcgacgtga  tcaccgcggt  cgacggcgct  ccgatcaact  cggccaccgc  gatggcggac  300
gcgcttaacg  ggcacatccc  cgggtgacgtc  atctcgggtg  cctggcaaac  caagtcgggc  360
ggcacgcgta  cagggaacgt  gacattggcc  gagggacccc  cggccgaatt  catgatccgg  420
gagaaatttg  cccactgcac  cgtgctaacc  attgcacaca  gattgaacac  cattattgac  480
agcgacaaga  taatggtttt  agattcagga  agactgaaag  aatatgatga  gccgatgttt  540
ttgctgcaaa  ataaagagag  cctattttac  aagatggtgc  aacaactggg  caaggcagaa  600
gccgctgccc  tcaactgaaac  agcaaaacag  agatgggggt  tcacccatgtt  ggccaggctg  660
gtctcaaaact  cctga

```

&lt;210&gt; 680

&lt;211&gt; 291

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 680

```

atggggatcc  gggagaaatt  tgccactgac  accgtgctaa  ccattgcaca  cagattgaac  60
accattattg  acagcgacaa  gataatgggt  ttagattcag  gaagactgaa  agaatatgat  120
gagccgtatg  ttttgctgca  aaataaagag  agcctatttt  acaagatggt  gcaacaactg  180
ggcaaggcag  aagccgctgc  cctcactgaa  acagcaaaac  agagatgggg  tttcaccatg  240
ttggccaggc  tgggtctcaa  ctccctcgag  caccaccacc  accaccactg  a

```

&lt;210&gt; 681

&lt;211&gt; 1074

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 681

```

atgtcagcca  ttgagagggt  gtcagaggca  atcgtcagca  tccgaagaat  ccagaccttt  60
ttgctacttg  atgagatata  acagcgcaac  cgtcagctgc  cgtcagatgg  taaaaagatg  120
gtgcatgtgc  aggattttac  tgcttttttg  gataaggcat  cagagacccc  aactctacaa  180
ggcctttcct  ttactgtcag  acctggcgaa  ttgttagctg  tggtcggccc  cgtggggagca  240
gggaagtcac  cactgttaag  tgccgtgttc  ggggaattgg  cccaagtca  cgggctgggtc  300
agcgtgcatg  gaagaattgc  ctatgtgtct  cagcagccct  ggggtgttct  gggaactctg  360
aggagtaata  ttttatttgg  gaagaaatac  gaaaaggaaac  gatatgaaaa  agtcataaaag  420
gcttgtgtct  tgaaaaagga  ttacacgtg  ttggaggatg  gtgatctgac  tgtgatagga  480
gatcggggaa  ccacgtgag  tggagggcag  aaagcacggg  taaaccttgc  aagagcagtg  540
tatcaagatg  ctgacatcta  tctcctggac  gatcctctca  gtgcagtaga  tgcggaagtt  600
agcagacact  tgttcgaact  gtgtatttgc  caaattttgc  atgagaagat  cacaatttta  660
gtgactcatc  agttgcagta  cctcaaagct  gcaagtcaga  ttctgatatt  gaaagatggt  720
aaaatggtgc  agaaggggac  ttacactgag  ttcctaaaat  ctggtataga  ttttggctcc  780
cttttaaaga  aggataatga  ggaaagtga  caacctccag  ttccaggaaac  tcccacacta  840
aggaatcgta  ctttctcaga  gtcttcgggt  tgggtctcaac  aatcttctag  accctccttg  900
aaagatggtg  ctctggagag  ccaagataca  gagaatgtcc  cagttacact  atcagaggag  960
aaccgttctg  aaggaaaagt  tggttttcag  gcctataaga  attacttcag  agctggtgct  1020
cactggattg  tcttcatttt  ccttatttct  gagcaccacc  accaccacca  ctga

```

&lt;210&gt; 682

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 682

```

Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu
      5                                10                        15

```

```

Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala

```



20	25	30
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala		
35	40	45
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val		
50	55	60
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr		
65	70	75
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr		
85	90	95
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser		
100	105	110
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr		
115	120	125
Leu Ala Glu Gly Pro Pro Ala Glu Phe Met Ile Arg Glu Lys Phe Ala		
130	135	140
His Cys Thr Val Leu Thr Ile Ala His Arg Leu Asn Thr Ile Ile Asp		
145	150	155
Ser Asp Lys Ile Met Val Leu Asp Ser Gly Arg Leu Lys Glu Tyr Asp		
165	170	175
Glu Pro Tyr Val Leu Leu Gln Asn Lys Glu Ser Leu Phe Tyr Lys Met		
180	185	190
Val Gln Gln Leu Gly Lys Ala Glu Ala Ala Ala Leu Thr Glu Thr Ala		
195	200	205
Lys Gln Arg Trp Gly Phe Thr Met Leu Ala Arg Leu Val Ser Asn Ser		
210	215	220

&lt;210&gt; 683

&lt;211&gt; 357

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 683

Met Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg Arg
5 10 15

Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg Gln
20 25 30

Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr Ala
35 40 45

Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser Phe
---

270

50	55	60
Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly Ala 65 70 75 80		
Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro Ser 85 90 95		
His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln Gln 100 105 110		
Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly Lys 115 120 125		
Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala Leu 130 135 140		
Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile Gly 145 150 155 160		
Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln Lys Ala Arg Val Asn Leu 165 170 175		
Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp Pro 180 185 190		
Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu Cys 195 200 205		
Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His Gln 210 215 220		
Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp Gly 225 230 235 240		
Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly Ile 245 250 255		
Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln Pro 260 265 270		
Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu Ser 275 280 285		
Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly Ala 290 295 300		
Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu Glu 305 310 315 320		
Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr Phe 325 330 335		
Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Glu His 340 345 350		
His His His His His 355		

&lt;210&gt; 684

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 684

Met Gly Ile Arg Glu Lys Phe Ala His Cys Thr Val Leu Thr Ile Ala  
                                   5                                  10                                  15

His Arg Leu Asn Thr Ile Ile Asp Ser Asp Lys Ile Met Val Leu Asp  
                                   20                                  25                                  30

Ser Gly Arg Leu Lys Glu Tyr Asp Glu Pro Tyr Val Leu Leu Gln Asn  
                                   35                                  40                                  45

Lys Glu Ser Leu Phe Tyr Lys Met Val Gln Gln Leu Gly Lys Ala Glu  
                                   50                                  55                                  60

Ala Ala Ala Leu Thr Glu Thr Ala Lys Gln Arg Trp Gly Phe Thr Met  
                                   65                                  70                                  75                                  80

Leu Ala Arg Leu Val Ser Asn Ser Leu Glu His His His His His His  
                                   85                                  90                                  95

&lt;210&gt; 685

&lt;211&gt; 35

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 685

cgcccatggg gatccgggag aaatttgccc actgc

35

&lt;210&gt; 686

&lt;211&gt; 35

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 686

cgctcgagg gagtttgaga ccagcctggc caaca

35

&lt;210&gt; 687

&lt;211&gt; 38

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

<400> 687  
gcatggacca tatgtcagcc attgagaggg tgtcagag

38

<210> 688  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 688  
ccgctcgaga ataaggaaaa tgaagacaat ccag

34

<210> 689  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 689  
gttgaattca tgcacggggcc ccaggtg

27

<210> 690  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 690  
cccctcgagt cactatgggtc tgcctcttga

30

<210> 691  
<211> 915  
<212> DNA  
<213> Homo sapiens

<400> 691  
atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccaggggtggg 60  
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagcttccc 120  
accgttcata tcggggcctac cgccttcctc ggcttggtg ttgtcgacaa caacggcaac 180  
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcgg catctccacc 240  
ggcgacgtga tcaccgcgt cgacggcgct ccgatcaact cggccaccgc gatggcggac 300  
gcgcttaacg ggcacatccc cggtgacgtc atctcgggtga cctggcaaac caagtcgggc 360  
ggcacgcgta cagggaaagt gacattggcc gagggacccc cggccgaatt catgcaoggg 420  
cccaggtgc tggcacgctg ctccgagtg gcttgctctg ccttggctgc cacctctgcg 480  
ggggtgcgtc tggagggggt ggaccggcca ccaaccttac ccagtcaagg aagtggatgg 540  
ccatgttccc acagcctgag tggctgccac ctgatggctg atggagcaaa ggccttagga 600  
aaagcagatg gcccttggcc ctacctttt gttagaagaa ctgatgttcc atgtcctgca 660  
gcgagtgagg ttggtggctg tgccccagc tcctggcgcg ccctcgaga ggtgactggt 720

tgctctttgg gccctcttgg ccttgcccag catgcacaag cctcagtgtc actactgtgc 780  
 tacaaatgga gccatatagg ggaaacgagc agccatctca ggagcaagggt gtatgctgcc 840  
 ttggggggct ccagtccttg cctcaagggt cttatgtcac tgtgggcttc ttggttgtca 900  
 agaggcagac catag 915

<210> 692

<211> 304

<212> PRT

<213> Homo sapiens

<400> 692

Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu  
 5 10 15

Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala  
 20 25 30

Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala  
 35 40 45

Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val  
 50 55 60

Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr  
 65 70 75 80

Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr  
 85 90 95

Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser  
 100 105 110

Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr  
 115 120 125

Leu Ala Glu Gly Pro Pro Ala Glu Phe Met His Gly Pro Gln Val Leu  
 130 135 140

Ala Arg Cys Ser Glu Cys Ala Cys Pro Ala Leu Ala Ala Thr Ser Ala  
 145 150 155 160

Gly Val Arg Leu Glu Gly Val Asp Arg Pro Pro Thr Leu Pro Ser Gln  
 165 170 175

Gly Ser Gly Trp Pro Cys Ser His Ser Leu Ser Gly Cys His Leu Met  
 180 185 190

Ala Asp Gly Ala Lys Ala Leu Gly Lys Ala Asp Gly Pro Trp Pro Tyr  
 195 200 205

Leu Phe Val Arg Arg Thr Asp Val Pro Cys Pro Ala Ala Ser Glu Val  
 210 215 220

Gly Gly Cys Ala Pro Ser Ser Trp Arg Ala Leu Ala Glu Val Thr Gly  
 225 230 235 240

Cys Ser Leu Gly Pro Leu Gly Leu Ala Gln His Ala Gln Ala Ser Val  
 245 250 255

Leu Leu Leu Cys Tyr Lys Trp Ser His Ile Gly Glu Thr Ser Ser His  
260 265 270

Leu Arg Ser Lys Val Tyr Ala Ala Phe Gly Gly Ser Ser Pro Cys Leu  
275 280 285

Lys Gly Leu Met Ser Leu Trp Ala Ser Trp Leu Ser Arg Gly Arg Pro  
290 295 300

```
<210> 693
<211> 24
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> PCR primer

<400> 693  
cgaagtcacg tggaggccag cctc 24

```
<210> 694
<211> 29
<212> DNA
<213> Artificial Sequence
```

<220>  
<223> PCR primer

<400> 694  
cctgaccgaa ttcattaact ggcttgac . 29

```
<210> 695
<211> 166
<212> PRT
<213> Homo sapiens
```

```
<220>
<221> VARIANT
<222> (1)...(166)
<223> Xaa = Any Amino Acid
```

<400> 695																
Met	Gly	His	His	His	His	His	His	Val	Glu	Ala	Ser	Leu	Ser	Val	Arg	
1				5					10					15		
His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu	Leu	Ala	Asn	Asp	Leu	Met	Leu	Ile	
			20					25					30			
Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu	Ser	Asp	Thr	Ile	Arg	Ser	Ile	Ser	
		35					40					45				
Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala	Gly	Asn	Ser	Cys	Leu	Val	Ser	Gly	
	50					55					60					
Trp	Gly	Leu	Leu	Ala	Asn	Gly	Arg	Met	Pro	Thr	Val	Leu	Gln	Cys	Val	
65					70					75				80		
Asn	Val	Ser	Val	Val	Ser	Glu	Glu	Val	Cys	Ser	Lys	Leu	Tyr	Asp	Pro	

275

	85		90		95
Leu Tyr His Pro Ser Met Phe Cys Ala Gly Gly Gln Xaa Gln Xaa					
	100		105		110
Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro Leu Ile Cys Asn Gly Tyr					
	115		120		125
Leu Gln Gly Leu Val Ser Phe Gly Lys Ala Pro Cys Gly Gln Val Gly					
	130		135		140
Val Pro Gly Val Tyr Thr Asn Leu Cys Lys Phe Thr Glu Trp Ile Glu					
	145		150		155
Lys Thr Val Gln Ala Ser					160
	165				

&lt;210&gt; 696

&lt;211&gt; 504

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(504)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 696

atgggccaac	atcatcatca	tcacgtggag	gccagcctct	ccgtacggca	cccagagtac	60
aacagaccct	tgctcgctaa	cgacctcatg	ctcatcaagt	tggaacgaatc	cggtgtccgag	120
tctgacacca	tccggagcat	cagcattgct	tcgcagtgcc	ctaccgcggg	gaaactcttg	180
ctcgtttctg	gctgggggtct	gctggcgaac	ggcagaatgc	ctaccgtgct	gcagtgcgtg	240
aacgtgtcgg	tggtgtctga	ggaggtctgc	agtaagctct	atgacccgct	gtaccacccc	300
agcatgttct	gcgccggcgg	agggcaanac	cagaangact	cctgcaacgg	tgactctggg	360
gggcccctga	tctgcaacgg	gtacttgacg	ggccttggtg	ctttcggaaa	agccccgtgt	420
ggccaagttg	gcgtgccagg	tgtctacacc	aacctctgca	aattcactga	gtggatagag	480
aaaaccgtcc	aggccagtta	atga				504

&lt;210&gt; 697

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 697

ctcagggttc cggagccgcg g 21

&lt;210&gt; 698

&lt;211&gt; 35

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 698

ctatagaatt cattaccaa aagctgggct ccagc 35

&lt;210&gt; 699

<211> 241  
 <212> PRT  
 <213> Homo sapiens

<400> 699

Met	Gln	His	His	His	His	His	His	Leu	Arg	Val	Pro	Glu	Pro	Arg	Pro
1				5					10					15	
Gly	Glu	Ala	Lys	Ala	Glu	Gly	Ala	Ala	Pro	Pro	Thr	Pro	Ser	Lys	Pro
			20					25					30		
Leu	Thr	Ser	Phe	Leu	Ile	Gln	Asp	Ile	Leu	Arg	Asp	Gly	Ala	Gln	Arg
		35					40					45			
Gln	Gly	Gly	Arg	Thr	Ser	Ser	Gln	Arg	Gln	Arg	Asp	Pro	Glu	Pro	Glu
	50					55					60				
Pro	Glu	Pro	Glu	Pro	Glu	Gly	Gly	Arg	Ser	Arg	Ala	Gly	Ala	Gln	Asn
65					70					75					80
Asp	Gln	Leu	Ser	Thr	Gly	Pro	Arg	Ala	Ala	Pro	Glu	Glu	Ala	Glu	Thr
				85					90					95	
Leu	Ala	Glu	Thr	Glu	Pro	Glu	Arg	His	Leu	Gly	Ser	Tyr	Leu	Leu	Asp
			100					105					110		
Ser	Glu	Asn	Thr	Ser	Gly	Ala	Leu	Pro	Arg	Leu	Pro	Gln	Thr	Pro	Lys
		115					120					125			
Gln	Pro	Gln	Lys	Arg	Ser	Arg	Ala	Ala	Phe	Ser	His	Thr	Gln	Val	Ile
	130					135					140				
Glu	Leu	Glu	Arg	Lys	Phe	Ser	His	Gln	Lys	Tyr	Leu	Ser	Ala	Pro	Glu
145					150					155					160
Arg	Ala	His	Leu	Ala	Lys	Asn	Leu	Lys	Leu	Thr	Glu	Thr	Gln	Val	Lys
				165					170					175	
Ile	Trp	Phe	Gln	Asn	Arg	Arg	Tyr	Lys	Thr	Lys	Arg	Lys	Gln	Leu	Ser
			180				185						190		
Ser	Glu	Leu	Gly	Asp	Leu	Glu	Lys	His	Ser	Ser	Leu	Pro	Ala	Leu	Lys
		195					200					205			
Glu	Glu	Ala	Phe	Ser	Arg	Ala	Ser	Leu	Val	Ser	Val	Tyr	Asn	Ser	Tyr
	210					215					220				
Pro	Tyr	Tyr	Pro	Tyr	Leu	Tyr	Cys	Val	Gly	Ser	Trp	Ser	Pro	Ala	Phe
225					230					235					240
Trp															

<210> 700  
 <211> 729  
 <212> DNA  
 <213> Homo sapiens

<400> 700

atgcagcatc	accaccatca	ccacctcagg	gttcgggagc	cgcgggcccg	ggaggcgaaa	60
gcgagggggg	ccgcgcgcgc	gaccccgctc	aagccgctca	cgtccttcct	catccaggac	120
atcctgcggg	acggcgcgca	gcggaaggc	ggccgcacga	gcagccagag	acagcgcgac	180
ccggagccgg	agccagagcc	agagccagag	ggaggacgca	gccgcgccgg	ggcgcagaac	240
gaccagctga	gcaccggggc	ccgcgcgcgc	ccggatgagg	ccgagacgct	ggcagagacc	300
gagccagaaa	ggcacttggg	gtcttatctg	ttggactctg	aaaacacttc	aggcgcctt	360
ccaaggcttc	cccaaacc	taagcagccg	cagaagcgct	cccagactgc	cttctccac	420
actcaggtga	tcgagttgga	gaggaagttc	agccatcaga	agtacgtg	ggcccctgaa	480
cgggcccacc	tgccaagaa	cctcaagctc	acggagaccc	aagtgaagat	atgggtccag	540
aacagacgct	ataagactaa	gcgaaagcag	ctctcctcgg	agctgggaga	cttgaggaga	600
cactcctttt	tgccggccct	gaaagaggag	gccttctccc	gggcctccct	ggtctccgtg	660
tataacagct	atccttacta	cccatacctg	cactgcgtgg	gcagctggag	cccagctttt	720
tggtaatga						729



<210> 701  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 701  
 ctactaagcg ctggagtgag ggatcag

27

<210> 702  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 702  
 catcgagaat tcactactct ctgactagat gtc

33

<210> 703  
 <211> 161  
 <212> PRT  
 <213> Homo sapiens

<400> 703  
 Met Gln His His His His His Ala Gly Val Arg Asp Gln Gly Gln  
 1 5 10 15  
 Gly Ala Arg Trp Pro His Thr Gly Lys Arg Gly Pro Leu Leu Gln Gly  
 20 25 30  
 Leu Thr Trp Ala Thr Gly Gly His Cys Phe Ser Ser Glu Glu Ser Gly  
 35 40 45  
 Ala Val Asp Gly Ala Gly Gln Lys Lys Asp Arg Ala Trp Leu Arg Cys  
 50 55 60  
 Pro Glu Ala Val Ala Gly Phe Pro Leu Gly Ser Asp Cys Arg Glu Gly  
 65 70 75 80  
 Gly Arg Gln Gly Cys Gly Gly Ser Asp Asp Glu Asp Asp Leu Gly Val  
 85 90 95  
 Ala Pro Gly Leu Ala Pro Ala Trp Ala Leu Thr Gln Pro Pro Ser Gln  
 100 105 110  
 Ser Pro Gly Pro Gln Ser Leu Pro Ser Thr Pro Ser Ser Ile Trp Pro  
 115 120 125  
 Gln Trp Val Ile Leu Ile Thr Glu Leu Thr Ile Pro Ser Pro Ala His  
 130 135 140  
 Gly Pro Pro Trp Leu Pro Asn Ala Leu Glu Arg Gly His Leu Val Arg  
 145 150 155 160  
 Glu

<210> 704  
 <211> 489  
 <212> DNA  
 <213> Homo sapiens

278

<400> 704  
 atgcagcatc accaccatca ccacgctgga gtgagggatc agggggcaggg cgcgagatgg 60  
 cctcacacag ggaagagagg gccctcctg cagggcctca cctgggccac aggaggacac 120  
 tgcttttccct ctgaggagtc aggagctgtg gatgggtctg gacagaagaa ggacagggcc 180  
 tggctcaggt gtccagaggc tgtcgctggc ttccctttgg gatcagactg cagggaggga 240  
 gggcggcagg gttgtggggg gaggtagcat gaggatgacc tgggggtggc tccaggcctt 300  
 gccctgcct gccccctcac ccagcctccc tcacagtctc ctggccctca gtctctcccc 360  
 tccactccat cctccatctg gctcagtggt gtcattctga tcaactgaact gaccataccc 420  
 agccctgccc acggccctcc atggctcccc aatgccctgg agaggggaca tctagtcaga 480  
 gagtagtga 489

<210> 705  
 <211> 132  
 <212> PRT  
 <213> Homo sapiens

<400> 705  
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe  
 1 5 10 15  
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser  
 20 25 30  
 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly  
 35 40 45  
 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val  
 50 55 60  
 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val  
 65 70 75 80  
 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala  
 85 90 95  
 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp  
 100 105 110  
 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu  
 115 120 125  
 Gly Pro Pro Ala  
 130

<210> 706  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 706  
 ggggaattca tcacctatgt gccgcctctg c

31

<210> 707  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

40

<210> 708

<211> 1203

<212> DNA

<213> Homo sapiens

<400> 708

atgcatcacc	atcaccatca	cacggccgcg	tccgataact	tccagctgtc	ccaggggtggg	60
cagggattcg	ccattccgat	cgggcaggcg	atggcgatcg	cgggccagat	caagcttccc	120
accgttcata	tcgggcctac	cgccttcctc	ggcttgggtg	ttgtcgacaa	caacggcaac	180
ggcgcacgag	tccaacgcgt	ggtcgggagc	gctccggcgg	caagtctcgg	catctccacc	240
ggcgacgtga	tcaccgcggt	cgaaggcgct	ccgatcaact	cggccaccgc	gatggcggac	300
gcgcttaacg	ggcatcatcc	cggtgacgtc	atctcggtga	cctggcaaac	caagtcgggc	360
ggcacgcgta	caggaacgt	gacattggcc	gagggacccc	cggccgaatt	catcacctat	420
gtgccgcctc	tgctgctgga	agtgggggta	gaggagaagt	tcatgaccat	ggtgctgggc	480
attggtccag	tgctgggcct	ggtctgtgtc	ccgctcctag	gctcagccag	tgaccactgg	540
cgtggacgct	atggccgccc	ccggcccttc	atctgggcac	tgtccttggg	catcctgctg	600
agcctctttc	tcatcccaag	ggccggctgg	ctagcagggc	tgctgtgcc	ggatcccagg	660
cccctggagc	tggcactgct	catcctgggc	gtggggctgc	tggacttctg	tggccaggtg	720
tgcttcactc	cactggaggc	cctgctctct	gacctcttcc	gggacccgga	ccactgtcgc	780
caggcctact	ctgtctatgc	cttcatgata	agtcttgggg	gctgcctggg	ctacctctg	840
cctgccattg	actgggacac	cagtgccctg	gccccctacc	tgggaccca	ggaggagtgc	900
ctctttggcc	tgtcaccct	catcttcctc	acctcgctag	cggccacact	gctggtggct	960
gaggaggcag	cgctggggcc	caccgagcca	gcagaagggc	tgtcggcccc	ctccttgtcg	1020
ccccactgct	gtccatgccg	ggcccgcctt	gctttccgga	acctgggcgc	cctgcttccc	1080
cggctgcacc	agctgtgctg	ccgcatgccc	cgcacctctg	gccggtcttt	cgtggctgag	1140
ctgtgcagct	ggatggcact	catgaccttc	acgctgtttt	acacggattt	cgtgggcgag	1200
tga						1203

<210> 709

<211> 400

<212> PRT

<213> Homo sapiens

<400> 709

Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu  
5 10 15

Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala  
20 25 30

Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala  
35 40 45

Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val  
50 55 60

Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr  
65 70 75 80

Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr  
85 90 95

Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser

Val	Thr	Trp	Gln	Thr	Lys	Ser	Gly	Gly	Thr	Arg	Thr	Gly	Asn	Val	Thr
		115					120					125			
Leu	Ala	Glu	Gly	Pro	Pro	Ala	Glu	Phe	Ile	Thr	Tyr	Val	Pro	Pro	Leu
	130					135					140				
Leu	Leu	Glu	Val	Gly	Val	Glu	Glu	Lys	Phe	Met	Thr	Met	Val	Leu	Gly
145					150					155					160
Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys	Val	Pro	Leu	Leu	Gly	Ser	Ala
				165					170					175	
Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly	Arg	Arg	Arg	Pro	Phe	Ile	Trp
			180					185					190		
Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser	Leu	Phe	Leu	Ile	Pro	Arg	Ala
		195					200					205			
Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro	Asp	Pro	Arg	Pro	Leu	Glu	Leu
	210					215					220				
Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	Leu	Leu	Asp	Phe	Cys	Gly	Gln	Val
225					230					235					240
Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu	Ser	Asp	Leu	Phe	Arg	Asp	Pro
				245					250					255	
Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val	Tyr	Ala	Phe	Met	Ile	Ser	Leu
			260					265					270		
Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro	Ala	Ile	Asp	Trp	Asp	Thr	Ser
		275					280					285			
Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln	Glu	Glu	Cys	Leu	Phe	Gly	Leu
		290				295					300				
Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val	Ala	Ala	Thr	Leu	Leu	Val	Ala
305					310					315					320
Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu	Pro	Ala	Glu	Gly	Leu	Ser	Ala
				325					330					335	
Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro	Cys	Arg	Ala	Arg	Leu	Ala	Phe
			340					345					350		
Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	Leu	His	Gln	Leu	Cys	Cys	Arg
		355					360					365			
Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val	Ala	Glu	Leu	Cys	Ser	Trp
	370					375					380				
Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	Thr	Asp	Phe	Val	Gly	Glu
385					390					395					400

<210> 710  
<211> 20  
<212> PRT  
<213> Homo sapiens

<400> 710  
Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val  
                    5                    10                    15

Ser Val Arg Val  
                    20

<210> 711  
<211> 60  
<212> DNA  
<213> Homo sapiens

<400> 711  
ctgctccac ctccaccgc gctctgcggg gcctctgcct gtgatgtctc cgtacgtgtg 60

<210> 712  
<211> 10  
<212> PRT  
<213> Homo sapiens

<400> 712  
Ala Ser Ala Cys Asp Val Ser Val Arg Val  
                    5                    10

<210> 713  
<211> 30  
<212> DNA  
<213> Homo sapiens

<400> 713  
gcctctgcct gtgatgtctc cgtacgtgtg 30

<210> 714  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 714  
Ala Ser Ala Cys Asp Val Ser Val Arg  
1                    5

<210> 715  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 715  
Ser Ala Cys Asp Val Ser Val Arg Val  
                    5

<210> 716  
<211> 27

<212> DNA  
<213> Homo sapiens

<400> 716  
tctgcctgtg atgtctccgt acgtgtg

27

<210> 717  
<211> 19  
<212> PRT  
<213> Homo sapiens

<400> 717  
Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro Leu Leu Gly Ser  
                    5                    10                    15

Ala Ser Asp

<210> 718  
<211> 19  
<212> PRT  
<213> Homo sapiens

<400> 718  
Val Pro Pro Leu Leu Leu Glu Val Gly Val Glu Glu Lys Phe Met Thr  
                    5                    10                    15

Met Val Leu

<210> 719  
<211> 19  
<212> PRT  
<213> Homo sapiens

<400> 719  
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala  
                    5                    10                    15

Gln Leu Leu

<210> 720  
<211> 57  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(57)  
<223> n = A,T,C or G

<400> 720  
ggnathggnc cngtnytngg nytngtntgy gtnccnytny tnggnwsngc nwsngay

57

<210> 721  
<211> 57  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(57)  
<223> n = A,T,C or G

<400> 721  
gtgccnccny tnytnytnga rgtnggngtn gargaraart tyatgacnat ggtnytn 57

<210> 722  
<211> 57  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(57)  
<223> n = A,T,C or G

<400> 722  
atggtncarm gnytnctgggt nwsnmgnytn ytnmgncaym gnaargenca rytnytn 57

<210> 723  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 723  
Val Leu Gln Cys Val Asn Val Ser Val  
1 5

<210> 724  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 724  
Arg Met Pro Thr Val Leu Gln Cys Val  
1 5

<210> 725  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 725  
Asn Leu Cys Lys Phe Thr Glu Trp Ile  
1 5

<210> 726  
<211> 9  
<212> PRT

<213> Homo sapiens

<400> 726

Met Leu Ile Lys Leu Asp Glu Ser Val

1 5

<210> 727

<211> 9

<212> PRT

<213> Homo sapiens

<400> 727

Leu Leu Ala Asn Asp Leu Met Leu Ile

1 5

<210> 728

<211> 10

<212> PRT

<213> Homo sapiens

<400> 728

Leu Leu Ala Asn Gly Arg Met Pro Thr Val

1 5 10

<210> 729

<211> 10

<212> PRT

<213> Homo sapiens

<400> 729

Leu Met Leu Ile Lys Leu Asp Glu Ser Val

1 5 10

<210> 730

<211> 10

<212> PRT

<213> Homo sapiens

<400> 730

Val Leu Gln Cys Val Asn Val Ser Val Val

1 5 10

<210> 731

<211> 10

<212> PRT

<213> Homo sapiens

<400> 731

Gly Leu Leu Ala Asn Gly Arg Met Pro Thr

1 5 10

<210> 732

<211> 10

<212> PRT

<213> Homo sapiens

<400> 732

Thr Val Leu Gln Cys Val Asn Val Ser Val



285

1 5 10

<210> 733  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 733  
 Gly Val Leu Val His Pro Gln Trp Val  
 1 5

<210> 734  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 734  
 Val Leu Val His Pro Gln Trp Val Leu  
 1 5

<210> 735  
 <211> 1195  
 <212> DNA  
 <213> Homo sapiens

<400> 735  
 ccgagactca cgggtcaagct aaggcgaaga gtgggtggct gaagccatac tattttatag 60  
 aattaatgga aagcagaaaa gacatcacia accaagaaga actttggaaa atgaagccta 120  
 ggagaaatgt agaagaagac gattatttgc ataaggacac gggagagacc agcatgctaa 180  
 aaagacctgt gcttttgcac ttgcacaaaa cagcccatgc tgatgaattt gactgccctt 240  
 cagaacttca gcacacacag gaactctttc cacagtggca cttgccaatt aaaatagctg 300  
 ctattatagc atctctgact tttctttaca ctcttctgag ggaagtaatt caccctttag 360  
 caacttccca tcaacaatat ttttataaaa ttccaatcct ggtcatcaac aaagtcttgc 420  
 caatgggtttc catcactctc ttggcattgg tttacctgcc aggtgtgata gcagcaattg 480  
 tccaacttca taatggaacc aagtataaga agtttccaca ttggttggat aagtggatgt 540  
 taacaagaaa gcagtttggg cttctcagtt tcttttttgc tgtactgcat gcaatttata 600  
 gtctgtctta cccaatgagg cgatcctaca gatacaagtt gctaaactgg gcatatcaac 660  
 aggtccaaca aaataaagaa gatgcctgga ttgagcatga tgtttggaga atggagattt 720  
 atgtgtctct gggaattgtg ggattggcaa tactggctct gttggctgtg acatctattc 780  
 catctgtgag tgactctttg acatggagag aatttcacta tattcagagc aagctaggaa 840  
 ttgtttccct tctactgggc acaatacacg cattgatttt tgccctggaat aagtggatag 900  
 atataaaaca atttgtatgg tatacacctc caacttttat gatagctgtt ttccttccaa 960  
 ttgttgcct gatattttaa agcatactat tcctgccatg cttgaggaag aagatactga 1020  
 agattagaca tggttgggaa gacgtcacca aaattaacaa aactgagata tgttcccagt 1080  
 tgtagaatta ctgtttacac acatttttgt tcaatattga tatattttat caccaacatt 1140  
 tcaagtttgt atttgtaaat aaaatgatta ttcaaggaaa aaaaaaaaaa aaaaa 1195

<210> 736  
 <211> 339  
 <212> PRT  
 <213> Homo sapiens

<400> 736  
 Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys Met  
 5 10 15

Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr  
                     20                    25                    30  
 Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln  
                     35                    40                    45  
 Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr  
                     50                    55                    60  
 Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile  
                     65                    70                    75                    80  
 Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile His  
                     85                    90                    95  
 Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile Leu  
                     100                    105                    110  
 Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala Leu  
                     115                    120                    125  
 Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn Gly  
                     130                    135                    140  
 Thr Lys Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu Thr  
                     145                    150                    155                    160  
 Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His Ala  
                     165                    170                    175  
 Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu  
                     180                    185                    190  
 Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp  
                     195                    200                    205  
 Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile  
                     210                    215                    220  
 Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser  
                     225                    230                    235                    240  
 Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser Lys  
                     245                    250                    255  
 Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile Phe  
                     260                    265                    270  
 Ala Trp Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr Pro  
                     275                    280                    285  
 Pro Thr Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile Phe  
                     290                    295                    300  
 Lys Ser Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys Ile  
                     305                    310                    315                    320  
 Arg His Gly Trp Glu Asp Val Thr Lys Ile Asn Lys Thr Glu Ile Cys

325

330

335

Ser Gln Leu

&lt;210&gt; 737

&lt;211&gt; 2172

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 737

```

aaaattgaat attgagatac cattcttttag tgttaccttt tttaccacaca tgtgtttctg 60
aaaatattgg aattttattc atcttaaaaa ttggaccogg ccttatttac catctttaat 120
ccatttttagt actatgggtg agtacatgga attgaagtct ggcttaaatac ttcagaaagt 180
tatatatcta ttttatttta tttttttgag acagagtctc gctgtgtcac ccaggctgga 240
gtgcggtgcc acaatcttgg ctactgcaa cctctgagtc ccaggttcaa gcgataactca 300
tgccctcgcc tctgagtag ctgggactac aggcgtgcac caccacatct ggctaactct 360
tttttggtatt tttagtagag acgggggttc actgtggtct ccatctcctg acctcgtgat 420
ccgcctgcct cccaaagtgc tgggattaca ggcatgagcc accgcacaca gctgggactg 480
ggtaatttat aaagaaaaga ggtttaatga ctacagttc cgcattggctg gagaggcctc 540
aggaaactta caatcatggt ggaaggcgaa ggggaagcaa ggcacgtctt acatggtggc 600
aggagagaac gagtgggggg ggagactgcc acaaactttt tttttttgag acaagagtct 660
ggccctggtg cccaggctgg agtgcagtgg catgatctca gctcactgca acctctgcct 720
cacaggttca agcaattctc atgcctcagc ctcccgcata gctgggacca caggatgca 780
ccaccacacc tagctaattt ttgtagtttt agtagagatg ggggtctcact atgttgctca 840
ggctggtcta aaactcctgg gctccagcaa tccgcctgcc ttggcctccc aaagtgctgg 900
ggttacaggc ataagccacc acatccagcc tgccacatac ttttaacta tcaggctctca 960
tgagaactca tgcactatca caagaatagc atggggaaaa tcccccccat aatccaatca 1020
cctcccacca ggtctcctcc gacacgtggg attgggtggg gacacagagc caaacctgat 1080
cagatgctgc aggggctggg gacactgaga ccactcagac ctggtgtctc tgtcactctt 1140
ctgggctctg tctgtctcca ggacctccct ccccttccat ggtatagaag gaaagtgtctg 1200
taagtgcaa attgcacagg aactccttaa gacatacatc atccactcag cagttttagg 1260
ttcgagcaa aatggagtgg aaggaacaga aatttcctgt gcacctcc cgcgtgtctc 1320
tcgcatatcg gcatcctgca tccagagtgg tggactgggt acaggctatg aacctacact 1380
gatgcggcac caccaccag agtccacggg ttatgttggg tcacatttac tcttgctgtg 1440
gtatggtcta taggtttgga cagatgtccg ataatccttt ttacattttg gcatccttgg 1500
gtagctcgtc ttgtaggaat ggacttgctt caaagtggag gcaggcagat ccttcagacg 1560
ggtatatgga gccctgtttt cagttgcttt tctaattctc tcttatcgtt tacctcaaaa 1620
tcttctgag gtctcgcttc cttttaaaat ccttgtctac tttgcagcat cactctgaca 1680
ctccattgat tcctcagcac ctactgacta cacggttagg agtgcaaggg tagaattcat 1740
gttttattca tctttgggtc tgtagcacc agcaaagtgc tcagtaaag cgagtaatt 1800
gatttgacct ctgaacaaat acacactgta ctaagaatct acacaccgaa agacaaaaac 1860
aagacaaatt tgagtgttac aggtgtcacg cttggcatca cacatgtgcc tgtgtattcc 1920
tctaggtggg taccaggagc tctgccactg catgtccact agtgacgggt tcgctccacc 1980
accccagctg ggtagccgct gctctcacat aaggggtcca attaaaattg ccaggaataa 2040
attccccgg actttgactt ctcaagagct aagaaggttt gctgagtatt ctggcatgat 2100
gtttggtgat caaacaactg ctggccaaaa atgatgagta tttccccctc ttgctgaaga 2160
tgtgctccat ac

```

&lt;210&gt; 738

&lt;211&gt; 2455

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 738

```

cagcttaaaa atggtttctt gaaatcagtg attagcattc actcaccagt acccctacta 60
aggggtaggc actggtttgt actcctggga atacaggagt acaccagaat ttattttctg 120

```

```

ttattgcttt  tgttgcaaat  gccgtggctt  catctgagga  attctagaat  tcagaggggtg 180
tagccctcca  ctctgctgtc  ttgctatctg  ctctcattgc  atccgtttaa  cctgcattct  240
gaaagatgtt  tctcaggttt  ttccttgacg  attttcttct  tttctgattc  tgacaatgtt  300
ttaaatacatt  gtactgtggt  tatcatttct  ctgcatttat  tttacccatc  ttcttttgta  360
acttgtccta  ttgtctttta  atttctgcct  gttctttatg  gctttcaact  tcataaataa  420
catgttttct  caaatctctt  tgtgaattcc  agagagggcc  aggcacgggtg  gctcacatct  480
gtaatcccag  cactttgggg  aggctgagac  ggggtggatca  cttgaggtca  ggagtttgag  540
accagcctgg  ccaacatggt  gaaatcccgt  ttactaaaa  atacaaaaat  taccaggga  600
tggtggcggg  cgcctgtaat  cccaggtact  cgggaggctg  agggaggaga  atcgcttgaa  660
cctgggaggg  tgaggaggga  gaatcgcttg  aaccggggag  gcagaggttg  cagtgaaccg  720
agatcatgtt  gctgcactcc  agcctgggtc  acagagcaag  actctgcctc  aaaaacaaac  780
aaataaacia  aaaaacaaac  aaaacagaga  gattttgctg  caatgtacaa  ggagcaattt  840
gotcctttta  aaaaataatt  tttggccagg  cacagtgggt  cacacctgta  atcccagcac  900
tttggaagc  caaggtgggt  ggatcatttg  aggtcaggag  tttgagatca  gcctggccaa  960
catggtgaaa  cactatctct  attaaaaata  caaaaatgtg  ctcatgtgtg  tgggtgcacat  1020
ctgtaatctc  agcctccgc  atagctggga  ccacaggtat  gcaccaccac  acctagctaa  1080
ttttttagt  tttagtagag  atggggtctc  actatgttgc  tcaggctggt  ctaaaactcc  1140
tgggctccag  caatccgcct  gccttggcct  cccaaagtgc  tggggttaca  ggcataagcc  1200
accacatcca  gcctgccaca  tacttttaaa  ctatcaggtc  tcatgagaac  tcatgacta  1260
tcacaagaat  agcatgggga  aaatccccc  cataatocaa  tcacctcca  ccaggctctc  1320
tccgacacgt  gggattgggt  ggggacacag  agccaaaccg  tatcagatgc  tgcaggggt  1380
ggggacactg  agaccactca  gacctgggtg  ctctgtcact  cttctgggt  ctgtctgtct  1440
ccaggacctc  cctcccttc  catggtatag  aaggaaagtg  ctgtaagggtg  caaattgcac  1500
aggaactcct  taagacatac  atcatccact  cagcagtttt  aggttcgcag  caaaatggag  1560
tggaaggaa  agaaatttcc  tgtgcacccc  tcccgcgtgt  ctccgccata  tcggcatcct  1620
gcatccagag  tgggtggactg  gttacaggct  atgaacctac  actgatgcgg  caccaccacc  1680
cagagtccac  aggttatgtt  ggttcacatt  tactcttgct  gtggtatggt  ctataggttt  1740
ggacagatgt  ccgataatcc  tttttacatt  ttggcatcct  tgggtagctc  gtcttgtagg  1800
aatggacttg  cttcaaagtg  gaggcaggca  gatccttcag  acgggtatat  ggagccctgt  1860
tttcagttgc  ttttctaatt  ctctcttctc  gtttacctca  aaatcttct  gaggtctcgc  1920
ttccttttaa  aatccttgct  tactttgcag  catcactctg  aactccatt  gattcctcag  1980
cacctactga  ctacacgggt  aggagtcaa  ggttagaatt  catgttttat  tcacttttg  2040
gtctgtagca  ccagcaaag  tgcctagtaa  atgcgcagta  attgatttga  cctctgaaca  2100
aatacacact  gtactaagaa  tctacacacc  gaaagacaaa  aacaagacaa  atttgactgc  2160
tacaggtgtc  acgcttgga  tcacacatgt  gcctgtgtat  tcctctaggt  ggttaccagg  2220
agctctgcca  ctgcattgct  actagtgcag  gggtcgctcc  accacccag  ctgggtagcc  2280
gctgctctca  cataaggggt  ccaattaaaa  ttgccaggaa  taaattcccc  cggactttga  2340
cttctcaaga  gctaagaagg  tttgctgagt  attctggcat  gatgtttggt  gatcaaaaa  2400
ctgctggcca  aaaatgatga  gtatttcccc  ctcttgctga  agatgtgctc  catac  2455

```

&lt;210&gt; 739

&lt;211&gt; 2455

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 739

```

cagcttaaaa  atgggtttctt  gaaatcagtg  attagcattc  actcaccagt  acccctacta  60
aggggtaggc  actgggtttgt  actcctggga  atacaggagt  acaccagaat  ttattttctgc  120
ttattgcttt  tgttgcaaat  gccgtggctt  catctgagga  attctagaat  tcagaggggtg  180
tagccctcca  ctctgctgtc  ttgctatctg  ctctcattgc  atccgtttaa  cctgcattct  240
gaaagatgtt  tctcaggttt  ttccttgacg  attttcttct  tttctgattc  tgacaatgtt  300
ttaaatacatt  gtactgtggt  tatcatttct  ctgcatttat  tttacccatc  ttcttttgta  360
acttgtccta  ttgtctttta  atttctgcct  gttctttatg  gctttcaact  tcataaataa  420
catgttttct  caaatctctt  tgtgaattcc  agagagggcc  aggcacgggtg  gctcacatct  480
gtaatcccag  cactttgggg  aggctgagac  ggggtggatca  cttgaggtca  ggagtttgag  540
accagcctgg  ccaacatggt  gaaatcccgt  ttactaaaa  atacaaaaat  taccaggga  600
tggtggcggg  cgcctgtaat  cccaggtact  cgggaggctg  agggaggaga  atcgcttgaa  660
cctgggaggg  tgaggaggga  gaatcgcttg  aaccggggag  gcagaggttg  cagtgaaccg  720

```

```

agatcatgtt gctgcaactcc agcctgggtca acagagcaag actctgcctc aaaaacaaac 780
aaataaacia acaaaacaaac aaaacagaga gattttgctg caatgtacaa ggagcaattt 840
gctcctttta aaaaataatt tttggccagg cacagtggct cacacctgta atcccagcac 900
tttggaagc caaggtgggt ggatcatttg aggtcaggag tttgagatca gcctggccaa 960
catggtgaaa cactatctct attaaaaata caaaaatgtg ctcaagtgtg tgggtgcacat 1020
ctgtaatctc agcctcccg c atagctggga ccacaggat gcaccaccac acctagctaa 1080
ttttttagt tttagtagag atgggggtctc actatgttgc tcaggctgggt ctaaaactcc 1140
tgggctccag caatccgcct gccttggcct cccaaagtgc tgggggttaca ggcataagcc 1200
accacatcca gcctgccaca tactttttaa ctatcagggtc tcatgagaac tcatgacta 1260
tcacaagaat agcatgggga aaatccccc cataatccaa tcacctccca ccaggctctc 1320
tccgacacgt gggattgggt ggggacacag agccaaaccg tatcagatgc tgcaggggct 1380
ggggacactg agaccactca gacctgggt ctctgtcact cttctgggct ctgtctgtct 1440
ccaggacctc cctccccttc catggtatag aaggaaagt ctgtaagggt caaattgcac 1500
aggaactcct taagacatac atcatccact cagcagtttt aggttcgcag caaaatggag 1560
tggaaggaac agaaatttcc tgtgcacccc tccccgctgt ctccgccata tcggcatcct 1620
gcatccagag tgggtgactg gttacaggct atgaacctac actgatgcgg caccaccacc 1680
cagagctccac aggttatgtt ggttcacatt tactcttgc gtggtaggt ctatagggtt 1740
ggacagatgt ccgataatcc tttttacatt ttggcatcct tgggtagctc gtctttagg 1800
aatggacttg cttcaaagt gaggcaggca gatccttcag acgggtatat ggagccctgt 1860
tttcagttgc ttttctaatt ctctcttctc gtttacctca aaatcttctc gaggtctcgc 1920
ttccttttaa aatccttgc tactttgcag catcactctg acactccatt gattcctcag 1980
cacctactga ctacacggtt aggagtgcac gggtagaatt catgttttat tcatcttttg 2040
gtctgtagca cccagcaaag tgctcagtaa atgcgcagta attgatttga cctctgaaca 2100
aatacacact gtactaagaa tctacacacc gaaagacaaa aacaagacaa atttgagtgc 2160
tacagggtgc acgcttgga tcacacatgt gcctgtgtat tctctaggt ggttaccagg 2220
agctctgcca ctgcatgtcc actagtgcag gggtcgtcc accaccccag ctgggtagcc 2280
gctgctctca cataaggggt ccaattaaaa ttgccaggaa taaattcccc cggactttga 2340
cttctcaaga gctaagaagg tttgctgagt attctggcat gatgtttggt gatcaaacia 2400
ctgctggcca aaatgatga gtatttcccc ctcttgcgtga agatgtgctc catac 2455

```

&lt;210&gt; 740

&lt;211&gt; 62

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 740

```

Met Thr His Ser Ser Ala Trp Leu Glu Arg Pro Gln Glu Thr Tyr Asn
          5                      10                      15

```

```

His Gly Gly Arg Arg Arg Gly Ser Lys Ala Arg Leu Thr Trp Trp Gln
          20                      25                      30

```

```

Glu Arg Thr Ser Glu Gly Gly Asp Cys His Lys Leu Phe Phe Phe Glu
          35                      40                      45

```

```

Thr Arg Val Trp Pro Cys Cys Pro Gly Trp Ser Ala Val Ala
          50                      55                      60

```

&lt;210&gt; 741

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 741

```

Met Val Glu Gly Glu Gly Glu Ala Arg His Val Leu His Gly Gly Arg
          5                      10                      15

```

Arg Glu Arg Val Arg Gly Glu Thr Ala Thr Asn Phe Phe Phe Leu Arg  
                     20                    25                    30  
 Gln Glu Ser Gly Pro Val Ala Gln Ala Gly Val Gln Trp His Asp Leu  
                     35                    40                    45  
 Ser Ser Leu Gln Pro Leu Pro His Arg Phe Lys Gln Phe Ser Cys Leu  
                     50                    55                    60  
 Ser Leu Pro His Ser Trp Asp His Arg Tyr Ala Pro Pro His Leu Ala  
                     65                    70                    75                    80  
 Asn Phe Cys Ser Phe Ser Arg Asp Gly Val Ser Leu Cys Cys Ser Gly  
                     85                    90                    95  
 Trp Ser Lys Thr Pro Gly Leu Gln Gln Ser Ala Cys Leu Gly Leu Pro  
                     100                    105                    110  
 Lys Cys Trp Gly Tyr Arg His Lys Pro Pro His Pro Ala Cys His Ile  
                     115                    120                    125  
 Leu Leu Asn Tyr Gln Val Ser  
                     130                    135

&lt;210&gt; 742

&lt;211&gt; 77

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 742

Met His Tyr His Lys Asn Ser Met Gly Lys Ile Pro Pro Ile Ile Gln  
                     5                    10                    15  
 Ser Pro Pro Thr Arg Ser Pro Pro Thr Arg Gly Ile Gly Trp Gly His  
                     20                    25                    30  
 Arg Ala Lys Pro Tyr Gln Met Leu Gln Gly Leu Gly Thr Leu Arg Pro  
                     35                    40                    45  
 Leu Arg Pro Gly Val Ser Val Thr Leu Leu Gly Ser Val Cys Leu Gln  
                     50                    55                    60  
 Asp Leu Pro Pro Leu Pro Trp Tyr Arg Arg Lys Val Leu  
                     65                    70                    75

&lt;210&gt; 743

&lt;211&gt; 60

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 743

Met Leu Val His Ile Tyr Ser Cys Cys Gly Met Val Tyr Arg Phe Gly  
                     5                    10                    15  
 Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu Ala Ser Leu Gly Ser Ser  
                     20                    25                    30

Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp Arg Gln Ala Asp Pro Ser  
           35                          40                          45

Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu Leu Phe  
           50                          55                          60

<210> 744

<211> 76

<212> PRT

<213> Homo sapiens

<400> 744

Met Cys Leu Cys Ile Pro Leu Gly Gly Tyr Gln Glu Leu Cys His Cys  
                           5                          10                          15

Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg  
                           20                          25                          30

Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro  
                           35                          40                          45

Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly  
           50                          55                          60

Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys  
           65                          70                          75

<210> 745

<211> 76

<212> PRT

<213> Homo sapiens

<400> 745

Met Val Lys Ser Arg Phe Thr Lys Asn Thr Lys Ile Thr Gln Ala Trp  
                           5                          10                          15

Trp Arg Ala Pro Val Ile Pro Gly Thr Arg Glu Ala Glu Gly Gly Glu  
                           20                          25                          30

Ser Leu Glu Pro Gly Arg Leu Arg Glu Glu Asn Arg Leu Asn Pro Gly  
                           35                          40                          45

Gly Arg Gly Cys Ser Glu Pro Arg Ser Cys Cys Cys Thr Pro Ala Trp  
           50                          55                          60

Ser Thr Glu Gln Asp Ser Ala Ser Lys Thr Asn Lys  
           65                          70                          75

<210> 746

<211> 80

<212> PRT

<213> Homo sapiens

<400> 746

Met Leu Leu His Ser Ser Leu Val Asn Arg Ala Arg Leu Cys Leu Lys

5 10 15  
 Asn Lys Gln Ile Asn Lys Gln Thr Asn Lys Thr Glu Arg Phe Cys Cys  
 20 25 30  
 Asn Val Gln Gly Ala Ile Cys Ser Phe Lys Lys Ile Ile Phe Gly Gln  
 35 40 45  
 Ala Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Glu Ala Lys Val  
 50 55 60  
 Gly Gly Ser Phe Glu Val Arg Ser Leu Arg Ser Ala Trp Pro Thr Trp  
 65 70 75 80

&lt;210&gt; 747

&lt;211&gt; 72

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 747

Met His Tyr His Lys Asn Ser Met Gly Lys Ile Pro Pro His Asn Pro  
 5 10 15  
 Ile Thr Ser His Gln Val Ser Ser Asp Thr Trp Asp Trp Val Gly Thr  
 20 25 30  
 Gln Ser Gln Thr Val Ser Asp Ala Ala Gly Ala Gly Asp Thr Glu Thr  
 35 40 45  
 Thr Gln Thr Trp Cys Leu Cys His Ser Ser Gly Leu Cys Leu Ser Pro  
 50 55 60  
 Gly Pro Pro Ser Pro Ser Met Val  
 65 70

&lt;210&gt; 748

&lt;211&gt; 77

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 748

Met His Tyr His Lys Asn Ser Met Gly Lys Ile Pro Pro Ile Ile Gln  
 5 10 15  
 Ser Pro Pro Thr Arg Ser Pro Pro Thr Arg Gly Ile Gly Trp Gly His  
 20 25 30  
 Arg Ala Lys Pro Tyr Gln Met Leu Gln Gly Leu Gly Thr Leu Arg Pro  
 35 40 45  
 Leu Arg Pro Gly Val Ser Val Thr Leu Leu Gly Ser Val Cys Leu Gln  
 50 55 60  
 Asp Leu Pro Pro Leu Pro Trp Tyr Arg Arg Lys Val Leu  
 65 70 75



<210> 749  
 <211> 60  
 <212> PRT  
 <213> Homo sapiens

<400> 749  
 Met Leu Val His Ile Tyr Ser Cys Cys Gly Met Val Tyr Arg Phe Gly  
                             5                            10                            15  
 Gln Met Ser Asp Asn Pro Phe Tyr Ile Leu Ala Ser Leu Gly Ser Ser  
                             20                            25                            30  
 Ser Cys Arg Asn Gly Leu Ala Ser Lys Trp Arg Gln Ala Asp Pro Ser  
                             35                            40                            45  
 Asp Gly Tyr Met Glu Pro Cys Phe Gln Leu Leu Phe  
                             50                            55                            60

<210> 750  
 <211> 76  
 <212> PRT  
 <213> Homo sapiens

<400> 750  
 Met Cys Leu Cys Ile Pro Leu Gly Gly Tyr Gln Glu Leu Cys His Cys  
                             5                            10                            15  
 Met Ser Thr Ser Asp Gly Phe Ala Pro Pro Pro Gln Leu Gly Ser Arg  
                             20                            25                            30  
 Cys Ser His Ile Arg Gly Pro Ile Lys Ile Ala Arg Asn Lys Phe Pro  
                             35                            40                            45  
 Arg Thr Leu Thr Ser Gln Glu Leu Arg Arg Phe Ala Glu Tyr Ser Gly  
                             50                            55                            60  
 Met Met Phe Gly Asp Gln Thr Thr Ala Gly Gln Lys  
                             65                            70                            75

<210> 751  
 <211> 2479  
 <212> DNA  
 <213> Homo sapiens

<400> 751  
 gtcattattga acattccaga tacctatcat tactcgatgc tgttgataac agcaagatgg 60  
 ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat ggataccaac 120  
 cggaaaaccc ctatcccgcg cagcccactg tgggtcccac tgtctacgag gtgcatccgg 180  
 ctcagtacta cccgtccccc gtgcccaggt acgcccgcag ggtcctgacg caggcttcca 240  
 accccgtcgt ctgcacgcag cccaaatccc catccgggac agtgtgcacc tcaaagacta 300  
 agaaagcact gtgcatcacc ttgacctggg ggaccttcct cgtgggagct gcgctggccg 360  
 ctggcctact ctggaagtgc atgggcagca agtgctccaa ctctgggata gaggcgact 420  
 cctcaggtac ctgcatcaac ccctctaact ggtgtgatgg cgtgtcacac tgccccggcg 480  
 gggaggacga gaatcgggtgt gttgcctctt acggaccaa cttcatcctt cagatgtact 540  
 catctcagag gaagtctctg caccctgtgt gccaaagacga ctggaacgag aactacgggc 600

```

gggcggcctg cagggacatg ggctataaga ataattttta ctctagccaa ggaatagtgg 660
atgacagcgg atccaccagc tttatgaaac tgaacacaag tgccggcaat gtcgatatct 720
ataaaaaact gtaccacagt gatgcctgtt cttcaaaagc agtggtttct ttacgctgtt 780
tagcctgcgg ggtcaacttg aactcaagcc gccagagcag gatcgtgggc ggtgagagcg 840
cgctcccggg ggctggccc tggcaggcca gcctgcacgt ccagaacgtc cacgtgtgcg 900
gaggtcccat catcaccccc gagtggatcg tgacagccgc ccactgcgtg gaaaaacctc 960
ttaacaatcc atggcatttg acggcatttg cggggatttt gagacaatct ttcattgttct 1020
atggagccgg ataccaagta caaaaagtga tttctcatcc aaattatgac tccaagacca 1080
agaacaatga cattgcgctg atgaagctgc agaagcctct gactttcaac gacctagtga 1140
aaccagtgtg totgcccaac ccaggcatga tgetgcagcc agaacagctc tgctggattt 1200
ccgggtgggg ggccaccgag gagaaagggg agacctcaga agtgctgaac gctgccaaag 1260
tgcttctcat tgagacacag agatgcaaca gcagatatgt ctatgacaac ctgatcacac 1320
cagccatgat ctgtgccggc ttcttgcagg ggaacgtcga ttcttgccag ggtgacagt 1380
gagggcctct ggtcacttcg aacaacaata tctggtggct gataggggat acaagctggg 1440
gttctggctg tgccaaagct tacagaccag gagtgtacgg gaattgtgat gtattcacgg 1500
actggattta tcgacaaatg aaggcaaacg gctaattcac atggtcttcg tccttgacgt 1560
cgttttacaa gaaaacaatg gggctggttt tgcttccccg tgcattgatt actcttagag 1620
atgattcaga ggtcacttca tttttattaa acagtgaact tgtctggctt tggcactctc 1680
tgccatactg tgaggctgc agtggctccc ctgccagcc tgcctcctct aaccttctgt 1740
ccgcaagggg tgatggccgg ctggttgttg gcactggcgg tcaatttgtg aaggaagagg 1800
gttgaggctg gccccattg agatcttctt gctgagtcct ttccaggggc caattttgga 1860
tgagcatgga gctgtcactt ctcagctgct ggatgacttg agatgaaaaa ggagagacat 1920
ggaaagggag acagccaggt ggcacctgca gcggctgccc tctggggcca cttggtagtg 1980
tccccagcct acttcacaag gggattttgc tgatgggttc ttagagcctt agcagccctg 2040
gatggtggcc agaaataaag ggaccagccc ttcattgggtg gtgacgtggg agtcacttgt 2100
aagggaagca gaaacatttt tgttcttatg gggtgagaat atagacagtg cccttgggtg 2160
gaggaagca attgaaaagg aacttgccct gagcactcct ggtgcagggt tccacctgca 2220
cattgggtgg ggctcctggg agggagactc agccttcctc ctcactctcc ctgacctgca 2280
tcctagcacc ctggagagtg aatgccctt ggtccctggc agggcgccaa gtttggcacc 2340
atgtcgccct cttcaggcct gatagtcatt ggaaattgag gtccatgggg gaaatcaagg 2400
atgctcagtt taaggtacac tgtttccatg ttatgtttct acacattgat ggtggtgacc 2460
ctgagttcaa agccatctt

```

&lt;210&gt; 752

&lt;211&gt; 492

&lt;212&gt; PRT

&lt;213&gt; Homo .sapiens

&lt;400&gt; 752

```

Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
          5                                10                                15

```

```

Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
          20                                25                                30

```

```

Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
          35                                40                                45

```

```

Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
          50                                55                                60

```

```

Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
          65                                70                                75                                80

```

```

Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
          85                                90                                95

```

```

Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys

```

100					105					110					
Cys	Ser	Asn	Ser	Gly	Ile	Glu	Cys	Asp	Ser	Ser	Gly	Thr	Cys	Ile	Asn
		115					120					125			
Pro	Ser	Asn	Trp	Cys	Asp	Gly	Val	Ser	His	Cys	Pro	Gly	Gly	Glu	Asp
		130				135					140				
Glu	Asn	Arg	Cys	Val	Arg	Leu	Tyr	Gly	Pro	Asn	Phe	Ile	Leu	Gln	Met
145					150					155					160
Tyr	Ser	Ser	Gln	Arg	Lys	Ser	Trp	His	Pro	Val	Cys	Gln	Asp	Asp	Trp
			165						170					175	
Asn	Glu	Asn	Tyr	Gly	Arg	Ala	Ala	Cys	Arg	Asp	Met	Gly	Tyr	Lys	Asn
			180					185					190		
Asn	Phe	Tyr	Ser	Ser	Gln	Gly	Ile	Val	Asp	Asp	Ser	Gly	Ser	Thr	Ser
		195					200					205			
Phe	Met	Lys	Leu	Asn	Thr	Ser	Ala	Gly	Asn	Val	Asp	Ile	Tyr	Lys	Lys
	210					215					220				
Leu	Tyr	His	Ser	Asp	Ala	Cys	Ser	Ser	Lys	Ala	Val	Val	Ser	Leu	Arg
225					230					235					240
Cys	Leu	Ala	Cys	Gly	Val	Asn	Leu	Asn	Ser	Ser	Arg	Gln	Ser	Arg	Ile
			245						250					255	
Val	Gly	Gly	Glu	Ser	Ala	Leu	Pro	Gly	Ala	Trp	Pro	Trp	Gln	Val	Ser
			260					265					270		
Leu	His	Val	Gln	Asn	Val	His	Val	Cys	Gly	Gly	Ser	Ile	Ile	Thr	Pro
		275					280					285			
Glu	Trp	Ile	Val	Thr	Ala	Ala	His	Cys	Val	Glu	Lys	Pro	Leu	Asn	Asn
	290					295					300				
Pro	Trp	His	Trp	Thr	Ala	Phe	Ala	Gly	Ile	Leu	Arg	Gln	Ser	Phe	Met
305					310					315					320
Phe	Tyr	Gly	Ala	Gly	Tyr	Gln	Val	Gln	Lys	Val	Ile	Ser	His	Pro	Asn
			325						330					335	
Tyr	Asp	Ser	Lys	Thr	Lys	Asn	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Gln
			340					345					350		
Lys	Pro	Leu	Thr	Phe	Asn	Asp	Leu	Val	Lys	Pro	Val	Cys	Leu	Pro	Asn
		355					360					365			
Pro	Gly	Met	Met	Leu	Gln	Pro	Glu	Gln	Leu	Cys	Trp	Ile	Ser	Gly	Trp
	370					375					380				
Gly	Ala	Thr	Glu	Glu	Lys	Gly	Lys	Thr	Ser	Glu	Val	Leu	Asn	Ala	Ala
385					390					395					400
Lys	Val	Leu	Leu	Ile	Glu	Thr	Gln	Arg	Cys	Asn	Ser	Arg	Tyr	Val	Tyr
			405						410					415	

Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly  
420 425 430

Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser  
435 440 445

Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly  
450 455 460

Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe  
465 470 475 480

Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly  
485 490

<210> 753

<211> 683

<212> DNA

<213> Homo sapiens

<400> 753

```
gtcatattga acattccaga tacctatcat tactcgatgc tgttgataac agcaagatgg 60
ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaaccat ggataccaac 120
cggaaaaccc ctatcccgca cagcccaactg tggccccac tgtctacgag gtgcatccgg 180
ctcagtacta cccgtccccc gtgccccagt acgccccgag ggtcctgacg caggcttcca 240
accccgctcg ctgcacgcag cccaaatccc catccgggac agtgtgcacc tcaaagacta 300
agaaagcact gtgcatcacc ttgaccctgg ggaccttct cgtgggagct gcgctggccg 360
ctggcctact ctggaagttc atgggcagca agtgctccaa ctctgggata gagtgcgact 420
cctcaggtac ctgcatcaac ccctctaact ggtgtgatgg cgtgtcacac tgccccggcg 480
gggaggacga gaatcgggtg gttcgccctt acggacaaa cttcatcctt cagatgtact 540
catctcagag gaagtcctgg caccctgtgt gccaaagacga ctggaacgag aactacgggc 600
gggcggcctg cagggacatg ggctataaga ataattttta ctctagccaa ggaatagtgg 660
atgacagcgg atccaccagc ttt 683
```

<210> 754

<211> 209

<212> PRT

<213> Homo sapiens

<400> 754

```
Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
1 5 10 15
Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
20 25 30
Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
35 40 45
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
50 55 60
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
65 70 75 80
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
85 90 95
```

297

Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys  
                   100                  105                  110  
 Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn  
                   115                  120                  125  
 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp  
                   130                  135                  140  
 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met  
 145                  150                  155                  160  
 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp  
                   165                  170                  175  
 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn  
                   180                  185                  190  
 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser  
                   195                  200                  205  
 Phe

<210> 755  
 <211> 27  
 <212> PRT  
 <213> Homo sapiens

<400> 755  
 Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly Thr  
   1                  5                  10                  15  
 Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg  
                   20                  25

<210> 756  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 756  
 ggatccgccg ccaccatgtc actttctagc ctgct

35

<210> 757  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 757  
 gtcgactcag ctggaccaca gccgcag

27

<210> 758  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> PCR primer

<400> 758  
ggatccgccg ccaccatggg ctgcaggctg ctct

34

<210> 759  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 759  
gtcgactcag aaatcctttc tcttgac

27

<210> 760  
<211> 936  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...()  
<223> n = A,T,C or G

<400> 760  
atgggctgca ggctgntctg ctgtgcggtt ctctgtctcc tgggagcggg ccccatggaa 60  
acgggaggtta cgcagacacc aagacacctg gtcatgggaa tgacaaataa gaagtctttg 120  
aaatgtgaac aacatctggg tcataacgct atgtattggt acaagcaaag tgctaagaag 180  
ccactggagc tcatgtttgt ctacagtctt gaagaacggg ttgaaaacaa cagtgtgcca 240  
agtcgcttct cacctgaatg ccccaacagc tctcacttat tccttcacct acacaccctg 300  
cagccagaag actcggccct gtatctctgc gccagcagcc aagaccggac aagcagctcc 360  
tacgagcagt acttcgggcc gggcaccagg ctccaggtca cagaggacct gaaaaacgtg 420  
ttcccacccg aggtcgctgt gtttgagcca tcagaagcag agatctccca caccctaaag 480  
gccacactgg tgtgcctggc cacaggcttc taccocgacc acgtggagct gagctggtgg 540  
gtgaatggga aggaggtgca cagtggggtc agcacagacc cgcagcccct caaggagcag 600  
cccgccctca atgactccag atactgctg agcagccgcc tgagggtctc ggccaccttc 660  
tggcagaacc cccgcaacca cttccgctgt caagtccagt tctacgggct ctcggagaat 720  
gacgagtgga cccaggatag ggccaaacct gtcaccaga tcgtcagcgc cgaggcctgg 780  
ggtagagcag actgtggctt cacctccgag tcttaccagc aaggggtcct gtctgccacc 840  
atcctctatg agatcttgct agggaaggcc accttgatat ccgtgctggt cagtgccttc 900  
gtgctgatgg ccatgggtcaa gagaaaggat ttctga 936

<210> 761  
<211> 834  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...()  
<223> n = A,T,C or G

<400> 761  
atgtcacttt ctagcctgct naaggtgggc acagcttcac tgtggctagg acctggcatt 60  
gccagaaga taactcaaac ccaaccagga atgttcgtgc aggaaaagga ggctgtgact 120  
ctggactgca catatgacac cagtgatcaa agttatgggc tcttctggta caagcagccc 180

```

agcagtgggg aaatgatattt tcttatttat caggggtctt atgacgagca aaatgcaaca 240
gaaggtcgct actcattgaa tttccagaag gcaagaaaat ccgccaacct tgtcatctcc 300
gcttcacaac tgggggactc agcaatgtat ttctgtgcaa tgagagaggg cgcgggagga 360
ggaaacaaac tcacctttgg gacaggcact cagctaaaag tggaactcaa tatccagaac 420
cctgaccctg ccgtgtacca gctgagagac tctaaatcca gtgacaagtc tgtctgccta 480
ttcaccgatt ttgattctca aacaaatgtg tcacaaagta aggattctga tgtgtatatc 540
acagacaaaa ctgtgctaga catgaggtct atggacttca agagcaacag tgctgtggcc 600
tgagagcaaca aatctgactt tgcatgtgca aacgccttca acaacagcat tattccagaa 660
gacaccttct tccccagccc agaaagttcc tgtgatgtca agctgggtcga gaaaagcttt 720
gaaacagata cgaacctaaa ctttcaaac ctgtcagtga ttgggttccg aatcctctc 780
ctgaaagtgg ccgggtttaa tctgctcatg acgtgcggc tgtgtgtccag ctga 834

```

&lt;210&gt; 762

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; variant

&lt;222&gt; (1)...(311)

&lt;223&gt; Xaa = Any amino acid

&lt;400&gt; 762

```

Met Gly Cys Arg Leu Xaa Cys Cys Ala Val Leu Cys Leu Leu Gly Ala
      5                                10                                15

```

```

Val Pro Met Glu Thr Gly Val Thr Gln Thr Pro Arg His Leu Val Met
      20                                25                                30

```

```

Gly Met Thr Asn Lys Lys Ser Leu Lys Cys Glu Gln His Leu Gly His
      35                                40                                45

```

```

Asn Ala Met Tyr Trp Tyr Lys Gln Ser Ala Lys Lys Pro Leu Glu Leu
      50                                55                                60

```

```

Met Phe Val Tyr Ser Leu Glu Glu Arg Val Glu Asn Asn Ser Val Pro
      65                                70                                75                                80

```

```

Ser Arg Phe Ser Pro Glu Cys Pro Asn Ser Ser His Leu Phe Leu His
      85                                90                                95

```

```

Leu His Thr Leu Gln Pro Glu Asp Ser Ala Leu Tyr Leu Cys Ala Ser
      100                                105                                110

```

```

Ser Gln Asp Arg Thr Ser Ser Ser Tyr Glu Gln Tyr Phe Gly Pro Gly
      115                                120                                125

```

```

Thr Arg Leu Thr Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu
      130                                135                                140

```

```

Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys
      145                                150                                155                                160

```

```

Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu
      165                                170                                175

```

```

Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
      180                                185                                190

```

300

Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr  
 195 200 205

Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro  
 210 215 220

Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn  
 225 230 235 240

Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser  
 245 250 255

Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr  
 260 265 270

Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly  
 275 280 285

Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala  
 290 295 300

Met Val Lys Arg Lys Asp Phe  
 305 310

<210> 763

<211> 277

<212> PRT

<213> Homo sapiens

<400> 763

Met Ser Leu Ser Ser Leu Leu Lys Val Val Thr Ala Ser Leu Trp Leu  
 5 10 15

Gly Pro Gly Ile Ala Gln Lys Ile Thr Gln Thr Gln Pro Gly Met Phe  
 20 25 30

Val Gln Glu Lys Glu Ala Val Thr Leu Asp Cys Thr Tyr Asp Thr Ser  
 35 40 45

Asp Gln Ser Tyr Gly Leu Phe Trp Tyr Lys Gln Pro Ser Ser Gly Glu  
 50 55 60

Met Ile Phe Leu Ile Tyr Gln Gly Ser Tyr Asp Glu Gln Asn Ala Thr  
 65 70 75 80

Glu Gly Arg Tyr Ser Leu Asn Phe Gln Lys Ala Arg Lys Ser Ala Asn  
 85 90 95

Leu Val Ile Ser Ala Ser Gln Leu Gly Asp Ser Ala Met Tyr Phe Cys  
 100 105 110

Ala Met Arg Glu Gly Ala Gly Gly Gly Asn Lys Leu Thr Phe Gly Thr  
 115 120 125

Gly Thr Gln Leu Lys Val Glu Leu Asn Ile Gln Asn Pro Asp Pro Ala  
 130 135 140



Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu  
145 150 155 160

Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser  
165 170 175

Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp  
180 185 190

Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala  
195 200 205

Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe  
210 215 220

Pro Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe  
225 230 235 240

Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe  
245 250 255

Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu  
260 265 270

Arg Leu Trp Ser Ser  
275

<210> 764

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 764

```

atgtacaacc tgttgctgtc ctacgacaga catggggacc acctgcagcc cctggacctc 60
gtgcccgaatc accagggtct cacccttttc aagctggctg gactggaggg taacactgtg 120
atgtttcagc acctgatgca gaagcggagc cacaccagc ggacgtatgg accactgacc 180
tcgactctct atgacctcac agagatcgac tcctcagggg atgagcagtc cctgctggaa 240
cttatcatca ccaccaagaa gcgggaggct cgccagatcc tggaccagac gccgggtgaag 300
gagctgggtga gcctcaagtga gaagcgggtac gggcgggcgt acttctgcat gctgggtgcc 360
atatatctgc tgtacatcat ctgcttcacc atgtgctgca tctaccgccc cctcaagccc 420
aggaccaata accgcacgag ccccggggac aacacctctt tacagcagaa gctacttcag 480
gaagcctaca tgacccttaa ggacgatata cggctgggtcg gggagctggg gactgtcatt 540
ggggctatca tcatcctgct ggtagagggt ccagacatct tcagaatggg ggtcactcgc 600
ttctttggac agaccatcct tgggggccc aatcatgtcc tcatcatcac ctatgccttc 660
atggtgctgg tgaccatggt gatgcggctc atcagtgcc a gcggggagggt ggtacccatg 720
tcctttgcac tcgtgctggg ctggtgcaac gtcagtact tcgcccagg attccagatg 780
ctaggccctc tcaccatcat gattcagaag atgatttttg gcgacctgat gcgattctgc 840
tggtgatgg ctgtggtcat cctgggcttt gcttcagcct tctatatcat cttccagaca 900
gaggaccccg aggagctagg ccactttctac gactacccca tggccctgtt cagcaccttc 960
gagctgttcc ttaccatcat cgatggccca gccaaactaca acgtggacct gcccttcattg 1020
tatagcatca cctatgctgc ctttgccatc atcgccacac tgcctcatgct caacctcctc 1080
attgccatga tggggcacac tcactggcga gtggcccatg agcgggatga gctgtggagg 1140
gcccgatttg tggccaccac ggtgatgctg gagcgggaagc tgccctcgtg cctgtggcct 1200
cgctccggga tctgcggacg ggagtatggc ctgggagacc gctggttcct gcgggtggaa 1260
gacaggcaag atctcaaccg gcagcggatc caacgctacg cacaggcctt ccacaccccg 1320
ggctctgagg atttggaaca agactcagtg gaaaaactag agctgggctg tcccttcagc 1380

```

```

ccccacctgt cccttcctat gccctcagtg tctcgaagta cctcccgcag cagtgccaat 1440
tgggaaaggc ttccggcaagg gaccctgagg agagacctgc gtgggataat caacaggggt 1500
ctggaggacg gggagagctg ggaatatcag atctga 1536

```

&lt;210&gt; 765

&lt;211&gt; 1533

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 765

```

atgtacaacc tggtgctgtc ctacgacaga catggggacc acctgcagcc cctggacctc 60
gtgcccacac accaggggtc caccctttc aagctggctg gaggaggagg taacactgtg 120
atgtttcagc acctgatgca gaagcgggaag cacaccagtg ggacgtatgg accactgacc 180
tcgactctct atgacctcac agagatcgac tcctcagggg atgagcagtc cctgctggaa 240
cttatcatca ccaccaagaa gcgggaggct cgcagatcc tggaccagac gccggtgaag 300
gagctggtga gcctcaagtg gaagcgggtac gggcgccgt acttctgcat gctgggtgcc 360
atatatctgc tgtacatcat ctgcttcacc atgtgctgca tctaccgcc cctcaagccc 420
aggaccaata accgcacgag ccccggggac aacacctct tacagcagaa gctacttcag 480
gaagcctaca tgacccttaa ggacgatata cggctggtcg gggagctggt gactgtcatt 540
ggggctatca tcatcctgct ggtagagggt ccagacatct tcagaatggg ggtcactcgc 600
ttctttggac agaccatcct tgggggcccc ttccatgtcc tcatcatcac ctatgccttc 660
atggtgctgg tgaccatggt gatgcggctc atcagtgccg gcggggaggt ggtacccatg 720
tcctttgcac tcgtgctggg ctggtgcaac gtcagtact tcgcccagg attccagatg 780
ctaggcccct tcaccatcat gattcagaag atgattttt gcgacctgat gcgattctgc 840
tggctgatgg ctgtggtcat cctgggcttt gcttcagcct tctatatcat cttccagaca 900
gaggaccccg aggagctagg ccacttctac gactacccca tggccctgtt cagcaccttc 960
gagctgttcc ttaccatcat cgatggccca gccaaactaca acgtggacct gcccttcatt 1020
tacagcatca cctatgctgc ctttgccatc atcgccacac tgctcatgct caacctcctc 1080
attgccatga tggcgacac tcaactggga gtggcccatg agcgggatga gctgtggagg 1140
gccagattg tggccaccac ggtgatgctg gaggcgaagc tgcctcgctg cctgtggcct 1200
cgctccggga tctgcggacg ggagtatggc ctgggagacc gctggttcct gcgggtggaa 1260
gacaggcaag atctcaaccg gcagcggatc caacgctacg cacaggcctt ccacaccggg 1320
ggctctgagg atttgacaa agactcagtg gaaaaactag agctgggctg tcccttcagc 1380
ccccacctgt cccttcctat gccctcagtg tctcgaagta cctcccgcag cagtgccaat 1440
tgggaaaggc ttccggcaagg gaccctgagg agagacctgc gtgggataat caacaggggt 1500
ctggaggacg gggagagctg ggaatatcag atc 1536

```

&lt;210&gt; 766

&lt;211&gt; 511

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 766

```

Met Tyr Asn Leu Leu Ser Tyr Asp Arg His Gly Asp His Leu Gln
          5              10              15

```

```

Pro Leu Asp Leu Val Pro Asn His Gln Gly Leu Thr Pro Phe Lys Leu
          20              25              30

```

```

Ala Gly Val Glu Gly Asn Thr Val Met Phe Gln His Leu Met Gln Lys
          35              40              45

```

```

Arg Lys His Thr Gln Trp Thr Tyr Gly Pro Leu Thr Ser Thr Leu Tyr
          50              55              60

```

```

Asp Leu Thr Glu Ile Asp Ser Ser Gly Asp Glu Gln Ser Leu Leu Glu
          65              70              75              80

```

Leu	Ile	Ile	Thr	Thr	Lys	Lys	Arg	Glu	Ala	Arg	Gln	Ile	Leu	Asp	Gln	85	90	95
Thr	Pro	Val	Lys	Glu	Leu	Val	Ser	Leu	Lys	Trp	Lys	Arg	Tyr	Gly	Arg	100	105	110
Pro	Tyr	Phe	Cys	Met	Leu	Gly	Ala	Ile	Tyr	Leu	Leu	Tyr	Ile	Ile	Cys	115	120	125
Phe	Thr	Met	Cys	Cys	Ile	Tyr	Arg	Pro	Leu	Lys	Pro	Arg	Thr	Asn	Asn	130	135	140
Arg	Thr	Ser	Pro	Arg	Asp	Asn	Thr	Leu	Leu	Gln	Gln	Lys	Leu	Leu	Gln	145	150	155
Glu	Ala	Tyr	Met	Thr	Pro	Lys	Asp	Asp	Ile	Arg	Leu	Val	Gly	Glu	Leu	165	170	175
Val	Thr	Val	Ile	Gly	Ala	Ile	Ile	Ile	Leu	Leu	Val	Glu	Val	Pro	Asp	180	185	190
Ile	Phe	Arg	Met	Gly	Val	Thr	Arg	Phe	Phe	Gly	Gln	Thr	Ile	Leu	Gly	195	200	205
Gly	Pro	Phe	His	Val	Leu	Ile	Ile	Thr	Tyr	Ala	Phe	Met	Val	Leu	Val	210	215	220
Thr	Met	Val	Met	Arg	Leu	Ile	Ser	Ala	Ser	Gly	Glu	Val	Val	Pro	Met	225	230	235
Ser	Phe	Ala	Leu	Val	Leu	Gly	Trp	Cys	Asn	Val	Met	Tyr	Phe	Ala	Arg	245	250	255
Gly	Phe	Gln	Met	Leu	Gly	Pro	Phe	Thr	Ile	Met	Ile	Gln	Lys	Met	Ile	260	265	270
Phe	Gly	Asp	Leu	Met	Arg	Phe	Cys	Trp	Leu	Met	Ala	Val	Val	Ile	Leu	275	280	285
Gly	Phe	Ala	Ser	Ala	Phe	Tyr	Ile	Ile	Phe	Gln	Thr	Glu	Asp	Pro	Glu	290	295	300
Glu	Leu	Gly	His	Phe	Tyr	Asp	Tyr	Pro	Met	Ala	Leu	Phe	Ser	Thr	Phe	305	310	315
Glu	Leu	Phe	Leu	Thr	Ile	Ile	Asp	Gly	Pro	Ala	Asn	Tyr	Asn	Val	Asp	325	330	335
Leu	Pro	Phe	Met	Tyr	Ser	Ile	Thr	Tyr	Ala	Ala	Phe	Ala	Ile	Ile	Ala	340	345	350
Thr	Leu	Leu	Met	Leu	Asn	Leu	Leu	Ile	Ala	Met	Met	Gly	Asp	Thr	His	355	360	365
Trp	Arg	Val	Ala	His	Glu	Arg	Asp	Glu	Leu	Trp	Arg	Ala	Gln	Ile	Val	370	375	380
Ala	Thr	Thr	Val	Met	Leu	Glu	Arg	Lys	Leu	Pro	Arg	Cys	Leu	Trp	Pro			

385                      390                      395                      400  
 Arg Ser Gly Ile Cys Gly Arg Glu Tyr Gly Leu Gly Asp Arg Trp Phe  
                                  405                                   410                                   415  
 Leu Arg Val Glu Asp Arg Gln Asp Leu Asn Arg Gln Arg Ile Gln Arg  
                                  420                                   425                                   430  
 Tyr Ala Gln Ala Phe His Thr Arg Gly Ser Glu Asp Leu Asp Lys Asp  
                                  435                                   440                                   445  
 Ser Val Glu Lys Leu Glu Leu Gly Cys Pro Phe Ser Pro His Leu Ser  
                                  450                                   455                                   460  
 Leu Pro Met Pro Ser Val Ser Arg Ser Thr Ser Arg Ser Ser Ala Asn  
                                  465                                   470                                   475                                   480  
 Trp Glu Arg Leu Arg Gln Gly Thr Leu Arg Arg Asp Leu Arg Gly Ile  
                                  485                                   490                                   495  
 Ile Asn Arg Gly Leu Glu Asp Gly Glu Ser Trp Glu Tyr Gln Ile  
                                  500                                   505                                   510

&lt;210&gt; 767

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 767

Met Tyr Asn Leu Leu Leu Ser Tyr Asp Arg His Gly Asp His Leu Gln  
                                  5                                   10                                   15  
 Pro Leu Asp Leu Val Pro Asn His Gln Gly Leu Thr Pro Phe Lys Leu  
                                  20                                   25                                   30  
 Ala Gly Val Glu Gly Asn Thr Val Met Phe Gln His Leu Met Gln Lys  
                                  35                                   40                                   45  
 Arg Lys His Thr Gln Trp Thr Tyr Gly Pro Leu Thr Ser Thr Leu Tyr  
                                  50                                   55                                   60  
 Asp Leu Thr Glu Ile Asp Ser Ser Gly Asp Glu Gln Ser Leu Leu Glu  
                                  65                                   70                                   75                                   80  
 Leu Ile Ile Thr Thr Lys Lys Arg Glu Ala Arg Gln Ile Leu Asp Gln  
                                  85                                   90                                   95  
 Thr Pro Val Lys Glu Leu Val Ser Leu Lys Trp Lys Arg Tyr Gly Arg  
                                  100                                   105                                   110  
 Pro Tyr Phe Cys Met Leu Gly Ala Ile Tyr Leu Leu Tyr Ile Ile Cys  
                                  115                                   120                                   125  
 Phe Thr Met Cys Cys Ile  
                                  130

305

&lt;210&gt; 768

&lt;211&gt; 55

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 768

Ala Tyr Arg Pro Leu Lys Pro Arg Thr Asn Asn Arg Thr Ser Pro Arg  
                                   5                                  10                                  15

Asp Asn Thr Leu Leu Gln Gln Lys Leu Leu Gln Glu Ala Tyr Met Thr  
                                   20                                  25                                  30

Pro Lys Asp Asp Ile Arg Leu Val Gly Glu Leu Val Thr Val Ile Gly  
                                   35                                  40                                  45

Ala Ile Ile Ile Leu Leu Val  
                                   50                                  55

&lt;210&gt; 769

&lt;211&gt; 39

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 769

Glu Val Pro Asp Ile Phe Arg Met Gly Val Thr Arg Phe Phe Gly Gln  
                                   5                                  10                                  15

Thr Ile Leu Gly Gly Pro Phe His Val Leu Ile Ile Thr Tyr Ala Phe  
                                   20                                  25                                  30

Met Val Leu Val Thr Met Val  
                                   35

&lt;210&gt; 770

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 770

Met Arg Leu Ile Ser Ala Ser Gly Glu Val Val Pro Met Ser Phe Ala  
                                   5                                  10                                  15

Leu Val Leu

&lt;210&gt; 771

&lt;211&gt; 52

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 771

Gly Trp Cys Asn Val Met Tyr Phe Ala Arg Gly Phe Gln Met Leu Gly  
                                   5                                  10                                  15

Pro Phe Thr Ile Met Ile Gln Lys Met Ile Phe Gly Asp Leu Met Arg

	20		25		30
Phe Cys Trp Leu Met Ala Val Val Ile Leu Gly Phe Ala Ser Ala Phe					
	35		40		45
Tyr Ile Ile Phe					
	50				

&lt;210&gt; 772

&lt;211&gt; 213

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 772

Gln Thr Glu Asp Pro Glu Glu Leu Gly His Phe Tyr Asp Tyr Pro Met					
	5		10		15
Ala Leu Phe Ser Thr Phe Glu Leu Phe Leu Thr Ile Ile Asp Gly Pro					
	20		25		30
Ala Asn Tyr Asn Val Asp Leu Pro Phe Met Tyr Ser Ile Thr Tyr Ala					
	35		40		45
Ala Phe Ala Ile Ile Ala Thr Leu Leu Met Leu Asn Leu Leu Ile Ala					
	50		55		60
Met Met Gly Asp Thr His Trp Arg Val Ala His Glu Arg Asp Glu Leu					
	65		70		75
Trp Arg Ala Gln Ile Val Ala Thr Thr Val Met Leu Glu Arg Lys Leu					
	85		90		95
Pro Arg Cys Leu Trp Pro Arg Ser Gly Ile Cys Gly Arg Glu Tyr Gly					
	100		105		110
Leu Gly Asp Arg Trp Phe Leu Arg Val Glu Asp Arg Gln Asp Leu Asn					
	115		120		125
Arg Gln Arg Ile Gln Arg Tyr Ala Gln Ala Phe His Thr Arg Gly Ser					
	130		135		140
Glu Asp Leu Asp Lys Asp Ser Val Glu Lys Leu Glu Leu Gly Cys Pro					
	145		150		155
Phe Ser Pro His Leu Ser Leu Pro Met Pro Ser Val Ser Arg Ser Thr					
	165		170		175
Ser Arg Ser Ser Ala Asn Trp Glu Arg Leu Arg Gln Gly Thr Leu Arg					
	180		185		190
Arg Asp Leu Arg Gly Ile Ile Asn Arg Gly Leu Glu Asp Gly Glu Ser					
	195		200		205
Trp Glu Tyr Gln Ile					
	210				

<210> 773  
 <211> 1302  
 <212> DNA  
 <213> Homo sapiens

<400> 773

```

tggacaaagg gggtcacaca ttcccttccat acggttgagc ctctacctgc ctgggtgctgg 60
tcacagttca gcttcttcat gatggtggat cccaatggca atgaatccag tgctacatac 120
ttcatcctaa taggcctccc tgggttagaa gaggtcagc tctggttggc ctteccattg 180
tgctccctct acctatttgc tgtgctaggt aaottgacaa tcatctacat tgtgctgact 240
gagcacagcc tgcattgagcc catgtatata tttctttgca tgctttcagg cattgacatc 300
ctcatctcca cctcatccat gcccaaaatg ctggccatct tctggttcaa ttccactacc 360
atccagtttg atgcttgtct gctacagatg tttgccatcc actccttata tggcatggaa 420
tccacagtgc tgcctggccat ggcttttgac cgctatgtgg ccatctgtca cccactgcgc 480
catgccacag tacttacgtt gcctcgtgtc accaaaattg gtgtggctgc tgtggtgcgg 540
ggggctgcac tgatggcacc ccttcctgtc ttcataaagc agctgccctt ctgccgtccc 600
aatactcctt cccattccta ctgcctacac caagatgtca tgaagctggc ctgtgatgat 660
atccgggtca atgtcgtcta tggccttata gtcacatct cggccattgg cctggactca 720
cttctcatct ccttctcata tctgcttatt cttaagactg tgttgggctt gacacgtgaa 780
gcccaggcca aggcatattg cacttgcgtc tctcatgtgt gtgctgtgtt catattctat 840
gtacctttca ttggattgtc catggtgcat cgcttttagc agcggcgtga ctctccgctg 900
cccgctcatct tggccaatat ctatctgctg gttcctcctg tgctcaaccc aattgtctat 960
ggagtgaaga caaaggagat tcgacagcgc atccttcgac ttttccatgt ggccacacac 1020
gcttcagagc cctaggtgtc agtgatcaaa ctctctttcc attcagagtc ctctgattca 1080
gattttaatg ttaacatttt ggaagacagt attcagaaaa aaaatttcct taataaaaaa 1140
acaactcaga tcttccaaat atgaaactgg ttgggggaatc tccatttttt caatattatt 1200
ttcttcttgg ttttcttggc acatataatt attaataccc tgactagggt gtggtttgag 1260
ggttattact tttcatttta ccatgcagtc caaatctaaa ct 1302

```

<210> 774  
 <211> 2061  
 <212> DNA  
 <213> Homo sapiens

<400> 774

```

acgattcgac agcgcaccc tgcacttttc catgtggcca cacacgcttc agagccctag 60
gtgtcagtga tcaaaacttct tttccattca gagtcctctg attcagattt taatgttaac 120
atthttggaag acagtattca gaaaaaaaat ttcttaata aaaatacaac tcagatcctt 180
caaatatgaa actggttggg gaatctccat tttttcaata ttattttctt ctttgttttc 240
ttgctacata taattattaa taccctgact aggttgtggt tggagggtta ttacttttca 300
ttttaccatg cagtcctaat ctaaaactgct tctactgatg gtttacagca ttctgagata 360
agaatggtac atctagagaa catttgccaa aggcctaagc acggcaaagg aaaataaaca 420
cagaatataa taaaatgaga taatctagct taaaactata acttcctctt cagaactccc 480
aaccacattg gatctcagaa aaatgctgtc ttcaaaatga cttctacaga gaagaaataa 540
tttttcctct ggacactagc acttaagggg aagattggaa gtaaagcctt gaaaagagta 600
catttaccta cgttaatgaa agttgacaca ctgttctgag agttttcaca gcatatggac 660
cctgtttttc ctatttaatt ttcttatcaa ccttttaatt aggcaaagat attattagta 720
ccctcattgt agccatggga aaattgatgt tcagtgggga tcagtgaatt aaatggggct 780
atacaagtat aaaaattaaa aaaaaaggac ttcattgcca atctcatatg atgtggaaga 840
actgttagag agaccaacag gtagtggtg tagagatttc cagagtctta cattttctag 900
aggaggtatt taatttcttc tcactcatcc agtgtgtgat ttaggaattt cctggcaaca 960
gaactcatgg cttaatccc actagctatt gcttattgtc ctggtccaat tgccaattac 1020
ctgtgtcttg gaagaagtga tttctagggt caccattatg gaagattctt attcagaaag 1080
tctgcatagg gcttatagca agttatttat ttttaaaagt tccatagggt attctgatag 1140
gcagtgaggt tagggagcca ccagttatga tgggaagtat ggaatggcag gtcttgaaga 1200
taacattggc cttttgagtg tgactcgtag ctggaaagtg agggaatctt caggaccatg 1260
ctttatttgg ggctttgtgc agtatggaac agggactttg agaccaggaa agcaatctga 1320

```

```

cttaggcattg ggaatcaggc atttttgctt ctgaggggct attaccaagg gttaataggt 1380
ttcatcttca acaggatatg acaacagtgt taaccaagaa actcaaatta caaataactaa 1440
aacatgtgat catatatgtg gtaagtttca ttttcttttt caatcctcag gttccctgat 1500
atggattcct ataacatgct ttcatccctt tttgtaatgg atatcatatt tggaaatgcc 1560
tatttaatac ttgtatttgc tgctggactg taagcccatg agggcactgt ttattattga 1620
atgtcatctc tgttcatcat tgactgctct ttgctcatca ttgaatcccc cagcaaagtg 1680
cctagaacat aatagtgcct atgcttgaca ccggttattt ttcatcaaac ctgattcctt 1740
ctgtcctgaa cacatagcca ggcaattttc cagccttctt tgagttgggt attattaaat 1800
tctggccatt acttccaatg tgagtggaa gacatgtgc aatttctata cctggctcat 1860
aaaaccctcc catgtgcagc ctttcatgtt gacattaaat gtgacttggg aagctatgtg 1920
ttacacagag taaatcacca gaagcctgga tttctgaaaa aactgtgcag agccaaacct 1980
ctgtcatttg caactccac ttgtatttgt acgaggcagt tggataagtg aaaaataaag 2040
tactattgtg tcaagtctct g 2061

```

&lt;210&gt; 775

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 775

```

atgatgggtg atcccaatgg caatgaatcc agtgctacat acttcatcct aataggcctc 60
cctggtttag aagaggctca gttctgggtg gccttcccat tgtgctccct ctaccttatt 120
gctgtgctag gtaacttgac aatcatctac attgtgcgga ctgagcacag cctgcatgag 180
cccatgtata tatttctttg catgctttca ggcattgaca tcctcatctc cacctcatcc 240
atgccccaaa tgctggccat cttctgggtc aattccacta ccatccagtt tgatgcttgt 300
ctgctacaga tgtttgccat ccactcctta tctggcatgg aatccacagt gctgctggcc 360
atggcttttg accgctatgt ggccatctgt caccactgc gccatgccac agtacttaag 420
ttgcctcgtg tcacccaaat tgggtgtggc gctgtggtgc ggggggctgc actgatggca 480
ccccttcttg tcttcatcaa gcagctgcc ttctgccgct ccaatatcct ttcccattcc 540
tactgcctac accaagatgt catgaagctg gcctgtgatg atatccgggt caatgtcgtc 600
tatggcctta tcgtcatcat ctccgccatt ggcctggact cacttctcat ctcttctca 660
tatctgctta ttcttaagac tgtgttgggc ttgacacgtg aagcccaggc caaggcattt 720
ggcacttgcg tctctcatgt gtgtgctgtg ttcatattct atgtaccttt cattggattg 780
tccatgggtg atcgcttttag caagcggcgt gactctccgc tgcccgtcat cttggccaat 840
atctatctgc tggttcctcc tgtgtccaac ccaattgtct atggagtga gacaaaggag 900
attcgacagc gcactccttg acttttccat gtggccacac acgcttcaga gccctag 957

```

&lt;210&gt; 776

&lt;211&gt; 954

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 776

```

atgatgggtg atcccaatgg caatgaatcc agtgctacat acttcatcct aataggcctc 60
cctggtttag aagaggctca gttctgggtg gccttcccat tgtgctccct ctaccttatt 120
gctgtgctag gtaacttgac aatcatctac attgtgcgga ctgagcacag cctgcatgag 180
cccatgtata tatttctttg catgctttca ggcattgaca tcctcatctc cacctcatcc 240
atgccccaaa tgctggccat cttctgggtc aattccacta ccatccagtt tgatgcttgt 300
ctgctacaga tgtttgccat ccactcctta tctggcatgg aatccacagt gctgctggcc 360
atggcttttg accgctatgt ggccatctgt caccactgc gccatgccac agtacttaag 420
ttgcctcgtg tcacccaaat tgggtgtggc gctgtggtgc ggggggctgc actgatggca 480
ccccttcttg tcttcatcaa gcagctgcc ttctgccgct ccaatatcct ttcccattcc 540
tactgcctac accaagatgt catgaagctg gcctgtgatg atatccgggt caatgtcgtc 600
tatggcctta tcgtcatcat ctccgccatt ggcctggact cacttctcat ctcttctca 660
tatctgctta ttcttaagac tgtgttgggc ttgacacgtg aagcccaggc caaggcattt 720
ggcacttgcg tctctcatgt gtgtgctgtg ttcatattct atgtaccttt cattggattg 780
tccatgggtg atcgcttttag caagcggcgt gactctccgc tgcccgtcat cttggccaat 840

```



<400> 777																
Met	Met	Val	Asp	Pro	Asn	Gly	Asn	Glu	Ser	Ser	Ala	Thr	Tyr	Phe	Ile	
				5					10					15		
Leu	Ile	Gly	Leu	Pro	Gly	Leu	Glu	Glu	Ala	Gln	Phe	Trp	Leu	Ala	Phe	
			20					25					30			
Pro	Leu	Cys	Ser	Leu	Tyr	Leu	Ile	Ala	Val	Leu	Gly	Asn	Leu	Thr	Ile	
		35					40					45				
Ile	Tyr	Ile	Val	Arg	Thr	Glu	His	Ser	Leu	His	Glu	Pro	Met	Tyr	Ile	
	50					55					60					
Phe	Leu	Cys	Met	Leu	Ser	Gly	Ile	Asp	Ile	Leu	Ile	Ser	Thr	Ser	Ser	
65					70					75					80	
Met	Pro	Lys	Met	Leu	Ala	Ile	Phe	Trp	Phe	Asn	Ser	Thr	Thr	Ile	Gln	
				85					90					95		
Phe	Asp	Ala	Cys	Leu	Leu	Gln	Met	Phe	Ala	Ile	His	Ser	Leu	Ser	Gly	
			100					105					110			
Met	Glu	Ser	Thr	Val	Leu	Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	
		115					120					125				
Ile	Cys	His	Pro	Leu	Arg	His	Ala	Thr	Val	Leu	Thr	Leu	Pro	Arg	Val	
	130					135					140					
Thr	Lys	Ile	Gly	Val	Ala	Ala	Val	Val	Arg	Gly	Ala	Ala	Leu	Met	Ala	
145					150					155					160	
Pro	Leu	Pro	Val	Phe	Ile	Lys	Gln	Leu	Pro	Phe	Cys	Arg	Ser	Asn	Ile	
				165					170					175		
Leu	Ser	His	Ser	Tyr	Cys	Leu	His	Gln	Asp	Val	Met	Lys	Leu	Ala	Cys	
			180					185					190			
Asp	Asp	Ile	Arg	Val	Asn	Val	Val	Tyr	Gly	Leu	Ile	Val	Ile	Ile	Ser	
		195					200					205				
Ala	Ile	Gly	Leu	Asp	Ser	Leu	Leu	Ile	Ser	Phe	Ser	Tyr	Leu	Leu	Ile	
	210					215					220					
Leu	Lys	Thr	Val	Leu	Gly	Leu	Thr	Arg	Glu	Ala	Gln	Ala	Lys	Ala	Phe	
225					230					235					240	
Gly	Thr	Cys	Val	Ser	His	Val	Cys	Ala	Val	Phe	Ile	Phe	Tyr	Val	Pro	
				245					250					255		

Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro  
305 310 315

Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg His Ala Thr Val Leu  
5 10 15

311

Thr Leu Pro Arg  
20

<210> 782  
<211> 37  
<212> PRT  
<213> Homo sapiens

<400> 782  
Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile Leu Ser His Ser  
5 10 15

Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Asp Asp Ile Arg  
20 25 30

Val Asn Val Val Tyr  
35

<210> 783  
<211> 13  
<212> PRT  
<213> Homo sapiens

<400> 783  
Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys  
5 10

<210> 784  
<211> 10  
<212> PRT  
<213> Homo sapiens

<400> 784  
Val His Arg Phe Ser Lys Arg Arg Asp Ser  
5 10

<210> 785  
<211> 22  
<212> PRT  
<213> Homo sapiens

<400> 785  
Lys Thr Lys Glu Ile Arg Gln Arg Ile Leu Arg Leu Phe His Val Ala  
5 10 15

Thr His Ala Ser Glu Pro  
20

<210> 786  
<211> 3245  
<212> DNA  
<213> Homo sapiens

&lt;400&gt; 786

```

gtcgacccac gcgtccgcgc gagctaagca ggaggcggag gcgaggcgcg agggcgagg 60
gcggggagcg ccgcctggag cgcggcaggt catattgaac attccagata cctatcatta 120
ctcgatgctg ttgataacag caagatggct ttgaactcag ggtcaccacc agctattgga 180
ccttactatg aaaaccatgg ataccaaccg gaaaaccctt atcccgca cccactgtg 240
gtccccactg tctacgaggt gcatccggct cagtactacc cgtccccgt gccccagtac 300
gccccgaggg tcctgacgca ggcttccaac ccgtcgctet gcacgcagcc caaatcccca 360
tccgggacag tgtgcacctc aaagactaag aaagcactgt gcatcacctt gaccctgggg 420
accttcctcg tgggagctgc gctggccgct ggcctactct ggaagtcat gggcagcaag 480
tgctccaact ctgggataga gtgcgactcc tcaggtaoct gcatcaaccc ctctaactgg 540
tgtgatggcg tgtcacactg ccccgccggg gaggcagaga atcggtgtgt tcgcctctac 600
ggatcaaaact tcactcctca ggtgtactca tctcagagga agtcctggca ccctgtgtgc 660
caagacgact ggaacgagaa ctacgggagg ggcgcctgca gggacatggg ctataagaat 720
aatttttact ctagccaagg aatagtggat gacagcggat ccaccagctt tatgaaactg 780
aacacaagtg ccggcaatgt cgatatctat aaaaaactgt accacagtga tgcctgttct 840
tcaaaagcag tggtttcttt acgctgtata gcctgcgggg tcaacttgaa ctcaagccgc 900
cagagcagga tgtgggcgg cgagagcgcg ctcccgggg cctggccctg gcaggtcagc 960
ctgcacgtcc agaactcca cgtgtgcgga ggctccatca tcaacccgga gtggatcgtg 1020
acagccgccc actgcgtgga aaaacctctt aacaatccat ggcattggac ggcatttgcg 1080
gggattttga gacaactctt catgttctat ggagccggat accaagtaga aaaagtgatt 1140
tctcatccaa attatgactc caagaccaag aacaatgaca ttgcgtgat gaagctgcag 1200
aagcctctga ctttcaacga cctagtgaag ccagtgtgtc tgcccaaccc aggcagtgatg 1260
ctgcagccag aacagctctg ctggatttcc ggggtggggg ccaccgagga gaaagggag 1320
acctcagaag tgctgaacgc tgccaaggtg cttctcattg agacacagag atgcaacagc 1380
agatatgtct atgacaacct gatcacacca gccatgatct gtgcgggctt cctgcagggg 1440
aacgtcgatt cttgccaggg tgacagtgga gggcctctgg tcaactcgaa gaacaatatc 1500
tggtggctga taggggatac aagctggggt tctggctgtg ccaaagctta cagaccagga 1560
gtgtacggga atgtgatggt attcacggac tggatttatt gacaaatgag ggcagacggc 1620
taatccacat ggtcttcgtc cttgacgtcg ttttacaaga aaacaatggg gctggttttg 1680
cttccccgtg catgatttac tcttagagat gattcagagg tcacttcatt tttattaaac 1740
agtgaacttg tctggctttg gcactctctg ccattctgtg caggctgcag tggctcccct 1800
gcccagcctg ctctccctaa ccccttgctc gcaaggggtg atggccggct ggttgtgggc 1860
actggcggtc aagtgtggag gagaggggtg gaggtgccc cattgagatc ttctgtctga 1920
gtcctttcca ggggccaatt ttggtgagc atggagctgt cactctcag ctgctggatg 1980
acttgatag gaaaaggaga gacatggaag gggagacagc caggtggcac ctgcagcggc 2040
tgccctctgg ggcacttg tagtgtcccc agcctacctc tccacaaggg gattttgctg 2100
atgggttctt agagccttag cagccctgga tgggtggccag aaataaaggg accagccctt 2160
catgggtggt gacgtggtag tcacttgtaa ggggaacaga aacatttttg ttcttatggg 2220
gtgagaatat agacagtgcc cttggtgcga gggagcaat tgaaaaggaa cttgccctga 2280
gcactcctgg tgcaggtctc cacctgcaca ttgggtgggg ctctggggag ggagactcag 2340
ccttctctct catctccct gaccctgctc ctacaccct ggagagtga catgccctt 2400
ggtcctggca gggcgccaag tctggacca tgttggctc ttcaggcctg ctagtactg 2460
gaaattgagg tccatggggg aaatcaagga tgctcagttt aaggtacact gtttccatgt 2520
tatgtttcta cacattgcta cctcagtgc cctggaaaact tagcttttga tgtctccaag 2580
tagtccacct tcatttaact ctttgaaact gtatcatctt tgccaagtaa gagtgggtgc 2640
ctatttcagc tgccttgaca aaatgactgg ctctgactt aacgttctat aaatgaatgt 2700
gctgaagcaa agtgcccatg gtggcgcgca agaagagaaa gatgtgtttt gttttggact 2760
ctctgtggtc ccttccaatg ctgtgggttt ccaaccaggg gaagggtccc ttttgcatg 2820
ccaagtcca taaccatgag cactactcta ccattggtct gcctcctggc caagcaggct 2880
ggtttgcaag aatgaaatga atgattctac agctaggact taaccttgaa atggaaagtc 2940
ttgcaatccc atttgcagga tccgtctgtg cacatgcctc tgtagagagc agcattccca 3000
gggaccttg aaacagttgg cactgtaagg tgcttgctcc ccaagacaca tcctaaaagg 3060
tgttgtaatg gtgaaaacgt cttccttctt tattgccct tcttatttat gtgaacaact 3120
gtttgtcttt ttttgatct tttttaaact gtaaaagtca attgtgaaaa tgaatatcat 3180
gcaataaat tatgcgattt ttttttcaaa gtaaaaaaaa aaaaaaaaaa aaaaaggcg 3240
gcccgc 3245

```

<210> 787  
 <211> 1479  
 <212> DNA  
 <213> Homo sapiens

<400> 787

```

atggctttga actcagggtc accaccagct attggacctt actatgaaaa ccatggatac 60
caaccgaaaa acccctatcc cgcacagccc actgtggtcc ccactgtcta cgaggtgcat 120
ccggctcagt actaccgcgc ccccggtgcc cagtacgccc cgagggtcct gacgcaggct 180
tccaaccccc tegtctgcac gcagcccaaa tccccatccg ggacagtgtg cacctcaaag 240
actaagaaag cactgtgcat caccttgacc ctggggacct tcctcgtggg agctgcgctg 300
gccgctggcc tactctggaa gttcatgggc agcaagtgtc ccaactctgg gatagagtgc 360
gactcctcag gtacctgcat caaccctctt aactggtgtg atggcgtgtc aactgcccc 420
ggcggggagg acgagaatcg gtgtgttcgc ctctacggat caaacttcat ccttcagggtg 480
tactcatctc agaggaagtc ctggcaccct gtgtgccaag acgactggaa cgagaactac 540
gggcggggcg cctgcaggga catgggctat aagaataatt ttactctag ccaaggaata 600
gtggatgaca gcgatccac cagctttatg aaactgaaca caagtgcgg caatgtcgat 660
atctataaaa aactgtacca cagtgtgccc tgttcttcaa aagcagtggg ttctttacgc 720
tgtatagcct gcgggggtcaa cttgaactca agccgccaga gcaggattgt gggcggcgag 780
agcgcgctcc cgggggcctg gccctggcag gtcagcctgc acgtccagaa cgtccacgtg 840
tgccgaggct ccatcatcac ccccgagtgg atcgtgacag ccgcccactg cgtggaaaaa 900
cctcttaaca atccatggca ttggacggca tttgcgggga ttttgagaca atctttcatg 960
ttctatggag ccggatacca agtagaaaaa gtgatttctc atccaaatta tgactccaag 1020
accaagaaca atgacattgc gctgatgaag ctgcagaagc ctctgacttt caacgacctt 1080
gtgaaaccag tgtgtctgcc caaccaggc atgatgctgc agccagaaca gctctgctgg 1140
atttcggggt gggggggccac cgaggagaaa ggggaagacct cagaagtgtt gaacgctgcc 1200
aaggtgcttc tcattgagac acagagatgc aacagcagat atgtctatga caacctgatc 1260
acaccagcca tgatctgtgc cggcttccctg caggggaaacg tcgattcttg ccagggtgac 1320
agtggagggc ctctggtcac ttogaagaac aatatctggg ggctgatagg ggatacaagc 1380
tggggttctg gctgtgccaa agcttacaga ccaggagtgt acgggaatgt gatggtattc 1440
acggactgga ttatcgaca aatgagggga gacggctaa 1479

```

<210> 788  
 <211> 1476  
 <212> DNA  
 <213> Homo sapiens

<400> 788

```

atggctttga actcagggtc accaccagct attggacctt actatgaaaa ccatggatac 60
caaccgaaaa acccctatcc cgcacagccc actgtggtcc ccactgtcta cgaggtgcat 120
ccggctcagt actaccgcgc ccccggtgcc cagtacgccc cgagggtcct gacgcaggct 180
tccaaccccc tegtctgcac gcagcccaaa tccccatccg ggacagtgtg cacctcaaag 240
actaagaaag cactgtgcat caccttgacc ctggggacct tcctcgtggg agctgcgctg 300
gccgctggcc tactctggaa gttcatgggc agcaagtgtc ccaactctgg gatagagtgc 360
gactcctcag gtacctgcat caaccctctt aactggtgtg atggcgtgtc aactgcccc 420
ggcggggagg acgagaatcg gtgtgttcgc ctctacggat caaacttcat ccttcagggtg 480
tactcatctc agaggaagtc ctggcaccct gtgtgccaag acgactggaa cgagaactac 540
gggcggggcg cctgcaggga catgggctat aagaataatt ttactctag ccaaggaata 600
gtggatgaca gcgatccac cagctttatg aaactgaaca caagtgcgg caatgtcgat 660
atctataaaa aactgtacca cagtgtgccc tgttcttcaa aagcagtggg ttctttacgc 720
tgtatagcct gcgggggtcaa cttgaactca agccgccaga gcaggattgt gggcggcgag 780
agcgcgctcc cgggggcctg gccctggcag gtcagcctgc acgtccagaa cgtccacgtg 840
tgccgaggct ccatcatcac ccccgagtgg atcgtgacag ccgcccactg cgtggaaaaa 900
cctcttaaca atccatggca ttggacggca tttgcgggga ttttgagaca atctttcatg 960
ttctatggag ccggatacca agtagaaaaa gtgatttctc atccaaatta tgactccaag 1020
accaagaaca atgacattgc gctgatgaag ctgcagaagc ctctgacttt caacgacctt 1080
gtgaaaccag tgtgtctgcc caaccaggc atgatgctgc agccagaaca gctctgctgg 1140

```

```

atttccgggt ggggggccac cgaggagaaa ggggaagacct cagaagtgtc gaacgctgcc 1200
aaggtgcttc tcattgagac acagagatgc aacagcagat atgtctatga caacctgac 1260
acaccagcca tgatctgtgc cggcttcctg cagggggaacg tcgattcttg ccagggtgac 1320
agtggagggc ctctggtcac ttcgaagaac aatatctggt ggctgatagg ggatacaagc 1380
tggggttctg gctgtgccaa agcttacaga ccaggagtgt acgggaatgt gatgggtattc 1440
acggactgga tttatcgaca aatgagggca gacggc 1476

```

&lt;210&gt; 789

&lt;211&gt; 492

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 789

```

Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
      5      10      15
Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
      20      25      30
Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
      35      40      45
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
      50      55      60
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
      65      70      75      80
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
      85      90      95
Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
      100     105     110
Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
      115     120     125
Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
      130     135     140
Glu Asn Arg Cys Val Arg Leu Tyr Gly Ser Asn Phe Ile Leu Gln Val
      145     150     155     160
Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
      165     170     175
Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
      180     185     190
Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
      195     200     205
Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
      210     215     220
Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
      225     230     235     240
Cys Ile Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
      245     250     255
Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
      260     265     270
Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
      275     280     285
Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
      290     295     300
Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
      305     310     315     320
Phe Tyr Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn
      325     330     335
Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
      340     345     350

```

Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn  
                   355                                  360                                  365  
 Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp  
                   370                                  375                                  380  
 Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala  
 385                                  390                                  395                                  400  
 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr  
                                   405                                  410                                  415  
 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly  
                                   420                                  425                                  430  
 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser  
                                   435                                  440                                  445  
 Lys Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly  
                                   450                                  455                                  460  
 Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe  
 465                                  470                                  475                                  480  
 Thr Asp Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly  
                                   485                                  490

<210> 790  
 <211> 100  
 <212> PRT  
 <213> Homo sapiens

<400> 790  
 Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu  
                                   5                                  10                                  15  
 Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val  
                                   20                                  25                                  30  
 Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro  
                                   35                                  40                                  45  
 Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val  
                                   50                                  55                                  60  
 Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys  
                                   65                                  70                                  75                                  80  
 Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val  
                                   85                                  90                                  95  
 Gly Ala Ala Leu  
                                   100

<210> 791  
 <211> 393  
 <212> PRT  
 <213> Homo sapiens

<400> 791  
 Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys Ser Asn  
                                   5                                  10                                  15  
 Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro Ser Asn  
                                   20                                  25                                  30  
 Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu Asn Arg  
                                   35                                  40                                  45  
 Cys Val Arg Leu Tyr Gly Ser Asn Phe Ile Leu Gln Val Tyr Ser Ser  
                                   50                                  55                                  60  
 Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn Glu Asn  
                                   65                                  70                                  75                                  80

Tyr	Gly	Arg	Ala	85	Cys	Arg	Asp	Met	Gly	90	Tyr	Lys	Asn	Asn	Phe	Tyr
Ser	Ser	Gln	Gly	100	Ile	Val	Asp	Asp	Ser	105	Gly	Ser	Thr	Ser	Phe	Met
Leu	Asn	Thr	Ser	115	Ala	Gly	Asn	Val	Asp	120	Ile	Tyr	Lys	Lys	Leu	Tyr
Ser	Asp	Ala	Cys	130	Ser	Ser	Lys	Ala	Val	135	Val	Ser	Leu	Arg	Cys	Ile
Cys	Gly	Val	Asn	145	Leu	Asn	Ser	Ser	Arg	150	Gln	Ser	Arg	Ile	Val	Gly
Glu	Ser	Ala	Leu	165	Pro	Gly	Ala	Trp	Pro	170	Trp	Gln	Val	Ser	Leu	His
Gln	Asn	Val	His	180	Val	Cys	Gly	Gly	Ser	185	Ile	Ile	Thr	Pro	Glu	Trp
Val	Thr	Ala	Ala	195	His	Cys	Val	Glu	Lys	200	Pro	Leu	Asn	Asn	Pro	Trp
Trp	Thr	Ala	Phe	210	Ala	Gly	Ile	Leu	Arg	215	Gln	Ser	Phe	Met	Phe	Tyr
Ala	Gly	Tyr	Gln	225	Val	Glu	Lys	Val	Ile	230	Ser	His	Pro	Asn	Tyr	Asp
Lys	Thr	Lys	Asn	245	Asn	Asp	Ile	Ala	Leu	250	Met	Lys	Leu	Gln	Lys	Pro
Thr	Phe	Asn	Asp	260	Leu	Val	Lys	Pro	Val	265	Cys	Leu	Pro	Asn	Pro	Gly
Met	Leu	Gln	Pro	275	Glu	Gln	Leu	Cys	Trp	280	Ile	Ser	Gly	Trp	Gly	Ala
Glu	Glu	Lys	Gly	290	Lys	Thr	Ser	Glu	Val	295	Leu	Asn	Ala	Ala	Lys	Val
Leu	Ile	Glu	Thr	305	Gln	Arg	Cys	Asn	Ser	310	Arg	Tyr	Val	Tyr	Asp	Asn
Ile	Thr	Pro	Ala	325	Met	Ile	Cys	Ala	Gly	330	Phe	Leu	Gln	Gly	Asn	Val
Ser	Cys	Gln	Gly	340	Asp	Ser	Gly	Gly	Pro	345	Leu	Val	Thr	Ser	Lys	Asn
Ile	Trp	Trp	Leu	355	Ile	Gly	Asp	Thr	Ser	360	Trp	Gly	Ser	Gly	Cys	Ala
Ala	Tyr	Arg	Pro	370	Gly	Val	Tyr	Gly	Asn	375	Val	Met	Val	Phe	Thr	Asp
Ile	Tyr	Arg	Gln	385	Met	Arg	Ala	Asp	Gly	390						

<210> 792

<211> 595

<21.2> PRT

<213> Homo sapiens

<400> 792

Met	Ser	Phe	Leu	Asn	Phe	Thr	Ala	Val	Leu	Phe	Ala	Ala	Ser	Ser	Ala
1				5					10					15	
Leu	Ala	Ala	Pro	Val	Asn	Thr	Thr	Thr	Glu	Asp	Glu	Thr	Ala	Gln	Ile
			20					25					30		
Pro	Ala	Glu	Ala	Val	Ile	Gly	Tyr	Ser	Asp	Leu	Glu	Gly	Asp	Phe	Asp
		35					40					45			
Val	Ala	Val	Leu	Pro	Phe	Ser	Asn	Ser	Thr	Asn	Asn	Gly	Leu	Leu	Phe
		50				55					60				
Ile	Asn	Thr	Thr	Ile	Ala	Ser	Ile	Ala	Ala	Lys	Glu	Glu	Gly	Val	Ser
65					70					75					80



Leu Glu Lys Arg Glu Ala Glu Ala Met Val Leu Gly Ile Gly Pro Val  
 85 90 95  
 Leu Gly Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp  
 100 105 110  
 Arg Gly Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu  
 115 120 125  
 Gly Ile Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala  
 130 135 140  
 Gly Leu Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile  
 145 150 155 160  
 Leu Gly Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro  
 165 170 175  
 Leu Glu Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg  
 180 185 190  
 Gln Ala Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu  
 195 200 205  
 Gly Tyr Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro  
 210 215 220  
 Tyr Leu Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile  
 225 230 235 240  
 Phe Leu Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala  
 245 250 255  
 Leu Gly Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser  
 260 265 270  
 Pro His Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly  
 275 280 285  
 Ala Leu Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr  
 290 295 300  
 Leu Arg Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met  
 305 310 315 320  
 Thr Phe Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln  
 325 330 335  
 Gly Val Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp  
 340 345 350  
 Glu Gly Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile  
 355 360 365  
 Ser Leu Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly  
 370 375 380  
 Thr Arg Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala  
 385 390 395 400  
 Gly Ala Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala  
 405 410 415  
 Ala Leu Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr  
 420 425 430  
 Leu Ala Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr  
 435 440 445  
 Arg Gly Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser  
 450 455 460  
 Phe Leu Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val  
 465 470 475 480  
 Gly Ala Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly  
 485 490 495  
 Ala Ser Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr  
 500 505 510  
 Glu Ala Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile  
 515 520 525  
 Leu Asp Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met  
 530 535 540

[illegible]